



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 19, 2025 – 05:21 AM EDT

PDB ID : 3L2Y
Title : The structure of C-reactive protein bound to phosphoethanolamine
Authors : Mikolajek, H.; Kolstoe, S.E.; Wood, S.P.; Pepys, M.B.
Deposited on : 2009-12-15
Resolution : 2.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 1.21
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.004 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41.4

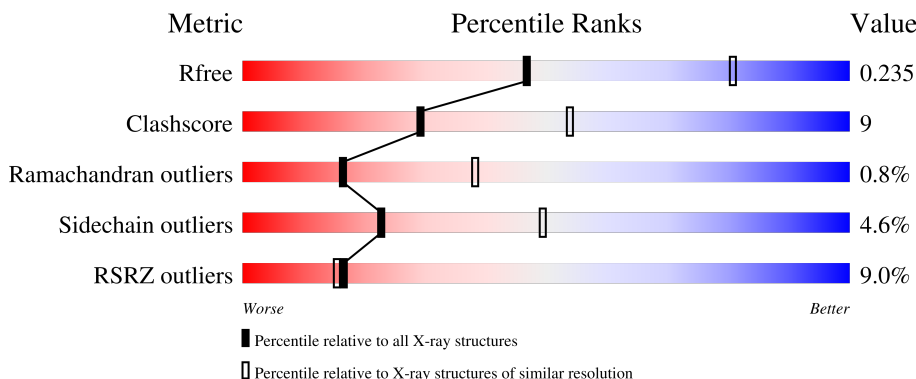
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	3333 (2.70-2.70)
Clashscore	180529	3684 (2.70-2.70)
Ramachandran outliers	177936	3633 (2.70-2.70)
Sidechain outliers	177891	3633 (2.70-2.70)
RSRZ outliers	164620	3333 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	206	 7% 80% 18% .
1	B	206	 8% 83% 16% .
1	C	206	 4% 82% 16% .
1	D	206	 6% 83% 16% .
1	E	206	 5% 80% 19% .

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Mol	Chain	Length	Quality of chain
1	F	206	
1	G	206	
1	H	206	
1	I	206	
1	J	206	
1	K	206	
1	L	206	
1	M	206	
1	N	206	
1	O	206	
1	P	206	
1	Q	206	
1	R	206	
1	S	206	
1	T	206	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 32993 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called C-reactive protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	B	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	C	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	D	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	E	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	F	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	G	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	H	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	I	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	J	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	K	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	L	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	M	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	N	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	O	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	P	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	206	Total 1632	C 1058	N 261	O 309	S 4	0	0	0
1	R	206	Total 1632	C 1058	N 261	O 309	S 4	0	0	0
1	S	206	Total 1632	C 1058	N 261	O 309	S 4	0	0	0
1	T	206	Total 1632	C 1058	N 261	O 309	S 4	0	0	0

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

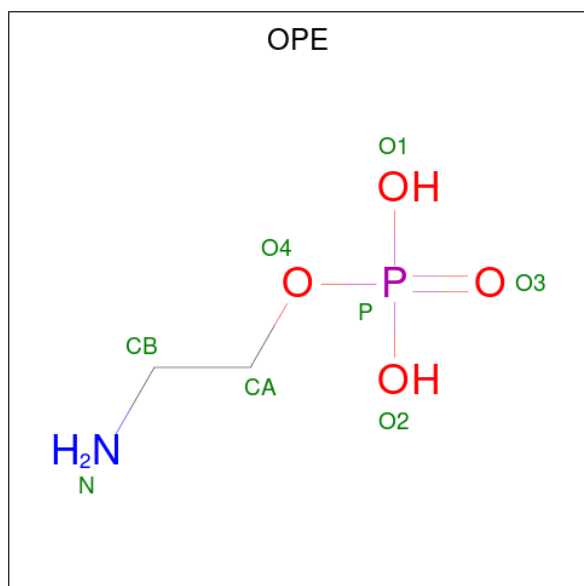
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total 2	Ca 2	0	0
2	B	2	Total 2	Ca 2	0	0
2	C	2	Total 2	Ca 2	0	0
2	D	2	Total 2	Ca 2	0	0
2	E	2	Total 2	Ca 2	0	0
2	F	2	Total 2	Ca 2	0	0
2	G	2	Total 2	Ca 2	0	0
2	H	2	Total 2	Ca 2	0	0
2	I	2	Total 2	Ca 2	0	0
2	J	2	Total 2	Ca 2	0	0
2	K	2	Total 2	Ca 2	0	0
2	L	2	Total 2	Ca 2	0	0
2	M	2	Total 2	Ca 2	0	0
2	N	2	Total 2	Ca 2	0	0
2	O	2	Total 2	Ca 2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	P	2	Total	Ca	0	0
			2	2		
2	Q	2	Total	Ca	0	0
			2	2		
2	R	2	Total	Ca	0	0
			2	2		
2	S	2	Total	Ca	0	0
			2	2		
2	T	2	Total	Ca	0	0
			2	2		

- Molecule 3 is PHOSPHORIC ACID MONO-(2-AMINO-ETHYL) ESTER (three-letter code: OPE) (formula: $C_2H_8NO_4P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			8	2	1	4	1		
3	B	1	Total	C	N	O	P	0	0
			8	2	1	4	1		
3	C	1	Total	C	N	O	P	0	0
			8	2	1	4	1		
3	D	1	Total	C	N	O	P	0	0
			8	2	1	4	1		
3	E	1	Total	C	N	O	P	0	0
			8	2	1	4	1		
3	F	1	Total	C	N	O	P	0	0
			8	2	1	4	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	G	1	Total	C	N	O	P	0	0
			8	2	1	4	1		
3	H	1	Total	C	N	O	P	0	0
			8	2	1	4	1		
3	I	1	Total	C	N	O	P	0	0
			8	2	1	4	1		
3	J	1	Total	C	N	O	P	0	0
			8	2	1	4	1		
3	K	1	Total	C	N	O	P	0	0
			8	2	1	4	1		
3	L	1	Total	C	N	O	P	0	0
			8	2	1	4	1		
3	M	1	Total	C	N	O	P	0	0
			8	2	1	4	1		
3	N	1	Total	C	N	O	P	0	0
			8	2	1	4	1		
3	O	1	Total	C	N	O	P	0	0
			8	2	1	4	1		
3	P	1	Total	C	N	O	P	0	0
			8	2	1	4	1		
3	Q	1	Total	C	N	O	P	0	0
			8	2	1	4	1		
3	R	1	Total	C	N	O	P	0	0
			8	2	1	4	1		
3	S	1	Total	C	N	O	P	0	0
			8	2	1	4	1		
3	T	1	Total	C	N	O	P	0	0
			8	2	1	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	11	Total	O	0	0
			11	11		
4	B	13	Total	O	0	0
			13	13		
4	C	12	Total	O	0	0
			12	12		
4	D	8	Total	O	0	0
			8	8		
4	E	12	Total	O	0	0
			12	12		

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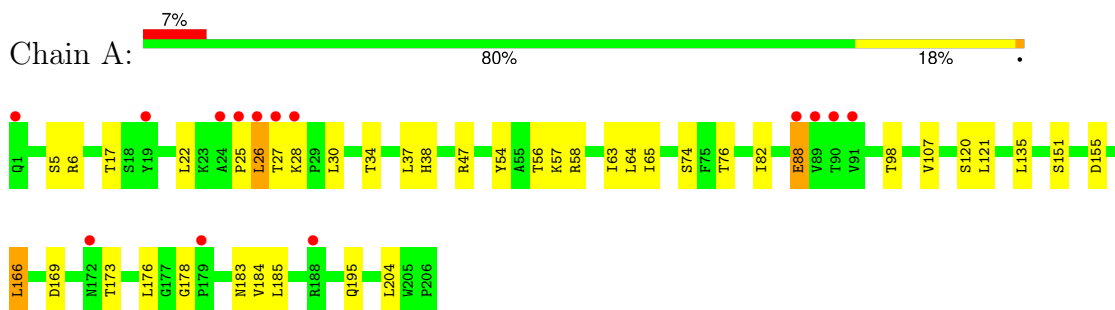
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	F	2	Total O 2 2	0	0
4	G	7	Total O 7 7	0	0
4	H	12	Total O 12 12	0	0
4	I	7	Total O 7 7	0	0
4	J	7	Total O 7 7	0	0
4	K	7	Total O 7 7	0	0
4	L	2	Total O 2 2	0	0
4	M	6	Total O 6 6	0	0
4	N	6	Total O 6 6	0	0
4	O	7	Total O 7 7	0	0
4	P	10	Total O 10 10	0	0
4	Q	2	Total O 2 2	0	0
4	R	3	Total O 3 3	0	0
4	S	4	Total O 4 4	0	0
4	T	15	Total O 15 15	0	0

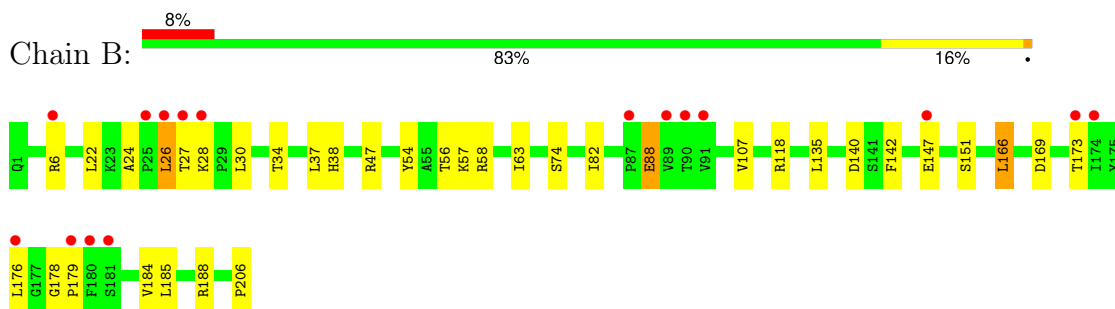
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

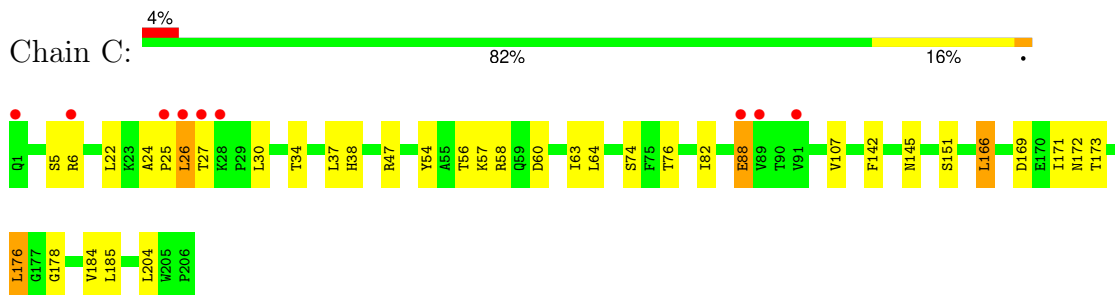
- Molecule 1: C-reactive protein



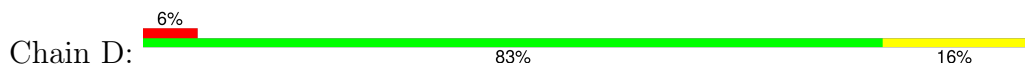
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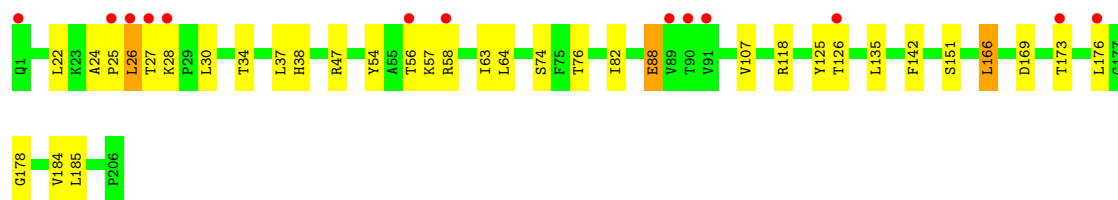


- Molecule 1: C-reactive protein

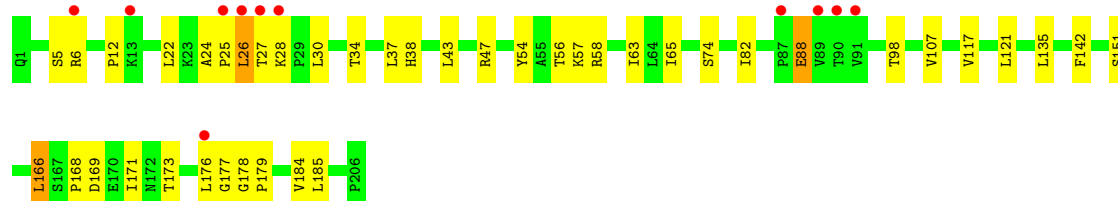
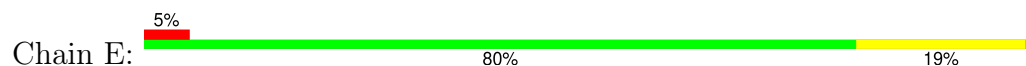


- Molecule 1: C-reactive protein

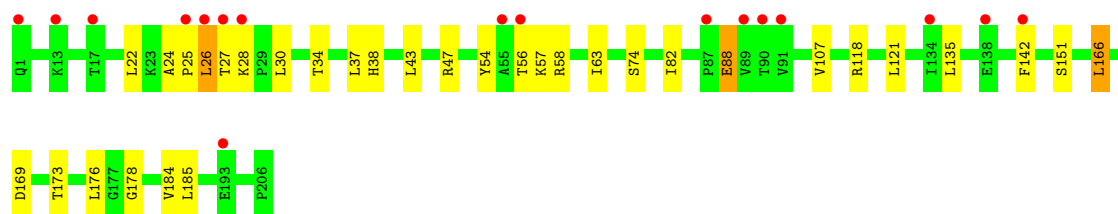
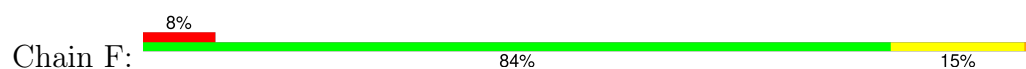




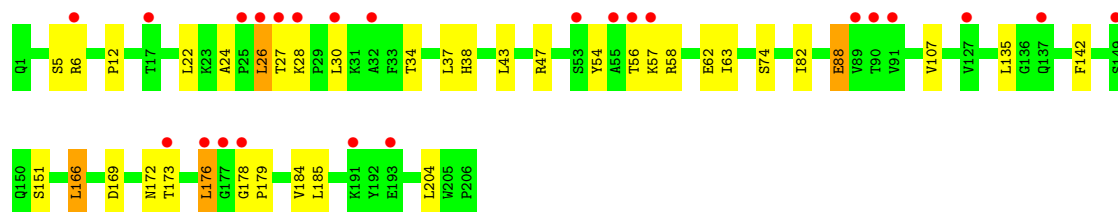
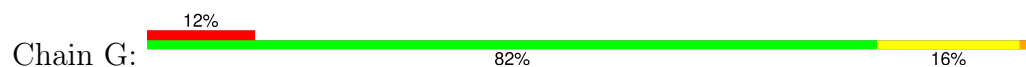
- Molecule 1: C-reactive protein



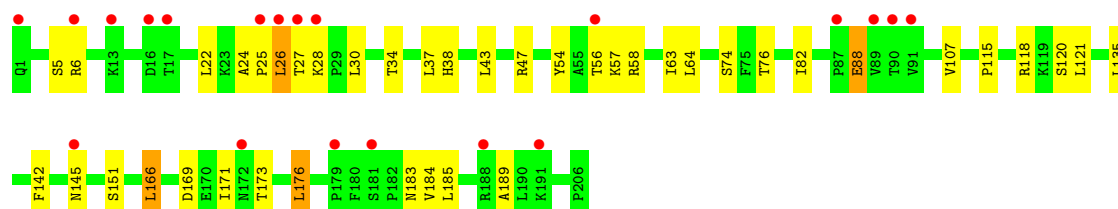
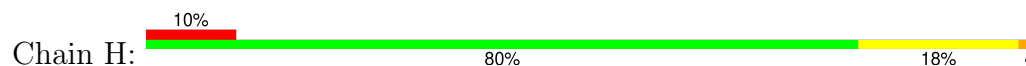
- Molecule 1: C-reactive protein



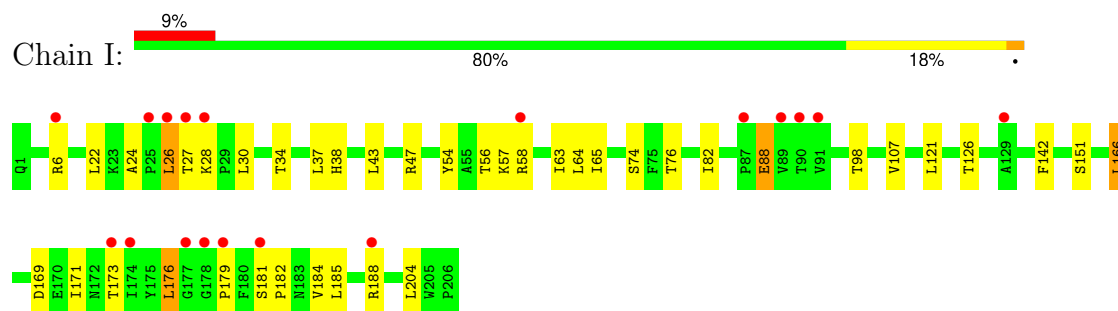
- Molecule 1: C-reactive protein



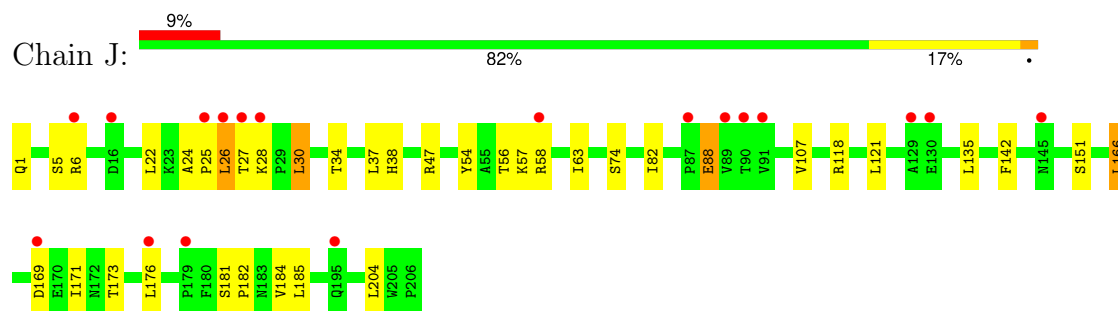
- Molecule 1: C-reactive protein



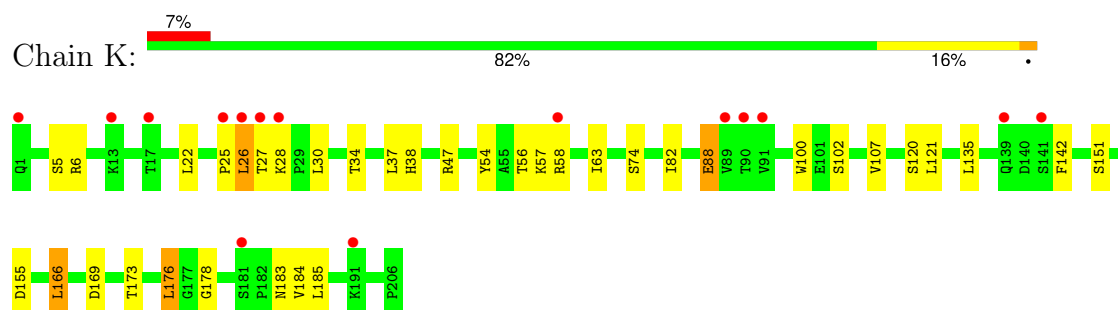
- Molecule 1: C-reactive protein



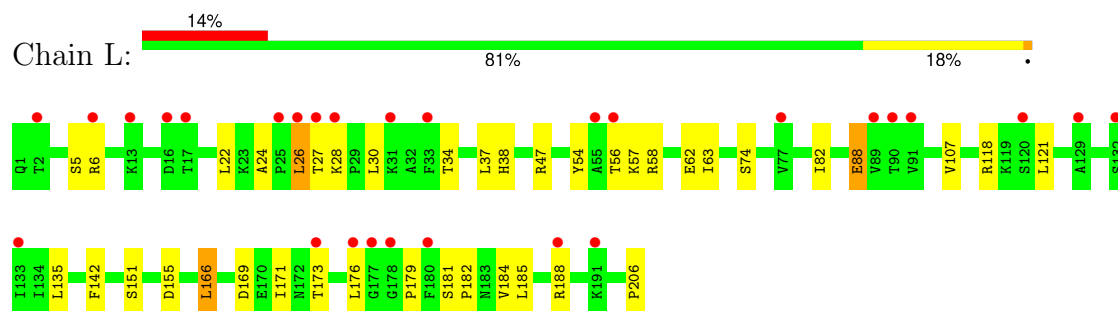
- Molecule 1: C-reactive protein



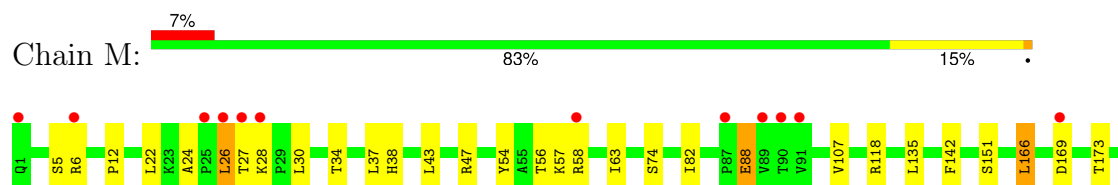
- Molecule 1: C-reactive protein



- Molecule 1: C-reactive protein

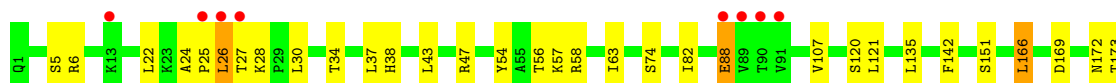
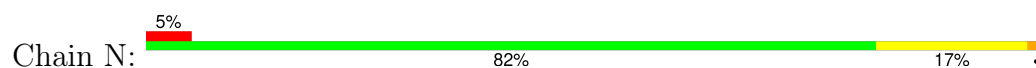


- Molecule 1: C-reactive protein

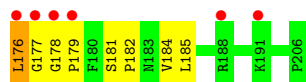
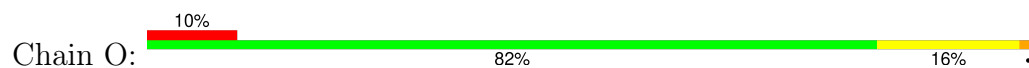




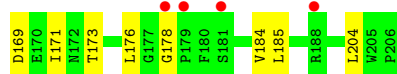
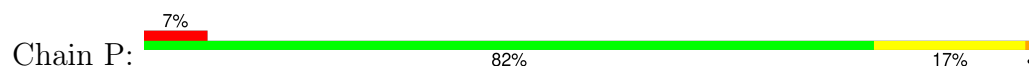
- Molecule 1: C-reactive protein



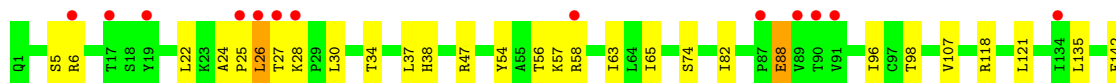
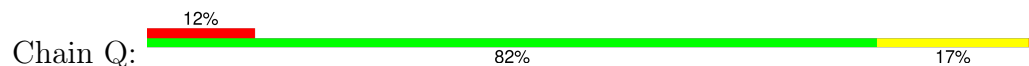
- Molecule 1: C-reactive protein



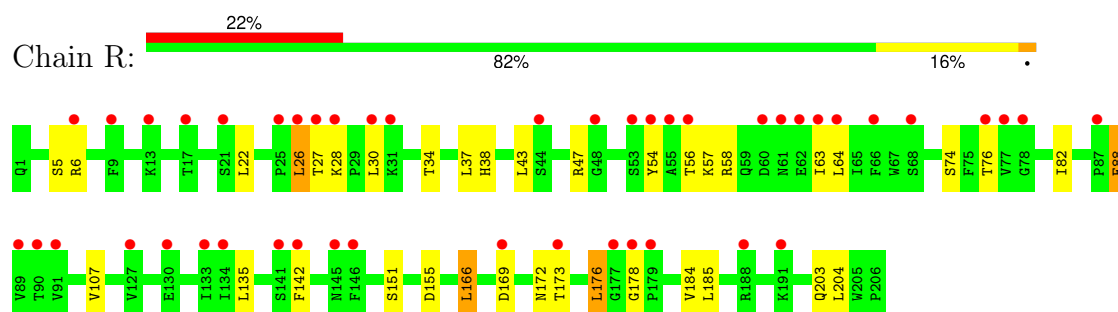
- Molecule 1: C-reactive protein



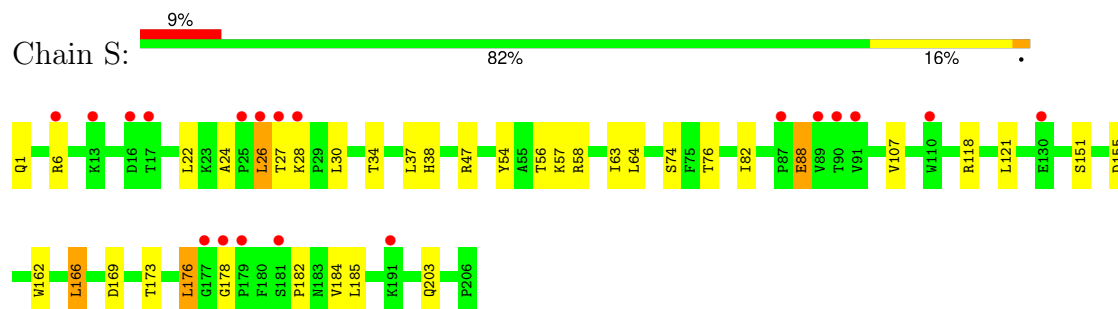
- Molecule 1: C-reactive protein



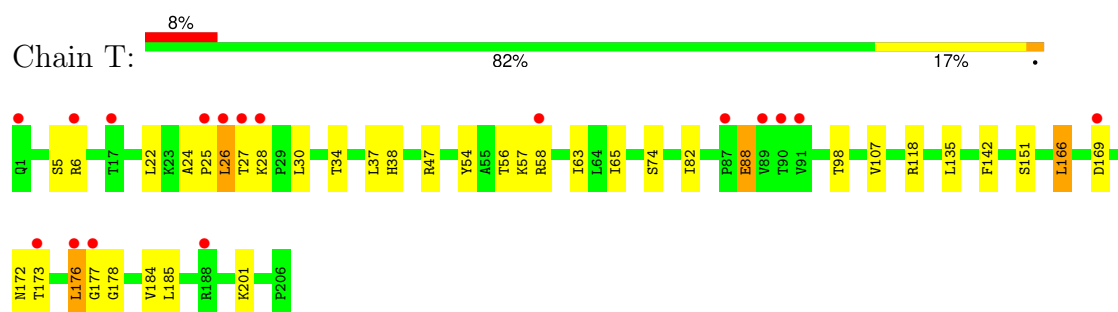
- Molecule 1: C-reactive protein



• Molecule 1: C-reactive protein



• Molecule 1: C-reactive protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	278.45Å 278.45Å 92.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	124.53 – 2.70 124.53 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.3 (124.53-2.70) 99.3 (124.53-2.70)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.85 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.6.4_486	Depositor
R, R_{free}	0.224 , 0.246 0.215 , 0.235	Depositor DCC
R_{free} test set	9717 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	60.3	Xtriage
Anisotropy	0.099	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 52.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.016 for h,-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	32993	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.88% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, OPE

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.44	0/1678	0.56	0/2279
1	B	0.46	0/1678	0.56	0/2279
1	C	0.43	0/1678	0.57	0/2279
1	D	0.42	0/1678	0.55	0/2279
1	E	0.44	0/1678	0.56	0/2279
1	F	0.46	0/1678	0.55	0/2279
1	G	0.45	0/1678	0.56	0/2279
1	H	0.42	0/1678	0.55	0/2279
1	I	0.44	0/1678	0.57	0/2279
1	J	0.44	0/1678	0.56	0/2279
1	K	0.43	0/1678	0.55	0/2279
1	L	0.46	0/1678	0.58	0/2279
1	M	0.41	0/1678	0.56	0/2279
1	N	0.43	0/1678	0.56	0/2279
1	O	0.43	0/1678	0.58	0/2279
1	P	0.45	0/1678	0.56	0/2279
1	Q	0.46	0/1678	0.56	0/2279
1	R	0.51	0/1678	0.58	0/2279
1	S	0.46	0/1678	0.57	0/2279
1	T	0.44	0/1678	0.57	0/2279
All	All	0.44	0/33560	0.56	0/45580

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1632	0	1593	32	0
1	B	1632	0	1593	31	2
1	C	1632	0	1593	30	0
1	D	1632	0	1593	26	0
1	E	1632	0	1593	31	2
1	F	1632	0	1593	25	0
1	G	1632	0	1593	26	0
1	H	1632	0	1593	37	0
1	I	1632	0	1593	59	0
1	J	1632	0	1593	28	0
1	K	1632	0	1593	29	0
1	L	1632	0	1593	35	0
1	M	1632	0	1593	24	0
1	N	1632	0	1593	25	0
1	O	1632	0	1593	30	0
1	P	1632	0	1593	28	0
1	Q	1632	0	1593	51	0
1	R	1632	0	1593	26	0
1	S	1632	0	1593	29	0
1	T	1632	0	1593	28	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	F	2	0	0	0	0
2	G	2	0	0	0	0
2	H	2	0	0	0	0
2	I	2	0	0	0	0
2	J	2	0	0	0	0
2	K	2	0	0	0	0
2	L	2	0	0	0	0
2	M	2	0	0	0	0
2	N	2	0	0	0	0
2	O	2	0	0	0	0
2	P	2	0	0	0	0
2	Q	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	R	2	0	0	0	0
2	S	2	0	0	0	0
2	T	2	0	0	0	0
3	A	8	0	6	0	0
3	B	8	0	6	0	0
3	C	8	0	6	0	0
3	D	8	0	6	0	0
3	E	8	0	6	0	0
3	F	8	0	6	0	0
3	G	8	0	6	0	0
3	H	8	0	6	0	0
3	I	8	0	6	0	0
3	J	8	0	6	0	0
3	K	8	0	6	0	0
3	L	8	0	6	0	0
3	M	8	0	6	0	0
3	N	8	0	6	0	0
3	O	8	0	6	0	0
3	P	8	0	6	0	0
3	Q	8	0	6	0	0
3	R	8	0	6	0	0
3	S	8	0	6	0	0
3	T	8	0	6	0	0
4	A	11	0	0	2	0
4	B	13	0	0	0	0
4	C	12	0	0	0	0
4	D	8	0	0	2	0
4	E	12	0	0	1	0
4	F	2	0	0	1	0
4	G	7	0	0	0	0
4	H	12	0	0	4	0
4	I	7	0	0	0	0
4	J	7	0	0	0	0
4	K	7	0	0	0	0
4	L	2	0	0	0	0
4	M	6	0	0	0	0
4	N	6	0	0	0	0
4	O	7	0	0	1	0
4	P	10	0	0	0	0
4	Q	2	0	0	0	0
4	R	3	0	0	0	0
4	S	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	T	15	0	0	0	0
All	All	32993	0	31980	552	2

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (552) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:188:ARG:NH2	1:Q:6:ARG:NH1	1.88	1.21
1:S:56:THR:HG22	1:S:58:ARG:H	1.14	1.08
1:H:56:THR:HG22	1:H:58:ARG:H	1.18	1.07
1:P:56:THR:HG22	1:P:58:ARG:H	1.18	1.07
1:L:56:THR:HG22	1:L:58:ARG:H	1.16	1.07
1:B:56:THR:HG22	1:B:58:ARG:H	1.16	1.05
1:C:56:THR:HG22	1:C:58:ARG:H	1.19	1.05
1:I:188:ARG:HH21	1:Q:6:ARG:NH1	1.48	1.05
1:Q:56:THR:HG22	1:Q:58:ARG:H	1.21	1.05
1:N:56:THR:HG22	1:N:58:ARG:H	1.16	1.05
1:I:6:ARG:HH12	1:Q:188:ARG:NH2	1.54	1.04
1:J:56:THR:HG22	1:J:58:ARG:H	1.17	1.04
1:I:188:ARG:NH2	1:Q:6:ARG:HH12	1.51	1.04
1:O:56:THR:HG22	1:O:58:ARG:H	1.24	1.02
1:E:56:THR:HG22	1:E:58:ARG:H	1.16	1.02
1:I:56:THR:HG22	1:I:58:ARG:H	1.21	1.02
1:D:56:THR:HG22	1:D:58:ARG:H	1.20	1.02
1:A:56:THR:HG22	1:A:58:ARG:H	1.23	1.01
1:G:56:THR:HG22	1:G:58:ARG:H	1.24	1.01
1:M:56:THR:HG22	1:M:58:ARG:H	1.24	1.01
1:R:56:THR:HG22	1:R:58:ARG:H	1.22	1.01
1:I:188:ARG:HH21	1:Q:6:ARG:HH11	1.06	1.01
1:T:56:THR:HG22	1:T:58:ARG:H	1.23	1.00
1:K:56:THR:HG22	1:K:58:ARG:H	1.23	1.00
1:F:56:THR:HG22	1:F:58:ARG:H	1.22	0.98
1:I:6:ARG:NH1	1:Q:188:ARG:HH21	1.60	0.98
1:H:173:THR:HG22	1:P:173:THR:HG22	1.46	0.97
1:I:188:ARG:CZ	1:Q:6:ARG:NH1	2.29	0.95
1:C:169:ASP:OD1	1:L:188:ARG:NH2	2.04	0.91
1:I:6:ARG:HH12	1:Q:188:ARG:HH21	0.93	0.90
1:H:27:THR:HG22	4:H:212:HOH:O	1.71	0.90
1:I:179:PRO:CB	1:Q:206:PRO:HB3	2.05	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:188:ARG:CZ	1:Q:6:ARG:HH12	1.89	0.81
1:B:188:ARG:NH2	1:M:169:ASP:OD1	2.15	0.80
1:F:82:ILE:HD11	1:F:107:VAL:HG21	1.65	0.78
1:S:56:THR:HG22	1:S:58:ARG:N	1.97	0.78
1:N:56:THR:HG22	1:N:58:ARG:N	1.97	0.78
1:I:179:PRO:CG	1:Q:206:PRO:CB	2.62	0.78
1:O:26:LEU:HD21	1:O:30:LEU:HD11	1.66	0.78
1:L:26:LEU:HD21	1:L:30:LEU:HD11	1.64	0.78
1:H:26:LEU:HD21	1:H:30:LEU:HD11	1.65	0.77
1:E:56:THR:HG22	1:E:58:ARG:N	1.96	0.77
1:I:26:LEU:HD21	1:I:30:LEU:HD11	1.65	0.77
1:G:26:LEU:HD21	1:G:30:LEU:HD11	1.67	0.77
1:A:26:LEU:HD21	1:A:30:LEU:HD11	1.67	0.77
1:R:26:LEU:HD21	1:R:30:LEU:HD11	1.67	0.77
1:K:26:LEU:HD21	1:K:30:LEU:HD11	1.65	0.77
1:G:82:ILE:HD11	1:G:107:VAL:HG21	1.65	0.77
1:C:26:LEU:HD21	1:C:30:LEU:HD11	1.65	0.76
1:B:56:THR:HG22	1:B:58:ARG:N	1.98	0.76
1:J:56:THR:HG22	1:J:58:ARG:N	1.98	0.76
1:J:82:ILE:HD11	1:J:107:VAL:HG21	1.67	0.76
1:I:82:ILE:HD11	1:I:107:VAL:HG21	1.67	0.76
1:I:179:PRO:CG	1:Q:206:PRO:HB3	2.16	0.76
1:S:26:LEU:HD21	1:S:30:LEU:HD11	1.68	0.75
1:S:82:ILE:HD11	1:S:107:VAL:HG21	1.68	0.75
1:C:56:THR:HG22	1:C:58:ARG:N	2.00	0.75
1:Q:56:THR:HG22	1:Q:58:ARG:N	2.01	0.75
1:P:82:ILE:HD11	1:P:107:VAL:HG21	1.69	0.75
1:J:26:LEU:HD21	1:J:30:LEU:HD11	1.68	0.75
1:D:26:LEU:HD21	1:D:30:LEU:HD11	1.69	0.75
1:D:82:ILE:HD11	1:D:107:VAL:HG21	1.69	0.74
1:H:173:THR:CG2	1:P:173:THR:HG22	2.16	0.74
1:M:82:ILE:HD11	1:M:107:VAL:HG21	1.69	0.74
1:N:82:ILE:HD11	1:N:107:VAL:HG21	1.69	0.74
1:M:26:LEU:HD21	1:M:30:LEU:HD11	1.66	0.74
1:H:6:ARG:NH1	4:H:210:HOH:O	2.15	0.74
1:Q:26:LEU:HD21	1:Q:30:LEU:HD11	1.69	0.74
1:F:26:LEU:HD21	1:F:30:LEU:HD11	1.69	0.74
1:N:26:LEU:HD21	1:N:30:LEU:HD11	1.70	0.74
1:R:56:THR:HG22	1:R:58:ARG:N	2.01	0.74
1:R:82:ILE:HD11	1:R:107:VAL:HG21	1.70	0.74
1:A:82:ILE:HD11	1:A:107:VAL:HG21	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:179:PRO:HG2	1:Q:206:PRO:CB	2.17	0.73
1:H:56:THR:HG22	1:H:58:ARG:N	2.00	0.73
1:I:188:ARG:NE	1:Q:6:ARG:NH1	2.35	0.73
1:D:56:THR:HG22	1:D:58:ARG:N	2.00	0.73
1:D:126:THR:H	1:H:145:ASN:HD21	1.35	0.73
1:F:56:THR:HG22	1:F:58:ARG:N	2.01	0.73
1:O:82:ILE:HD11	1:O:107:VAL:HG21	1.71	0.73
1:T:82:ILE:HD11	1:T:107:VAL:HG21	1.70	0.73
1:C:145:ASN:HD21	1:I:126:THR:H	1.37	0.73
1:A:56:THR:HG22	1:A:58:ARG:N	2.02	0.73
1:L:82:ILE:HD11	1:L:107:VAL:HG21	1.69	0.73
1:P:56:THR:HG22	1:P:58:ARG:N	2.00	0.73
1:Q:82:ILE:HD11	1:Q:107:VAL:HG21	1.71	0.73
1:P:26:LEU:HD21	1:P:30:LEU:HD11	1.71	0.72
1:C:82:ILE:HD11	1:C:107:VAL:HG21	1.72	0.72
1:K:82:ILE:HD11	1:K:107:VAL:HG21	1.72	0.72
1:T:26:LEU:HD21	1:T:30:LEU:HD11	1.71	0.72
1:A:25:PRO:HD2	1:O:179:PRO:HG2	1.70	0.72
1:A:88:GLU:O	1:A:88:GLU:HG3	1.90	0.72
1:L:56:THR:HG22	1:L:58:ARG:N	1.98	0.71
1:H:82:ILE:HD11	1:H:107:VAL:HG21	1.71	0.71
1:O:56:THR:HG22	1:O:58:ARG:N	2.02	0.71
1:E:82:ILE:HD11	1:E:107:VAL:HG21	1.72	0.71
1:G:56:THR:HG22	1:G:58:ARG:N	2.04	0.71
1:D:88:GLU:HG3	1:D:88:GLU:O	1.91	0.71
1:T:56:THR:HG22	1:T:58:ARG:N	2.04	0.71
1:E:26:LEU:HD21	1:E:30:LEU:HD11	1.71	0.70
1:R:88:GLU:O	1:R:88:GLU:HG3	1.89	0.70
1:I:6:ARG:NH1	1:Q:188:ARG:HE	1.90	0.70
1:K:56:THR:HG22	1:K:58:ARG:N	2.03	0.70
1:B:34:THR:HG21	1:B:166:LEU:HD22	1.74	0.70
1:B:26:LEU:HD21	1:B:30:LEU:HD11	1.73	0.70
1:I:56:THR:HG22	1:I:58:ARG:N	2.02	0.70
1:R:34:THR:HG21	1:R:166:LEU:HD22	1.74	0.70
1:F:88:GLU:O	1:F:88:GLU:HG3	1.91	0.69
1:J:88:GLU:O	1:J:88:GLU:HG3	1.92	0.69
1:M:88:GLU:O	1:M:88:GLU:HG3	1.93	0.69
1:E:88:GLU:O	1:E:88:GLU:HG3	1.92	0.69
1:H:88:GLU:O	1:H:88:GLU:HG3	1.91	0.69
1:E:179:PRO:HG2	1:K:25:PRO:HD2	1.75	0.68
1:J:34:THR:HG21	1:J:166:LEU:HD22	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:88:GLU:HG3	1:B:88:GLU:O	1.92	0.68
1:Q:88:GLU:HG3	1:Q:88:GLU:O	1.91	0.68
1:P:34:THR:HG21	1:P:166:LEU:HD22	1.76	0.67
1:T:88:GLU:O	1:T:88:GLU:HG3	1.93	0.67
1:I:179:PRO:HG2	1:Q:206:PRO:HB3	1.75	0.67
1:B:82:ILE:HD11	1:B:107:VAL:HG21	1.75	0.67
1:I:88:GLU:HG3	1:I:88:GLU:O	1.94	0.67
1:P:88:GLU:O	1:P:88:GLU:HG3	1.93	0.66
1:R:169:ASP:O	1:R:173:THR:HG23	1.95	0.66
1:G:88:GLU:HG3	1:G:88:GLU:O	1.96	0.66
1:S:88:GLU:HG3	1:S:88:GLU:O	1.93	0.66
1:K:88:GLU:O	1:K:88:GLU:HG3	1.93	0.66
1:L:88:GLU:HG3	1:L:88:GLU:O	1.94	0.66
1:N:88:GLU:HG3	1:N:88:GLU:O	1.94	0.66
1:O:88:GLU:O	1:O:88:GLU:HG3	1.94	0.66
1:A:173:THR:HG22	1:K:173:THR:HG22	1.78	0.65
1:B:206:PRO:HB3	1:L:179:PRO:CG	2.26	0.65
1:E:168:PRO:HD3	4:E:207:HOH:O	1.96	0.65
1:I:179:PRO:CG	1:Q:206:PRO:HB2	2.27	0.65
1:C:88:GLU:O	1:C:88:GLU:HG3	1.94	0.65
1:F:184:VAL:HG12	1:F:185:LEU:HD13	1.78	0.64
1:H:34:THR:HG21	1:H:166:LEU:HD22	1.79	0.64
1:M:56:THR:HG22	1:M:58:ARG:N	2.04	0.64
1:I:34:THR:HG21	1:I:166:LEU:HD22	1.80	0.64
1:A:184:VAL:HA	1:O:179:PRO:HG3	1.79	0.64
1:F:34:THR:HG21	1:F:166:LEU:HD22	1.80	0.64
1:E:34:THR:HG21	1:E:166:LEU:HD22	1.80	0.63
1:H:189:ALA:HB2	1:T:176:LEU:HG	1.81	0.63
1:B:206:PRO:HB3	1:L:179:PRO:HG3	1.80	0.63
1:C:34:THR:HG21	1:C:166:LEU:HD22	1.81	0.63
1:M:34:THR:HG21	1:M:166:LEU:HD22	1.80	0.63
1:O:34:THR:HG21	1:O:166:LEU:HD22	1.81	0.62
1:C:145:ASN:ND2	1:I:126:THR:H	1.96	0.62
1:D:184:VAL:HG12	1:D:185:LEU:HD13	1.80	0.62
1:O:184:VAL:HG12	1:O:185:LEU:HD13	1.82	0.62
1:I:179:PRO:HB2	1:Q:206:PRO:HB3	1.81	0.61
1:P:169:ASP:O	1:P:173:THR:HG23	1.99	0.61
1:Q:34:THR:HG21	1:Q:166:LEU:HD22	1.82	0.61
1:L:34:THR:HG21	1:L:166:LEU:HD22	1.81	0.61
1:I:179:PRO:HG2	1:Q:206:PRO:HB2	1.80	0.61
1:R:155:ASP:OD2	1:S:118:ARG:NH1	2.32	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:26:LEU:HD12	1:L:27:THR:H	1.66	0.61
1:S:34:THR:HG21	1:S:166:LEU:HD22	1.83	0.61
1:N:184:VAL:HG12	1:N:185:LEU:HD13	1.82	0.61
1:D:126:THR:H	1:H:145:ASN:ND2	1.98	0.60
1:A:26:LEU:HD12	1:A:27:THR:H	1.66	0.60
1:Q:184:VAL:HG12	1:Q:185:LEU:HD13	1.82	0.60
1:K:34:THR:HG21	1:K:166:LEU:HD22	1.82	0.60
1:G:184:VAL:HG12	1:G:185:LEU:HD13	1.83	0.60
1:I:179:PRO:CB	1:Q:206:PRO:CB	2.78	0.60
1:K:26:LEU:HD12	1:K:27:THR:H	1.66	0.60
1:C:26:LEU:HD12	1:C:27:THR:H	1.65	0.60
1:J:184:VAL:HG12	1:J:185:LEU:HD13	1.84	0.60
1:B:184:VAL:HG12	1:B:185:LEU:HD13	1.84	0.59
1:B:26:LEU:HD12	1:B:27:THR:H	1.67	0.59
1:N:34:THR:HG21	1:N:166:LEU:HD22	1.84	0.59
1:E:184:VAL:HG12	1:E:185:LEU:HD13	1.84	0.59
1:I:6:ARG:HH12	1:Q:188:ARG:CZ	2.13	0.59
1:G:34:THR:HG21	1:G:166:LEU:HD22	1.83	0.59
1:H:27:THR:CG2	4:H:212:HOH:O	2.41	0.59
1:N:169:ASP:O	1:N:173:THR:HG23	2.03	0.58
1:F:25:PRO:HG3	4:F:207:HOH:O	2.03	0.58
1:T:34:THR:HG21	1:T:166:LEU:HD22	1.84	0.58
1:D:34:THR:HG21	1:D:166:LEU:HD22	1.85	0.58
1:P:26:LEU:HD12	1:P:27:THR:H	1.68	0.58
1:A:169:ASP:O	1:A:173:THR:HG23	2.03	0.58
1:B:6:ARG:NH1	1:L:188:ARG:HE	2.02	0.58
1:F:47:ARG:NH2	1:F:151:SER:O	2.37	0.58
1:I:26:LEU:HD12	1:I:27:THR:H	1.68	0.58
1:S:184:VAL:HG12	1:S:185:LEU:HD13	1.85	0.58
1:D:26:LEU:HD12	1:D:27:THR:H	1.69	0.57
1:I:188:ARG:NH2	1:R:169:ASP:OD1	2.36	0.57
1:J:47:ARG:NH2	1:J:151:SER:O	2.37	0.57
1:F:169:ASP:O	1:F:173:THR:HG23	2.04	0.57
1:M:184:VAL:HG12	1:M:185:LEU:HD13	1.86	0.57
1:J:26:LEU:HD12	1:J:27:THR:H	1.69	0.57
1:O:26:LEU:HD12	1:O:27:THR:H	1.70	0.57
1:K:169:ASP:O	1:K:173:THR:HG23	2.04	0.57
1:F:26:LEU:HD12	1:F:27:THR:H	1.70	0.57
1:L:184:VAL:HG12	1:L:185:LEU:HD13	1.87	0.57
1:M:26:LEU:HD12	1:M:27:THR:H	1.69	0.57
1:N:47:ARG:NH2	1:N:151:SER:O	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:188:ARG:HE	1:Q:6:ARG:NH1	2.02	0.57
1:R:26:LEU:HD12	1:R:27:THR:H	1.70	0.57
1:B:179:PRO:HG3	1:L:206:PRO:HB3	1.87	0.56
1:Q:47:ARG:NH2	1:Q:151:SER:O	2.37	0.56
1:A:34:THR:HG21	1:A:166:LEU:HD22	1.87	0.56
1:S:169:ASP:O	1:S:173:THR:HG23	2.05	0.56
1:T:184:VAL:HG12	1:T:185:LEU:HD13	1.87	0.56
1:H:183:ASN:HA	1:T:177:GLY:O	2.04	0.56
1:C:184:VAL:HG12	1:C:185:LEU:HD13	1.87	0.56
1:R:184:VAL:HG12	1:R:185:LEU:HD13	1.86	0.56
1:N:26:LEU:HD12	1:N:27:THR:H	1.70	0.56
1:C:169:ASP:O	1:C:173:THR:HG23	2.05	0.56
1:O:47:ARG:NH2	1:O:151:SER:O	2.39	0.56
1:I:184:VAL:HG12	1:I:185:LEU:HD13	1.87	0.56
1:H:26:LEU:HD12	1:H:27:THR:H	1.72	0.55
1:S:26:LEU:HD12	1:S:27:THR:H	1.71	0.55
1:P:184:VAL:HG12	1:P:185:LEU:HD13	1.87	0.55
1:E:179:PRO:HG3	1:K:184:VAL:HA	1.88	0.55
1:G:47:ARG:NH2	1:G:151:SER:O	2.40	0.55
1:L:169:ASP:O	1:L:173:THR:HG23	2.06	0.55
1:B:47:ARG:NH2	1:B:151:SER:O	2.40	0.55
1:E:26:LEU:HD12	1:E:27:THR:H	1.73	0.54
1:K:184:VAL:HG12	1:K:185:LEU:HD13	1.90	0.54
1:R:88:GLU:O	1:R:88:GLU:CG	2.55	0.54
1:H:169:ASP:O	1:H:173:THR:HG23	2.08	0.54
1:D:169:ASP:O	1:D:173:THR:HG23	2.08	0.54
1:H:88:GLU:O	1:H:88:GLU:CG	2.56	0.54
1:M:169:ASP:O	1:M:173:THR:HG23	2.07	0.54
1:T:169:ASP:O	1:T:173:THR:HG23	2.08	0.53
1:E:177:GLY:O	1:K:183:ASN:HA	2.09	0.53
1:G:26:LEU:HD12	1:G:27:THR:H	1.73	0.53
1:O:169:ASP:O	1:O:173:THR:HG23	2.08	0.53
1:I:6:ARG:NH1	1:Q:188:ARG:NE	2.56	0.53
1:Q:26:LEU:HD12	1:Q:27:THR:H	1.74	0.53
1:A:184:VAL:HG12	1:A:185:LEU:HD13	1.90	0.53
1:O:27:THR:HG23	1:O:28:LYS:H	1.73	0.53
1:T:27:THR:HG23	1:T:28:LYS:H	1.74	0.53
1:J:169:ASP:O	1:J:173:THR:HG23	2.09	0.53
1:T:26:LEU:HD12	1:T:27:THR:H	1.73	0.53
1:Q:37:LEU:C	1:Q:37:LEU:HD12	2.30	0.52
1:S:37:LEU:HD12	1:S:37:LEU:C	2.29	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:47:ARG:NH2	1:S:151:SER:O	2.42	0.52
1:S:88:GLU:O	1:S:88:GLU:CG	2.58	0.52
1:B:88:GLU:O	1:B:88:GLU:CG	2.58	0.52
1:I:47:ARG:NH2	1:I:151:SER:O	2.41	0.52
1:K:88:GLU:O	1:K:88:GLU:CG	2.57	0.52
1:M:47:ARG:NH2	1:M:151:SER:O	2.42	0.52
1:F:88:GLU:O	1:F:88:GLU:CG	2.57	0.52
1:P:204:LEU:HD11	1:Q:118:ARG:HG3	1.92	0.52
1:T:37:LEU:C	1:T:37:LEU:HD12	2.29	0.52
1:A:17:THR:HG22	4:A:213:HOH:O	2.09	0.52
1:D:88:GLU:O	1:D:88:GLU:CG	2.57	0.52
1:D:27:THR:HG23	1:D:28:LYS:H	1.74	0.52
1:I:88:GLU:O	1:I:88:GLU:CG	2.58	0.52
1:D:47:ARG:NH2	1:D:151:SER:O	2.43	0.52
1:E:47:ARG:NH2	1:E:151:SER:O	2.43	0.52
1:P:27:THR:HG23	1:P:28:LYS:H	1.75	0.52
1:B:169:ASP:O	1:B:173:THR:HG23	2.10	0.51
1:E:169:ASP:O	1:E:173:THR:HG23	2.08	0.51
1:F:37:LEU:C	1:F:37:LEU:HD12	2.30	0.51
1:K:27:THR:HG23	1:K:28:LYS:H	1.76	0.51
1:E:88:GLU:O	1:E:88:GLU:CG	2.57	0.51
1:P:47:ARG:NH2	1:P:151:SER:O	2.44	0.51
1:Q:88:GLU:O	1:Q:88:GLU:CG	2.57	0.51
1:I:37:LEU:HD12	1:I:37:LEU:C	2.31	0.51
1:T:88:GLU:O	1:T:88:GLU:CG	2.58	0.51
1:O:88:GLU:O	1:O:88:GLU:CG	2.59	0.51
1:P:88:GLU:O	1:P:88:GLU:CG	2.58	0.51
1:G:12:PRO:HB2	1:H:120:SER:HB2	1.91	0.51
1:E:27:THR:HG23	1:E:28:LYS:H	1.75	0.50
1:F:184:VAL:HG12	1:F:185:LEU:CD1	2.41	0.50
1:A:88:GLU:O	1:A:88:GLU:CG	2.56	0.50
1:A:183:ASN:HA	1:O:177:GLY:O	2.11	0.50
1:R:27:THR:HG23	1:R:28:LYS:H	1.76	0.50
1:T:47:ARG:NH2	1:T:151:SER:O	2.45	0.50
1:A:37:LEU:C	1:A:37:LEU:HD12	2.32	0.50
1:A:27:THR:HG23	1:A:28:LYS:H	1.76	0.50
1:G:27:THR:HG23	1:G:28:LYS:H	1.77	0.50
1:G:169:ASP:O	1:G:173:THR:HG23	2.11	0.50
1:H:115:PRO:HD2	4:H:207:HOH:O	2.11	0.49
1:J:88:GLU:O	1:J:88:GLU:CG	2.57	0.49
1:L:37:LEU:C	1:L:37:LEU:HD12	2.32	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:27:THR:HG23	1:M:28:LYS:H	1.76	0.49
1:E:179:PRO:HD2	1:K:25:PRO:HG2	1.94	0.49
1:B:37:LEU:HD12	1:B:37:LEU:C	2.32	0.49
1:G:88:GLU:O	1:G:88:GLU:CG	2.60	0.49
1:C:54:TYR:HB3	1:C:63:ILE:HB	1.94	0.49
1:I:27:THR:HG23	1:I:28:LYS:H	1.77	0.49
1:D:37:LEU:HD12	1:D:37:LEU:C	2.33	0.49
1:K:47:ARG:NH2	1:K:151:SER:O	2.45	0.49
1:Q:169:ASP:O	1:Q:173:THR:HG23	2.11	0.49
1:Q:184:VAL:HG12	1:Q:185:LEU:CD1	2.43	0.49
4:D:208:HOH:O	1:E:117:VAL:CG2	2.60	0.49
1:F:27:THR:HG23	1:F:28:LYS:H	1.77	0.49
1:K:26:LEU:HD12	1:K:27:THR:N	2.27	0.49
1:M:88:GLU:O	1:M:88:GLU:CG	2.58	0.49
1:O:37:LEU:C	1:O:37:LEU:HD12	2.32	0.49
1:I:169:ASP:O	1:I:173:THR:HG23	2.13	0.49
1:N:88:GLU:O	1:N:88:GLU:CG	2.58	0.49
1:L:88:GLU:O	1:L:88:GLU:CG	2.58	0.48
1:Q:27:THR:HG23	1:Q:28:LYS:H	1.78	0.48
1:A:47:ARG:NH2	1:A:151:SER:O	2.46	0.48
1:E:37:LEU:C	1:E:37:LEU:HD12	2.33	0.48
1:R:37:LEU:C	1:R:37:LEU:HD12	2.34	0.48
1:R:47:ARG:NH2	1:R:151:SER:O	2.45	0.48
1:S:27:THR:HG23	1:S:28:LYS:H	1.77	0.48
1:G:184:VAL:HG12	1:G:185:LEU:CD1	2.44	0.48
1:K:37:LEU:HD12	1:K:37:LEU:C	2.34	0.48
1:E:56:THR:CG2	1:E:57:LYS:N	2.77	0.48
1:J:27:THR:HG23	1:J:28:LYS:H	1.79	0.48
1:L:47:ARG:NH2	1:L:151:SER:O	2.47	0.48
1:N:56:THR:CG2	1:N:57:LYS:N	2.76	0.48
1:C:60:ASP:CG	1:I:58:ARG:NH2	2.67	0.48
1:G:37:LEU:HD12	1:G:37:LEU:C	2.34	0.48
1:B:206:PRO:CB	1:L:179:PRO:HG3	2.44	0.47
1:H:184:VAL:HG12	1:H:185:LEU:HD13	1.94	0.47
1:J:56:THR:CG2	1:J:57:LYS:N	2.77	0.47
1:L:26:LEU:HD12	1:L:27:THR:N	2.29	0.47
1:P:37:LEU:HD12	1:P:37:LEU:C	2.34	0.47
1:H:37:LEU:C	1:H:37:LEU:HD12	2.34	0.47
1:S:56:THR:CG2	1:S:57:LYS:N	2.77	0.47
1:A:65:ILE:HD11	1:A:98:THR:HG21	1.96	0.47
1:B:6:ARG:HH12	1:L:188:ARG:HE	1.60	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:24:ALA:HB2	1:D:185:LEU:HD11	1.95	0.47
1:F:24:ALA:HA	1:F:25:PRO:HD3	1.74	0.47
1:N:184:VAL:HG12	1:N:185:LEU:CD1	2.45	0.47
1:P:5:SER:O	1:P:6:ARG:HB3	2.15	0.47
1:G:179:PRO:HG2	1:P:25:PRO:HD2	1.95	0.47
1:H:24:ALA:HA	1:H:25:PRO:HD3	1.71	0.47
1:O:54:TYR:HB3	1:O:63:ILE:HB	1.96	0.47
1:A:26:LEU:HD12	1:A:27:THR:N	2.29	0.47
1:C:47:ARG:NH2	1:C:151:SER:O	2.47	0.47
1:H:5:SER:O	1:H:6:ARG:HB3	2.15	0.47
1:H:27:THR:HG23	1:H:28:LYS:H	1.80	0.47
1:N:24:ALA:HA	1:N:25:PRO:HD3	1.73	0.47
1:O:56:THR:CG2	1:O:57:LYS:N	2.78	0.47
1:A:120:SER:HB2	1:E:12:PRO:HB2	1.96	0.47
1:C:26:LEU:HD12	1:C:27:THR:N	2.30	0.47
4:D:208:HOH:O	1:E:117:VAL:HG23	2.15	0.47
1:F:54:TYR:HB3	1:F:63:ILE:HB	1.97	0.47
1:R:184:VAL:HG12	1:R:185:LEU:CD1	2.44	0.46
1:D:56:THR:CG2	1:D:57:LYS:N	2.78	0.46
1:K:155:ASP:OD2	1:L:118:ARG:NH1	2.44	0.46
1:M:37:LEU:C	1:M:37:LEU:HD12	2.35	0.46
1:S:54:TYR:HB3	1:S:63:ILE:HB	1.97	0.46
1:S:155:ASP:OD2	1:T:118:ARG:NH1	2.46	0.46
1:B:184:VAL:HG12	1:B:185:LEU:CD1	2.46	0.46
1:E:54:TYR:HB3	1:E:63:ILE:HB	1.96	0.46
1:J:54:TYR:HB3	1:J:63:ILE:HB	1.96	0.46
1:L:184:VAL:HG12	1:L:185:LEU:CD1	2.45	0.46
1:I:204:LEU:HD11	1:J:118:ARG:HG3	1.97	0.46
1:J:37:LEU:C	1:J:37:LEU:HD12	2.35	0.46
1:P:56:THR:CG2	1:P:57:LYS:N	2.78	0.46
1:A:27:THR:HG23	1:A:28:LYS:N	2.31	0.46
1:B:179:PRO:CG	1:L:206:PRO:HB3	2.46	0.46
1:J:181:SER:HA	1:J:182:PRO:HD3	1.82	0.46
1:Q:24:ALA:HB2	1:Q:185:LEU:HD11	1.98	0.46
1:J:24:ALA:HA	1:J:25:PRO:HD3	1.71	0.46
1:P:27:THR:HG23	1:P:28:LYS:N	2.31	0.46
1:A:56:THR:CG2	1:A:57:LYS:N	2.79	0.46
1:B:56:THR:CG2	1:B:57:LYS:N	2.78	0.46
1:O:184:VAL:HG12	1:O:185:LEU:CD1	2.46	0.46
1:B:54:TYR:HB3	1:B:63:ILE:HB	1.97	0.45
1:R:64:LEU:HB3	1:R:76:THR:HB	1.96	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:54:TYR:HB3	1:T:63:ILE:HB	1.98	0.45
1:R:54:TYR:HB3	1:R:63:ILE:HB	1.98	0.45
1:C:37:LEU:C	1:C:37:LEU:HD12	2.36	0.45
1:H:47:ARG:NH2	1:H:151:SER:O	2.49	0.45
1:H:56:THR:CG2	1:H:57:LYS:N	2.78	0.45
1:Q:56:THR:CG2	1:Q:57:LYS:N	2.79	0.45
1:D:64:LEU:HB3	1:D:76:THR:HB	1.99	0.45
1:J:5:SER:O	1:J:6:ARG:HB3	2.17	0.45
1:M:184:VAL:HG12	1:M:185:LEU:CD1	2.46	0.45
1:K:56:THR:CG2	1:K:57:LYS:N	2.79	0.45
1:P:26:LEU:HD12	1:P:27:THR:N	2.30	0.45
1:S:82:ILE:HG23	1:S:121:LEU:HD13	1.99	0.45
1:C:60:ASP:OD1	1:I:58:ARG:NH2	2.50	0.45
1:A:155:ASP:OD2	1:B:118:ARG:NH1	2.44	0.45
1:E:184:VAL:HG12	1:E:185:LEU:CD1	2.47	0.45
1:P:106:ILE:HD12	1:T:201:LYS:HE3	1.99	0.45
1:N:54:TYR:HB3	1:N:63:ILE:HB	1.98	0.45
1:S:184:VAL:HG12	1:S:185:LEU:CD1	2.47	0.45
1:A:5:SER:O	1:A:6:ARG:HB3	2.18	0.44
1:B:26:LEU:HD12	1:B:27:THR:N	2.31	0.44
1:D:125:TYR:CD1	1:H:145:ASN:ND2	2.81	0.44
1:I:24:ALA:C	1:I:26:LEU:H	2.21	0.44
1:S:24:ALA:HB2	1:S:185:LEU:HD11	2.00	0.44
1:B:27:THR:HG23	1:B:28:LYS:H	1.82	0.44
1:J:26:LEU:HD12	1:J:27:THR:N	2.31	0.44
1:J:184:VAL:HG12	1:J:185:LEU:CD1	2.46	0.44
1:N:37:LEU:HD12	1:N:37:LEU:C	2.38	0.44
1:G:54:TYR:HB3	1:G:63:ILE:HB	1.99	0.44
1:K:54:TYR:HB3	1:K:63:ILE:HB	1.98	0.44
1:A:25:PRO:HG2	1:O:179:PRO:HD2	2.00	0.44
1:E:24:ALA:HA	1:E:25:PRO:HD3	1.72	0.44
1:H:82:ILE:HG23	1:H:121:LEU:HD13	2.00	0.44
1:A:64:LEU:HB3	1:A:76:THR:HB	1.99	0.44
1:D:26:LEU:HD12	1:D:27:THR:N	2.32	0.44
1:O:26:LEU:HD12	1:O:27:THR:N	2.33	0.44
1:D:54:TYR:HB3	1:D:63:ILE:HB	2.00	0.44
1:O:27:THR:HG23	1:O:28:LYS:N	2.32	0.44
1:Q:54:TYR:HB3	1:Q:63:ILE:HB	2.00	0.44
1:F:26:LEU:HD12	1:F:27:THR:N	2.33	0.44
1:P:64:LEU:HB3	1:P:76:THR:HB	2.00	0.44
1:G:56:THR:CG2	1:G:57:LYS:N	2.80	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:26:LEU:HD12	1:I:27:THR:N	2.31	0.44
1:I:56:THR:CG2	1:I:57:LYS:N	2.81	0.44
1:I:64:LEU:HB3	1:I:76:THR:HB	2.00	0.44
1:N:27:THR:HG23	1:N:28:LYS:H	1.82	0.44
1:R:172:ASN:OD1	1:R:176:LEU:HD23	2.18	0.44
1:I:6:ARG:NH1	1:Q:188:ARG:NH2	2.33	0.43
1:M:24:ALA:HB2	1:M:185:LEU:HD11	2.00	0.43
1:S:162:TRP:CD1	1:S:182:PRO:HA	2.53	0.43
1:C:88:GLU:O	1:C:88:GLU:CG	2.59	0.43
1:C:184:VAL:HG12	1:C:185:LEU:CD1	2.48	0.43
1:D:184:VAL:HG12	1:D:185:LEU:CD1	2.46	0.43
1:E:5:SER:O	1:E:6:ARG:HB3	2.18	0.43
1:M:27:THR:HG23	1:M:28:LYS:N	2.33	0.43
1:O:176:LEU:HD13	1:O:176:LEU:HA	1.82	0.43
1:A:54:TYR:HB3	1:A:63:ILE:HB	2.01	0.43
1:G:172:ASN:OD1	1:G:176:LEU:HD23	2.17	0.43
1:I:54:TYR:HB3	1:I:63:ILE:HB	2.01	0.43
1:P:82:ILE:HG23	1:P:121:LEU:HD13	2.00	0.43
1:C:60:ASP:CG	1:I:58:ARG:HH22	2.22	0.43
1:N:5:SER:O	1:N:6:ARG:HB3	2.17	0.43
1:F:27:THR:HG23	1:F:28:LYS:N	2.34	0.43
1:S:27:THR:HG23	1:S:28:LYS:N	2.34	0.43
1:T:24:ALA:C	1:T:26:LEU:H	2.22	0.43
1:I:6:ARG:CZ	1:Q:188:ARG:HE	2.31	0.43
1:M:54:TYR:HB3	1:M:63:ILE:HB	2.00	0.43
1:G:204:LEU:HD11	1:H:118:ARG:HG3	2.01	0.43
1:K:176:LEU:HD13	1:K:176:LEU:HA	1.89	0.43
1:L:5:SER:O	1:L:6:ARG:HB3	2.19	0.43
1:M:12:PRO:HB2	1:N:120:SER:HB2	2.01	0.43
1:O:24:ALA:HB2	1:O:185:LEU:HD11	2.00	0.43
1:S:26:LEU:HD12	1:S:27:THR:N	2.33	0.43
1:H:166:LEU:HB3	1:H:171:ILE:HG13	2.00	0.43
1:L:56:THR:CG2	1:L:57:LYS:N	2.82	0.43
1:P:54:TYR:HB3	1:P:63:ILE:HB	2.00	0.43
1:S:24:ALA:C	1:S:26:LEU:H	2.22	0.43
1:F:56:THR:CG2	1:F:57:LYS:N	2.82	0.43
1:M:24:ALA:C	1:M:26:LEU:H	2.23	0.43
1:C:56:THR:CG2	1:C:57:LYS:N	2.81	0.42
1:C:60:ASP:OD2	1:I:58:ARG:NH2	2.51	0.42
1:J:82:ILE:HG23	1:J:121:LEU:HD13	2.01	0.42
1:S:64:LEU:HB3	1:S:76:THR:HB	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:24:ALA:HA	1:T:25:PRO:HD3	1.72	0.42
1:F:118:ARG:HG3	1:J:204:LEU:HD11	2.00	0.42
1:G:26:LEU:HD12	1:G:27:THR:N	2.34	0.42
1:I:181:SER:OG	1:R:172:ASN:OD1	2.37	0.42
1:O:5:SER:O	1:O:6:ARG:HB3	2.19	0.42
1:E:27:THR:HG23	1:E:28:LYS:N	2.35	0.42
1:I:65:ILE:HD11	1:I:98:THR:HG21	2.01	0.42
1:M:26:LEU:HD12	1:M:27:THR:N	2.34	0.42
1:R:27:THR:HG23	1:R:28:LYS:N	2.34	0.42
1:J:27:THR:HG23	1:J:28:LYS:N	2.35	0.42
1:K:82:ILE:HG23	1:K:121:LEU:HD13	2.00	0.42
1:K:120:SER:HB2	1:O:12:PRO:HB2	2.01	0.42
1:R:56:THR:CG2	1:R:57:LYS:N	2.82	0.42
1:H:54:TYR:HB3	1:H:63:ILE:HB	2.01	0.42
1:I:24:ALA:HB2	1:I:185:LEU:HD11	2.00	0.42
1:N:26:LEU:HD12	1:N:27:THR:N	2.33	0.42
1:N:82:ILE:HG23	1:N:121:LEU:HD13	2.01	0.42
1:R:26:LEU:HD12	1:R:27:THR:N	2.33	0.42
1:T:5:SER:O	1:T:6:ARG:HB3	2.19	0.42
1:C:24:ALA:HB2	1:C:185:LEU:HD11	2.02	0.42
1:K:27:THR:HG23	1:K:28:LYS:N	2.33	0.42
1:T:27:THR:HG23	1:T:28:LYS:N	2.34	0.42
1:B:24:ALA:C	1:B:26:LEU:H	2.23	0.42
1:C:24:ALA:HA	1:C:25:PRO:HD3	1.72	0.42
1:E:82:ILE:HG23	1:E:121:LEU:HD13	2.00	0.42
1:H:26:LEU:HD12	1:H:27:THR:N	2.33	0.42
1:M:56:THR:CG2	1:M:57:LYS:N	2.83	0.42
1:C:5:SER:O	1:C:6:ARG:HB3	2.20	0.42
1:K:5:SER:O	1:K:6:ARG:HB3	2.20	0.42
1:Q:5:SER:O	1:Q:6:ARG:HB3	2.20	0.42
1:Q:27:THR:HG23	1:Q:28:LYS:N	2.35	0.42
1:Q:82:ILE:HG23	1:Q:121:LEU:HD13	2.02	0.42
1:R:204:LEU:HD11	1:S:118:ARG:HG3	2.01	0.42
1:F:24:ALA:HB2	1:F:185:LEU:HD11	2.02	0.42
1:I:166:LEU:HB3	1:I:171:ILE:HG13	2.02	0.42
1:K:100:TRP:CH2	1:K:102:SER:HB2	2.55	0.42
1:L:27:THR:HG23	1:L:28:LYS:H	1.85	0.42
1:L:155:ASP:OD2	1:M:118:ARG:NH1	2.49	0.42
1:C:204:LEU:HD11	1:D:118:ARG:HG3	2.01	0.41
1:J:166:LEU:HB3	1:J:171:ILE:HG13	2.01	0.41
1:A:184:VAL:HG12	1:A:185:LEU:CD1	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:54:TYR:HB3	1:L:63:ILE:HB	2.01	0.41
1:L:62:GLU:HA	1:L:62:GLU:OE1	2.21	0.41
1:N:24:ALA:HB2	1:N:185:LEU:HD11	2.02	0.41
1:O:24:ALA:C	1:O:26:LEU:H	2.24	0.41
1:P:166:LEU:HB3	1:P:171:ILE:HG13	2.02	0.41
1:T:24:ALA:HB2	1:T:185:LEU:HD11	2.02	0.41
1:T:56:THR:CG2	1:T:57:LYS:N	2.83	0.41
1:T:65:ILE:HD11	1:T:98:THR:HG21	2.02	0.41
1:D:27:THR:HG23	1:D:28:LYS:N	2.33	0.41
1:H:27:THR:HG23	1:H:28:LYS:N	2.35	0.41
1:Q:184:VAL:O	1:Q:185:LEU:HD12	2.20	0.41
1:C:64:LEU:HB3	1:C:76:THR:HB	2.03	0.41
1:L:82:ILE:HG23	1:L:121:LEU:HD13	2.02	0.41
1:D:24:ALA:C	1:D:26:LEU:H	2.23	0.41
1:D:24:ALA:HA	1:D:25:PRO:HD3	1.70	0.41
1:O:181:SER:HA	1:O:182:PRO:HD3	1.85	0.41
1:T:172:ASN:OD1	1:T:176:LEU:HD23	2.21	0.41
1:C:166:LEU:HB3	1:C:171:ILE:HG13	2.02	0.41
1:G:27:THR:HG23	1:G:28:LYS:N	2.35	0.41
1:I:82:ILE:HG23	1:I:121:LEU:HD13	2.02	0.41
1:M:5:SER:O	1:M:6:ARG:HB3	2.21	0.41
1:N:181:SER:HA	1:N:182:PRO:HD3	1.80	0.41
1:A:195:GLN:HG3	4:A:213:HOH:O	2.20	0.41
1:E:24:ALA:HB2	1:E:185:LEU:HD11	2.03	0.41
1:L:166:LEU:HB3	1:L:171:ILE:HG13	2.03	0.41
1:N:56:THR:HG22	1:N:57:LYS:N	2.36	0.41
1:Q:96:ILE:HG21	1:Q:96:ILE:HD13	1.78	0.41
1:A:82:ILE:HG23	1:A:121:LEU:HD13	2.02	0.41
1:A:204:LEU:HD11	1:B:118:ARG:HG3	2.02	0.41
1:G:24:ALA:HB2	1:G:185:LEU:HD11	2.03	0.41
1:G:176:LEU:HD13	1:G:176:LEU:HA	1.87	0.41
1:H:24:ALA:HB2	1:H:185:LEU:HD11	2.03	0.41
1:H:176:LEU:HD13	1:H:176:LEU:HA	1.88	0.41
1:Q:24:ALA:HA	1:Q:25:PRO:HD3	1.71	0.41
1:T:26:LEU:HD12	1:T:27:THR:N	2.35	0.41
1:C:172:ASN:OD1	1:C:176:LEU:HD23	2.21	0.41
1:F:82:ILE:HG23	1:F:121:LEU:HD13	2.02	0.41
1:L:181:SER:HA	1:L:182:PRO:HD3	1.83	0.41
1:O:166:LEU:HB3	1:O:171:ILE:HG13	2.03	0.41
1:P:184:VAL:HG12	1:P:185:LEU:CD1	2.50	0.41
1:S:176:LEU:HD13	1:S:176:LEU:HA	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:6:ARG:HH12	1:L:188:ARG:NE	2.18	0.40
1:B:24:ALA:HB2	1:B:185:LEU:HD11	2.03	0.40
1:F:82:ILE:CD1	1:F:107:VAL:HG21	2.45	0.40
1:G:5:SER:O	1:G:6:ARG:HB3	2.21	0.40
1:L:24:ALA:C	1:L:26:LEU:H	2.24	0.40
1:B:206:PRO:HB3	1:L:179:PRO:CB	2.50	0.40
1:E:65:ILE:HD11	1:E:98:THR:HG21	2.03	0.40
1:I:181:SER:HA	1:I:182:PRO:HD3	1.82	0.40
1:J:82:ILE:CD1	1:J:107:VAL:HG21	2.44	0.40
1:K:184:VAL:HG12	1:K:185:LEU:CD1	2.51	0.40
1:S:1:GLN:OE1	1:S:1:GLN:N	2.52	0.40
1:I:27:THR:HG23	1:I:28:LYS:N	2.36	0.40
1:I:176:LEU:HD13	1:I:176:LEU:HA	1.81	0.40
1:J:1:GLN:OE1	1:J:1:GLN:N	2.50	0.40
1:J:24:ALA:HB2	1:J:185:LEU:HD11	2.03	0.40
1:O:12:PRO:HD2	4:O:207:HOH:O	2.21	0.40
1:P:82:ILE:CD1	1:P:107:VAL:HG21	2.47	0.40
1:Q:24:ALA:C	1:Q:26:LEU:H	2.24	0.40
1:E:166:LEU:HB3	1:E:171:ILE:HG13	2.02	0.40
1:G:62:GLU:HA	1:G:62:GLU:OE1	2.21	0.40
1:H:64:LEU:HB3	1:H:76:THR:HB	2.04	0.40
1:R:5:SER:O	1:R:6:ARG:HB3	2.22	0.40
1:R:6:ARG:HD3	1:R:203:GLN:HG2	2.04	0.40
1:T:184:VAL:HG12	1:T:185:LEU:CD1	2.49	0.40
1:F:24:ALA:C	1:F:26:LEU:H	2.24	0.40
1:N:172:ASN:OD1	1:N:176:LEU:HD23	2.21	0.40
1:Q:65:ILE:HD11	1:Q:98:THR:HG21	2.03	0.40
1:S:6:ARG:HD3	1:S:203:GLN:HG2	2.04	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:147:GLU:OE2	1:E:28:LYS:NZ[1_556]	1.91	0.29
1:B:140:ASP:OD2	1:E:28:LYS:CE[1_556]	2.18	0.02

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	204/206 (99%)	196 (96%)	7 (3%)	1 (0%)	25	49
1	B	204/206 (99%)	196 (96%)	6 (3%)	2 (1%)	13	33
1	C	204/206 (99%)	195 (96%)	7 (3%)	2 (1%)	13	33
1	D	204/206 (99%)	196 (96%)	6 (3%)	2 (1%)	13	33
1	E	204/206 (99%)	196 (96%)	6 (3%)	2 (1%)	13	33
1	F	204/206 (99%)	196 (96%)	6 (3%)	2 (1%)	13	33
1	G	204/206 (99%)	195 (96%)	7 (3%)	2 (1%)	13	33
1	H	204/206 (99%)	195 (96%)	8 (4%)	1 (0%)	25	49
1	I	204/206 (99%)	196 (96%)	7 (3%)	1 (0%)	25	49
1	J	204/206 (99%)	196 (96%)	7 (3%)	1 (0%)	25	49
1	K	204/206 (99%)	196 (96%)	6 (3%)	2 (1%)	13	33
1	L	204/206 (99%)	195 (96%)	8 (4%)	1 (0%)	25	49
1	M	204/206 (99%)	195 (96%)	7 (3%)	2 (1%)	13	33
1	N	204/206 (99%)	196 (96%)	6 (3%)	2 (1%)	13	33
1	O	204/206 (99%)	196 (96%)	6 (3%)	2 (1%)	13	33
1	P	204/206 (99%)	196 (96%)	7 (3%)	1 (0%)	25	49
1	Q	204/206 (99%)	196 (96%)	7 (3%)	1 (0%)	25	49
1	R	204/206 (99%)	196 (96%)	6 (3%)	2 (1%)	13	33
1	S	204/206 (99%)	196 (96%)	7 (3%)	1 (0%)	25	49
1	T	204/206 (99%)	196 (96%)	6 (3%)	2 (1%)	13	33
All	All	4080/4120 (99%)	3915 (96%)	133 (3%)	32 (1%)	16	38

All (32) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	178	GLY

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Mol	Chain	Res	Type
1	G	178	GLY
1	M	178	GLY
1	O	178	GLY
1	T	178	GLY
1	D	178	GLY
1	E	142	PHE
1	F	142	PHE
1	H	142	PHE
1	J	142	PHE
1	L	142	PHE
1	R	142	PHE
1	R	178	GLY
1	T	142	PHE
1	B	142	PHE
1	C	142	PHE
1	D	142	PHE
1	G	142	PHE
1	I	142	PHE
1	K	142	PHE
1	K	178	GLY
1	M	142	PHE
1	O	142	PHE
1	Q	142	PHE
1	A	178	GLY
1	F	178	GLY
1	N	142	PHE
1	S	178	GLY
1	B	178	GLY
1	N	178	GLY
1	P	178	GLY
1	C	178	GLY

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	180/180 (100%)	172 (96%)	8 (4%)	24	51
1	B	180/180 (100%)	172 (96%)	8 (4%)	24	51
1	C	180/180 (100%)	173 (96%)	7 (4%)	27	56
1	D	180/180 (100%)	172 (96%)	8 (4%)	24	51
1	E	180/180 (100%)	171 (95%)	9 (5%)	20	46
1	F	180/180 (100%)	171 (95%)	9 (5%)	20	46
1	G	180/180 (100%)	171 (95%)	9 (5%)	20	46
1	H	180/180 (100%)	171 (95%)	9 (5%)	20	46
1	I	180/180 (100%)	172 (96%)	8 (4%)	24	51
1	J	180/180 (100%)	171 (95%)	9 (5%)	20	46
1	K	180/180 (100%)	172 (96%)	8 (4%)	24	51
1	L	180/180 (100%)	172 (96%)	8 (4%)	24	51
1	M	180/180 (100%)	171 (95%)	9 (5%)	20	46
1	N	180/180 (100%)	171 (95%)	9 (5%)	20	46
1	O	180/180 (100%)	172 (96%)	8 (4%)	24	51
1	P	180/180 (100%)	171 (95%)	9 (5%)	20	46
1	Q	180/180 (100%)	172 (96%)	8 (4%)	24	51
1	R	180/180 (100%)	171 (95%)	9 (5%)	20	46
1	S	180/180 (100%)	173 (96%)	7 (4%)	27	56
1	T	180/180 (100%)	172 (96%)	8 (4%)	24	51
All	All	3600/3600 (100%)	3433 (95%)	167 (5%)	23	49

All (167) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	LEU
1	A	26	LEU
1	A	38	HIS
1	A	74	SER
1	A	88	GLU
1	A	135	LEU
1	A	166	LEU
1	A	176	LEU

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Mol	Chain	Res	Type
1	B	22	LEU
1	B	26	LEU
1	B	38	HIS
1	B	74	SER
1	B	88	GLU
1	B	135	LEU
1	B	166	LEU
1	B	176	LEU
1	C	22	LEU
1	C	26	LEU
1	C	38	HIS
1	C	74	SER
1	C	88	GLU
1	C	166	LEU
1	C	176	LEU
1	D	22	LEU
1	D	26	LEU
1	D	38	HIS
1	D	74	SER
1	D	88	GLU
1	D	135	LEU
1	D	166	LEU
1	D	176	LEU
1	E	22	LEU
1	E	26	LEU
1	E	38	HIS
1	E	43	LEU
1	E	74	SER
1	E	88	GLU
1	E	135	LEU
1	E	166	LEU
1	E	176	LEU
1	F	22	LEU
1	F	26	LEU
1	F	38	HIS
1	F	43	LEU
1	F	74	SER
1	F	88	GLU
1	F	135	LEU
1	F	166	LEU
1	F	176	LEU
1	G	22	LEU

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Mol	Chain	Res	Type
1	G	26	LEU
1	G	38	HIS
1	G	43	LEU
1	G	74	SER
1	G	88	GLU
1	G	135	LEU
1	G	166	LEU
1	G	176	LEU
1	H	22	LEU
1	H	26	LEU
1	H	38	HIS
1	H	43	LEU
1	H	74	SER
1	H	88	GLU
1	H	135	LEU
1	H	166	LEU
1	H	176	LEU
1	I	22	LEU
1	I	26	LEU
1	I	38	HIS
1	I	43	LEU
1	I	74	SER
1	I	88	GLU
1	I	166	LEU
1	I	176	LEU
1	J	22	LEU
1	J	26	LEU
1	J	30	LEU
1	J	38	HIS
1	J	74	SER
1	J	88	GLU
1	J	135	LEU
1	J	166	LEU
1	J	176	LEU
1	K	22	LEU
1	K	26	LEU
1	K	38	HIS
1	K	74	SER
1	K	88	GLU
1	K	135	LEU
1	K	166	LEU
1	K	176	LEU

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Mol	Chain	Res	Type
1	L	22	LEU
1	L	26	LEU
1	L	38	HIS
1	L	74	SER
1	L	88	GLU
1	L	135	LEU
1	L	166	LEU
1	L	176	LEU
1	M	22	LEU
1	M	26	LEU
1	M	38	HIS
1	M	43	LEU
1	M	74	SER
1	M	88	GLU
1	M	135	LEU
1	M	166	LEU
1	M	176	LEU
1	N	22	LEU
1	N	26	LEU
1	N	38	HIS
1	N	43	LEU
1	N	74	SER
1	N	88	GLU
1	N	135	LEU
1	N	166	LEU
1	N	176	LEU
1	O	22	LEU
1	O	26	LEU
1	O	38	HIS
1	O	74	SER
1	O	88	GLU
1	O	135	LEU
1	O	166	LEU
1	O	176	LEU
1	P	22	LEU
1	P	26	LEU
1	P	38	HIS
1	P	74	SER
1	P	88	GLU
1	P	135	LEU
1	P	155	ASP
1	P	166	LEU

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Mol	Chain	Res	Type
1	P	176	LEU
1	Q	22	LEU
1	Q	26	LEU
1	Q	38	HIS
1	Q	74	SER
1	Q	88	GLU
1	Q	135	LEU
1	Q	166	LEU
1	Q	176	LEU
1	R	22	LEU
1	R	26	LEU
1	R	38	HIS
1	R	43	LEU
1	R	74	SER
1	R	88	GLU
1	R	135	LEU
1	R	166	LEU
1	R	176	LEU
1	S	22	LEU
1	S	26	LEU
1	S	38	HIS
1	S	74	SER
1	S	88	GLU
1	S	166	LEU
1	S	176	LEU
1	T	22	LEU
1	T	26	LEU
1	T	38	HIS
1	T	74	SER
1	T	88	GLU
1	T	135	LEU
1	T	166	LEU
1	T	176	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 60 ligands modelled in this entry, 40 are monoatomic - leaving 20 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	OPE	S	4700	2	7,7,7	0.78	0	9,9,9	1.18	2 (22%)
3	OPE	T	2700	2	7,7,7	0.85	0	9,9,9	1.27	2 (22%)
3	OPE	B	950	2	7,7,7	1.02	0	9,9,9	1.01	0
3	OPE	K	500	2	7,7,7	0.84	0	9,9,9	1.27	2 (22%)
3	OPE	F	7700	2	7,7,7	0.71	0	9,9,9	1.63	3 (33%)
3	OPE	A	550	2	7,7,7	0.97	0	9,9,9	1.30	2 (22%)
3	OPE	I	800	2	7,7,7	0.78	0	9,9,9	1.22	1 (11%)
3	OPE	P	700	2	7,7,7	0.99	1 (14%)	9,9,9	1.25	1 (11%)
3	OPE	G	8700	2	7,7,7	0.76	0	9,9,9	1.21	1 (11%)
3	OPE	D	450	2	7,7,7	0.92	0	9,9,9	0.99	1 (11%)
3	OPE	N	900	2	7,7,7	1.00	0	9,9,9	0.90	0
3	OPE	Q	1700	2	7,7,7	0.84	0	9,9,9	1.64	2 (22%)
3	OPE	O	600	2	7,7,7	0.65	0	9,9,9	1.25	2 (22%)
3	OPE	C	650	2	7,7,7	0.94	0	9,9,9	1.27	2 (22%)
3	OPE	H	5700	2	7,7,7	1.00	0	9,9,9	1.34	2 (22%)
3	OPE	E	350	2	7,7,7	0.90	0	9,9,9	1.15	2 (22%)
3	OPE	J	6700	2	7,7,7	0.76	0	9,9,9	1.15	1 (11%)
3	OPE	M	400	2	7,7,7	0.93	0	9,9,9	0.88	0
3	OPE	R	3700	2	7,7,7	0.71	0	9,9,9	1.17	1 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	OPE	L	300	2	7,7,7	0.99	0	9,9,9	1.36	2 (22%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	OPE	S	4700	2	-	3/5/5/5	-
3	OPE	T	2700	2	-	0/5/5/5	-
3	OPE	B	950	2	-	0/5/5/5	-
3	OPE	K	500	2	-	1/5/5/5	-
3	OPE	F	7700	2	-	0/5/5/5	-
3	OPE	A	550	2	-	3/5/5/5	-
3	OPE	I	800	2	-	2/5/5/5	-
3	OPE	P	700	2	-	1/5/5/5	-
3	OPE	G	8700	2	-	4/5/5/5	-
3	OPE	D	450	2	-	3/5/5/5	-
3	OPE	N	900	2	-	0/5/5/5	-
3	OPE	Q	1700	2	-	0/5/5/5	-
3	OPE	O	600	2	-	3/5/5/5	-
3	OPE	C	650	2	-	3/5/5/5	-
3	OPE	H	5700	2	-	3/5/5/5	-
3	OPE	E	350	2	-	3/5/5/5	-
3	OPE	J	6700	2	-	3/5/5/5	-
3	OPE	M	400	2	-	0/5/5/5	-
3	OPE	R	3700	2	-	3/5/5/5	-
3	OPE	L	300	2	-	3/5/5/5	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	P	700	OPE	P-O3	-2.03	1.44	1.50

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	Q	1700	OPE	O4-P-O3	3.22	115.13	106.44
3	P	700	OPE	O4-CA-CB	3.05	120.32	109.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	8700	OPE	O4-CA-CB	3.00	120.16	109.17
3	F	7700	OPE	O4-P-O3	2.78	113.95	106.44
3	J	6700	OPE	O4-CA-CB	2.77	119.31	109.17
3	Q	1700	OPE	O4-CA-CB	2.75	119.25	109.17
3	I	800	OPE	O4-CA-CB	2.69	119.00	109.17
3	A	550	OPE	O4-P-O3	2.67	113.67	106.44
3	L	300	OPE	O4-P-O3	2.67	113.65	106.44
3	A	550	OPE	O4-CA-CB	2.65	118.85	109.17
3	T	2700	OPE	P-O4-CA	2.60	125.28	118.21
3	L	300	OPE	P-O4-CA	2.52	125.06	118.21
3	D	450	OPE	O4-CA-CB	2.50	118.31	109.17
3	H	5700	OPE	O4-CA-CB	2.49	118.30	109.17
3	R	3700	OPE	O4-CA-CB	2.43	118.06	109.17
3	H	5700	OPE	O4-P-O3	2.42	112.98	106.44
3	K	500	OPE	O4-CA-CB	2.42	118.02	109.17
3	F	7700	OPE	O4-CA-CB	2.40	117.96	109.17
3	O	600	OPE	O4-P-O3	2.37	112.85	106.44
3	S	4700	OPE	O4-P-O3	2.36	112.81	106.44
3	O	600	OPE	O4-CA-CB	2.32	117.67	109.17
3	K	500	OPE	O4-P-O3	2.31	112.69	106.44
3	S	4700	OPE	O4-CA-CB	2.29	117.55	109.17
3	F	7700	OPE	O2-P-O4	-2.25	100.80	106.67
3	C	650	OPE	O4-CA-CB	2.22	117.31	109.17
3	E	350	OPE	O2-P-O4	2.05	112.02	106.67
3	T	2700	OPE	O2-P-O4	2.04	111.98	106.67
3	C	650	OPE	P-O4-CA	2.03	123.74	118.21
3	E	350	OPE	O4-CA-CB	2.02	116.55	109.17

There are no chirality outliers.

All (38) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	550	OPE	CA-O4-P-O2
3	C	650	OPE	CA-O4-P-O1
3	C	650	OPE	CA-O4-P-O2
3	C	650	OPE	CA-O4-P-O3
3	D	450	OPE	CA-O4-P-O1
3	D	450	OPE	CA-O4-P-O2
3	D	450	OPE	CA-O4-P-O3
3	E	350	OPE	CA-O4-P-O1
3	E	350	OPE	CA-O4-P-O2
3	G	8700	OPE	O4-CA-CB-N

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Mol	Chain	Res	Type	Atoms
3	G	8700	OPE	CA-O4-P-O1
3	H	5700	OPE	CA-O4-P-O1
3	H	5700	OPE	CA-O4-P-O3
3	I	800	OPE	O4-CA-CB-N
3	J	6700	OPE	CA-O4-P-O1
3	J	6700	OPE	CA-O4-P-O2
3	J	6700	OPE	CA-O4-P-O3
3	K	500	OPE	O4-CA-CB-N
3	L	300	OPE	O4-CA-CB-N
3	L	300	OPE	CA-O4-P-O1
3	L	300	OPE	CA-O4-P-O2
3	O	600	OPE	CA-O4-P-O1
3	O	600	OPE	CA-O4-P-O2
3	O	600	OPE	CA-O4-P-O3
3	P	700	OPE	O4-CA-CB-N
3	R	3700	OPE	CA-O4-P-O1
3	R	3700	OPE	CA-O4-P-O3
3	S	4700	OPE	CA-O4-P-O1
3	S	4700	OPE	CA-O4-P-O2
3	S	4700	OPE	CA-O4-P-O3
3	A	550	OPE	CA-O4-P-O3
3	E	350	OPE	CA-O4-P-O3
3	G	8700	OPE	CA-O4-P-O3
3	A	550	OPE	CA-O4-P-O1
3	G	8700	OPE	CA-O4-P-O2
3	H	5700	OPE	CA-O4-P-O2
3	R	3700	OPE	CA-O4-P-O2
3	I	800	OPE	CA-O4-P-O2

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	206/206 (100%)	0.26	14 (6%) 25 23	34, 48, 83, 131	0
1	B	206/206 (100%)	0.29	16 (7%) 20 19	36, 48, 83, 133	0
1	C	206/206 (100%)	0.10	9 (4%) 39 38	35, 48, 80, 132	0
1	D	206/206 (100%)	0.22	13 (6%) 27 25	38, 49, 82, 133	0
1	E	206/206 (100%)	0.21	11 (5%) 33 31	34, 49, 83, 132	0
1	F	206/206 (100%)	0.71	17 (8%) 19 17	40, 54, 86, 132	0
1	G	206/206 (100%)	0.72	24 (11%) 10 10	38, 53, 86, 135	0
1	H	206/206 (100%)	0.26	20 (9%) 15 14	36, 48, 82, 131	0
1	I	206/206 (100%)	0.30	18 (8%) 17 16	36, 48, 81, 132	0
1	J	206/206 (100%)	0.30	18 (8%) 17 16	36, 49, 84, 133	0
1	K	206/206 (100%)	0.49	15 (7%) 22 20	40, 53, 84, 133	0
1	L	206/206 (100%)	0.84	28 (13%) 8 7	37, 51, 84, 133	0
1	M	206/206 (100%)	0.28	15 (7%) 22 20	38, 50, 83, 133	0
1	N	206/206 (100%)	0.20	11 (5%) 33 31	38, 50, 85, 133	0
1	O	206/206 (100%)	0.54	20 (9%) 15 14	37, 50, 83, 134	0
1	P	206/206 (100%)	0.31	15 (7%) 22 20	35, 47, 84, 133	0
1	Q	206/206 (100%)	0.81	25 (12%) 10 9	38, 52, 85, 135	0
1	R	206/206 (100%)	1.34	46 (22%) 3 3	42, 56, 88, 132	0
1	S	206/206 (100%)	0.66	19 (9%) 16 15	41, 53, 86, 133	0
1	T	206/206 (100%)	0.34	17 (8%) 19 17	35, 47, 80, 133	0
All	All	4120/4120 (100%)	0.46	371 (9%) 17 15	34, 50, 86, 135	0

All (371) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	K	25	PRO	6.1
1	G	6	ARG	5.9
1	A	25	PRO	5.7
1	B	27	THR	5.6
1	T	176	LEU	5.1
1	R	91	VAL	5.0
1	G	25	PRO	5.0
1	B	26	LEU	5.0
1	O	89	VAL	4.9
1	R	90	THR	4.9
1	P	27	THR	4.9
1	E	28	LYS	4.8
1	I	6	ARG	4.8
1	I	25	PRO	4.7
1	E	27	THR	4.6
1	Q	89	VAL	4.6
1	Q	26	LEU	4.6
1	O	91	VAL	4.6
1	T	25	PRO	4.6
1	A	27	THR	4.5
1	S	27	THR	4.5
1	R	28	LYS	4.5
1	R	25	PRO	4.5
1	L	6	ARG	4.5
1	Q	27	THR	4.5
1	H	25	PRO	4.4
1	Q	174	ILE	4.4
1	G	27	THR	4.4
1	F	91	VAL	4.4
1	J	195	GLN	4.4
1	C	27	THR	4.4
1	L	89	VAL	4.3
1	E	25	PRO	4.3
1	R	27	THR	4.3
1	R	26	LEU	4.3
1	R	54	TYR	4.2
1	F	26	LEU	4.2
1	P	91	VAL	4.2
1	Q	91	VAL	4.2
1	R	89	VAL	4.2
1	T	6	ARG	4.2
1	I	179	PRO	4.2
1	P	25	PRO	4.2

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Mol	Chain	Res	Type	RSRZ
1	T	58	ARG	4.1
1	S	25	PRO	4.1
1	Q	183	ASN	4.1
1	F	89	VAL	4.1
1	R	179	PRO	4.1
1	T	177	GLY	4.1
1	I	28	LYS	4.1
1	O	90	THR	4.0
1	L	91	VAL	4.0
1	M	91	VAL	4.0
1	L	90	THR	4.0
1	D	28	LYS	4.0
1	S	89	VAL	4.0
1	O	58	ARG	3.9
1	F	90	THR	3.9
1	K	1	GLN	3.9
1	O	176	LEU	3.9
1	O	28	LYS	3.8
1	J	27	THR	3.8
1	G	91	VAL	3.8
1	L	27	THR	3.8
1	T	91	VAL	3.8
1	B	25	PRO	3.7
1	D	25	PRO	3.7
1	F	87	PRO	3.7
1	B	89	VAL	3.7
1	I	27	THR	3.7
1	F	28	LYS	3.7
1	F	27	THR	3.7
1	N	26	LEU	3.7
1	K	27	THR	3.7
1	I	90	THR	3.6
1	M	90	THR	3.6
1	P	90	THR	3.6
1	T	1	GLN	3.6
1	Q	180	PHE	3.6
1	G	55	ALA	3.6
1	B	90	THR	3.6
1	D	90	THR	3.6
1	J	169	ASP	3.6
1	Q	25	PRO	3.6
1	E	90	THR	3.6

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Mol	Chain	Res	Type	RSRZ
1	L	26	LEU	3.6
1	S	26	LEU	3.6
1	Q	181	SER	3.5
1	F	25	PRO	3.5
1	I	173	THR	3.5
1	B	6	ARG	3.5
1	M	89	VAL	3.5
1	J	89	VAL	3.5
1	P	1	GLN	3.5
1	F	55	ALA	3.4
1	N	90	THR	3.4
1	J	26	LEU	3.4
1	A	89	VAL	3.4
1	R	178	GLY	3.4
1	C	26	LEU	3.4
1	F	56	THR	3.4
1	L	28	LYS	3.4
1	J	16	ASP	3.4
1	T	89	VAL	3.4
1	S	91	VAL	3.4
1	T	28	LYS	3.4
1	L	25	PRO	3.3
1	N	195	GLN	3.3
1	C	91	VAL	3.3
1	E	89	VAL	3.3
1	G	89	VAL	3.3
1	I	26	LEU	3.3
1	G	17	THR	3.3
1	M	27	THR	3.3
1	B	91	VAL	3.3
1	G	26	LEU	3.3
1	C	25	PRO	3.2
1	I	91	VAL	3.2
1	E	26	LEU	3.2
1	G	28	LYS	3.2
1	E	6	ARG	3.2
1	K	89	VAL	3.2
1	G	178	GLY	3.2
1	O	6	ARG	3.2
1	O	25	PRO	3.2
1	O	27	THR	3.2
1	B	28	LYS	3.2

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Mol	Chain	Res	Type	RSRZ
1	D	91	VAL	3.2
1	O	178	GLY	3.2
1	H	89	VAL	3.2
1	T	27	THR	3.1
1	J	91	VAL	3.1
1	A	1	GLN	3.1
1	K	91	VAL	3.1
1	O	55	ALA	3.1
1	A	179	PRO	3.1
1	Q	193	GLU	3.1
1	G	177	GLY	3.1
1	Q	58	ARG	3.1
1	G	56	THR	3.0
1	R	56	THR	3.0
1	B	179	PRO	3.0
1	N	89	VAL	3.0
1	M	25	PRO	3.0
1	G	127	VAL	3.0
1	E	176	LEU	2.9
1	G	193	GLU	2.9
1	S	6	ARG	2.9
1	T	90	THR	2.9
1	K	90	THR	2.9
1	L	17	THR	2.9
1	H	1	GLN	2.9
1	K	28	LYS	2.9
1	Q	90	THR	2.9
1	A	91	VAL	2.9
1	H	91	VAL	2.9
1	L	177	GLY	2.9
1	N	25	PRO	2.9
1	O	177	GLY	2.9
1	D	58	ARG	2.9
1	J	90	THR	2.9
1	P	89	VAL	2.9
1	A	28	LYS	2.8
1	L	13	LYS	2.8
1	H	181	SER	2.8
1	L	55	ALA	2.8
1	E	87	PRO	2.8
1	J	179	PRO	2.8
1	K	191	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
1	Q	188	ARG	2.8
1	Q	179	PRO	2.8
1	O	26	LEU	2.8
1	I	174	ILE	2.8
1	M	58	ARG	2.8
1	P	179	PRO	2.8
1	Q	176	LEU	2.8
1	B	174	ILE	2.8
1	P	6	ARG	2.8
1	Q	173	THR	2.8
1	R	169	ASP	2.8
1	H	145	ASN	2.7
1	R	62	GLU	2.7
1	R	130	GLU	2.7
1	C	89	VAL	2.7
1	L	56	THR	2.7
1	R	173	THR	2.7
1	S	90	THR	2.7
1	Q	19	TYR	2.7
1	S	130	GLU	2.7
1	B	181	SER	2.7
1	D	26	LEU	2.7
1	L	173	THR	2.7
1	I	58	ARG	2.7
1	L	191	LYS	2.7
1	M	28	LYS	2.7
1	R	31	LYS	2.7
1	J	25	PRO	2.7
1	N	176	LEU	2.7
1	B	173	THR	2.7
1	P	181	SER	2.7
1	D	27	THR	2.6
1	F	17	THR	2.6
1	R	141	SER	2.6
1	R	177	GLY	2.6
1	J	130	GLU	2.6
1	M	6	ARG	2.6
1	Q	6	ARG	2.6
1	G	90	THR	2.6
1	R	134	ILE	2.6
1	J	28	LYS	2.6
1	B	180	PHE	2.6

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Mol	Chain	Res	Type	RSRZ
1	J	58	ARG	2.6
1	R	6	ARG	2.6
1	K	17	THR	2.6
1	B	176	LEU	2.6
1	R	87	PRO	2.6
1	F	142	PHE	2.6
1	T	188	ARG	2.6
1	S	181	SER	2.5
1	M	179	PRO	2.5
1	S	87	PRO	2.5
1	I	188	ARG	2.5
1	E	91	VAL	2.5
1	D	1	GLN	2.5
1	R	60	ASP	2.5
1	H	172	ASN	2.5
1	H	90	THR	2.5
1	R	48	GLY	2.5
1	R	77	VAL	2.5
1	P	16	ASP	2.5
1	P	145	ASN	2.5
1	S	28	LYS	2.5
1	N	27	THR	2.5
1	G	53	SER	2.4
1	T	169	ASP	2.4
1	A	90	THR	2.4
1	G	30	LEU	2.4
1	B	87	PRO	2.4
1	H	188	ARG	2.4
1	J	6	ARG	2.4
1	L	132	SER	2.4
1	R	53	SER	2.4
1	R	55	ALA	2.4
1	M	169	ASP	2.4
1	L	178	GLY	2.4
1	M	178	GLY	2.4
1	R	76	THR	2.4
1	D	176	LEU	2.4
1	K	26	LEU	2.4
1	H	6	ARG	2.4
1	H	13	LYS	2.4
1	S	177	GLY	2.4
1	I	87	PRO	2.4

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Mol	Chain	Res	Type	RSRZ
1	L	31	LYS	2.4
1	N	91	VAL	2.4
1	H	16	ASP	2.4
1	L	16	ASP	2.4
1	R	61	ASN	2.4
1	H	56	THR	2.3
1	P	188	ARG	2.3
1	C	28	LYS	2.3
1	O	87	PRO	2.3
1	L	33	PHE	2.3
1	R	146	PHE	2.3
1	H	17	THR	2.3
1	L	188	ARG	2.3
1	R	191	LYS	2.3
1	D	89	VAL	2.3
1	G	149	SER	2.3
1	L	176	LEU	2.3
1	O	88	GLU	2.3
1	R	17	THR	2.3
1	K	58	ARG	2.3
1	M	1	GLN	2.3
1	Q	134	ILE	2.3
1	R	21	SER	2.3
1	F	13	LYS	2.3
1	H	191	LYS	2.3
1	D	56	THR	2.3
1	O	173	THR	2.3
1	Q	17	THR	2.3
1	H	87	PRO	2.3
1	Q	206	PRO	2.3
1	K	139	GLN	2.3
1	R	63	ILE	2.3
1	P	178	GLY	2.3
1	R	78	GLY	2.3
1	R	13	LYS	2.2
1	H	27	THR	2.2
1	O	17	THR	2.2
1	T	17	THR	2.2
1	H	179	PRO	2.2
1	Q	87	PRO	2.2
1	I	89	VAL	2.2
1	L	133	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	S	110	TRP	2.2
1	Q	28	LYS	2.2
1	M	26	LEU	2.2
1	K	141	SER	2.2
1	S	16	ASP	2.2
1	R	127	VAL	2.2
1	N	13	LYS	2.2
1	R	30	LEU	2.2
1	F	138	GLU	2.2
1	N	88	GLU	2.2
1	M	87	PRO	2.2
1	R	142	PHE	2.2
1	S	13	LYS	2.2
1	I	129	ALA	2.2
1	O	179	PRO	2.2
1	Q	175	TYR	2.2
1	F	1	GLN	2.2
1	F	134	ILE	2.2
1	E	13	LYS	2.2
1	P	28	LYS	2.2
1	T	26	LEU	2.2
1	I	177	GLY	2.2
1	L	120	SER	2.1
1	D	126	THR	2.1
1	C	1	GLN	2.1
1	G	191	LYS	2.1
1	K	13	LYS	2.1
1	H	26	LEU	2.1
1	A	188	ARG	2.1
1	A	88	GLU	2.1
1	I	181	SER	2.1
1	R	44	SER	2.1
1	R	68	SER	2.1
1	S	17	THR	2.1
1	L	77	VAL	2.1
1	R	133	ILE	2.1
1	R	64	LEU	2.1
1	C	6	ARG	2.1
1	O	188	ARG	2.1
1	I	178	GLY	2.1
1	J	87	PRO	2.1
1	S	179	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
1	O	191	LYS	2.1
1	T	173	THR	2.1
1	A	172	ASN	2.1
1	J	145	ASN	2.1
1	R	9	PHE	2.1
1	R	145	ASN	2.1
1	A	26	LEU	2.1
1	G	176	LEU	2.1
1	J	129	ALA	2.1
1	R	188	ARG	2.1
1	B	147	GLU	2.1
1	F	193	GLU	2.1
1	H	28	LYS	2.1
1	L	180	PHE	2.1
1	R	66	PHE	2.1
1	J	176	LEU	2.1
1	A	24	ALA	2.1
1	L	129	ALA	2.1
1	S	178	GLY	2.1
1	C	88	GLU	2.0
1	G	57	LYS	2.0
1	Q	146	PHE	2.0
1	A	19	TYR	2.0
1	G	32	ALA	2.0
1	M	177	GLY	2.0
1	N	177	GLY	2.0
1	T	87	PRO	2.0
1	P	13	LYS	2.0
1	S	191	LYS	2.0
1	D	173	THR	2.0
1	G	173	THR	2.0
1	L	2	THR	2.0
1	G	137	GLN	2.0
1	K	181	SER	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	OPE	R	3700	8/8	0.84	0.13	61,84,119,122	0
3	OPE	F	7700	8/8	0.89	0.14	62,72,85,100	0
2	CA	F	302	1/1	0.89	0.09	86,86,86,86	0
3	OPE	K	500	8/8	0.93	0.09	46,67,81,92	0
3	OPE	L	300	8/8	0.93	0.12	38,60,80,85	0
2	CA	R	302	1/1	0.93	0.09	80,80,80,80	0
2	CA	F	301	1/1	0.94	0.07	67,67,67,67	0
2	CA	G	302	1/1	0.94	0.08	71,71,71,71	0
3	OPE	G	8700	8/8	0.94	0.10	53,59,85,89	0
3	OPE	S	4700	8/8	0.94	0.15	27,61,65,92	0
3	OPE	Q	1700	8/8	0.95	0.11	44,66,83,85	0
2	CA	O	302	1/1	0.96	0.07	59,59,59,59	0
3	OPE	N	900	8/8	0.96	0.10	37,52,63,73	0
3	OPE	O	600	8/8	0.96	0.10	28,61,81,83	0
3	OPE	H	5700	8/8	0.97	0.10	37,44,55,91	0
3	OPE	J	6700	8/8	0.97	0.07	31,51,59,59	0
2	CA	G	301	1/1	0.97	0.04	56,56,56,56	0
2	CA	R	301	1/1	0.97	0.05	87,87,87,87	0
3	OPE	M	400	8/8	0.97	0.08	42,46,56,62	0
2	CA	K	302	1/1	0.97	0.07	72,72,72,72	0
3	OPE	D	450	8/8	0.97	0.09	33,40,55,60	0
3	OPE	P	700	8/8	0.97	0.10	22,36,55,56	0
3	OPE	E	350	8/8	0.97	0.07	37,55,75,76	0
2	CA	L	301	1/1	0.97	0.04	50,50,50,50	0
2	CA	M	302	1/1	0.97	0.07	53,53,53,53	0
3	OPE	T	2700	8/8	0.97	0.09	37,43,66,77	0
2	CA	H	302	1/1	0.98	0.04	47,47,47,47	0
2	CA	N	301	1/1	0.98	0.03	43,43,43,43	0
3	OPE	I	800	8/8	0.98	0.07	37,47,59,61	0
2	CA	O	301	1/1	0.98	0.04	49,49,49,49	0
2	CA	I	302	1/1	0.98	0.04	54,54,54,54	0
2	CA	Q	302	1/1	0.98	0.05	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	CA	J	301	1/1	0.98	0.04	52,52,52,52	0
2	CA	J	302	1/1	0.98	0.06	54,54,54,54	0
3	OPE	A	550	8/8	0.98	0.07	28,42,51,54	0
3	OPE	B	950	8/8	0.98	0.06	30,37,50,50	0
3	OPE	C	650	8/8	0.98	0.09	36,42,65,65	0
2	CA	K	301	1/1	0.98	0.04	69,69,69,69	0
2	CA	A	302	1/1	0.98	0.04	53,53,53,53	0
2	CA	H	301	1/1	0.98	0.03	46,46,46,46	0
2	CA	C	301	1/1	0.99	0.03	42,42,42,42	0
2	CA	L	302	1/1	0.99	0.03	53,53,53,53	0
2	CA	M	301	1/1	0.99	0.03	49,49,49,49	0
2	CA	D	301	1/1	0.99	0.04	48,48,48,48	0
2	CA	D	302	1/1	0.99	0.02	46,46,46,46	0
2	CA	N	302	1/1	0.99	0.02	44,44,44,44	0
2	CA	I	301	1/1	0.99	0.03	44,44,44,44	0
2	CA	E	301	1/1	0.99	0.03	47,47,47,47	0
2	CA	P	301	1/1	0.99	0.03	39,39,39,39	0
2	CA	P	302	1/1	0.99	0.02	41,41,41,41	0
2	CA	Q	301	1/1	0.99	0.03	49,49,49,49	0
2	CA	E	302	1/1	0.99	0.03	46,46,46,46	0
2	CA	A	301	1/1	0.99	0.03	47,47,47,47	0
2	CA	B	301	1/1	0.99	0.03	41,41,41,41	0
2	CA	S	301	1/1	0.99	0.04	50,50,50,50	0
2	CA	S	302	1/1	0.99	0.03	57,57,57,57	0
2	CA	T	301	1/1	0.99	0.04	43,43,43,43	0
2	CA	T	302	1/1	0.99	0.04	47,47,47,47	0
2	CA	B	302	1/1	0.99	0.03	39,39,39,39	0
2	CA	C	302	1/1	1.00	0.03	43,43,43,43	0

6.5 Other polymers ⓘ

There are no such residues in this entry.