



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 23, 2024 – 02:35 AM EDT

PDB ID : 3AJV
Title : Splicing endonuclease from *Aeropyrum pernix*
Authors : Yoshinari, S.; Watanabe, Y.; Okuda, M.; Shiba, T.; Inaoka, K.D.; Kurisu, G.
Deposited on : 2010-06-19
Resolution : 1.70 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:

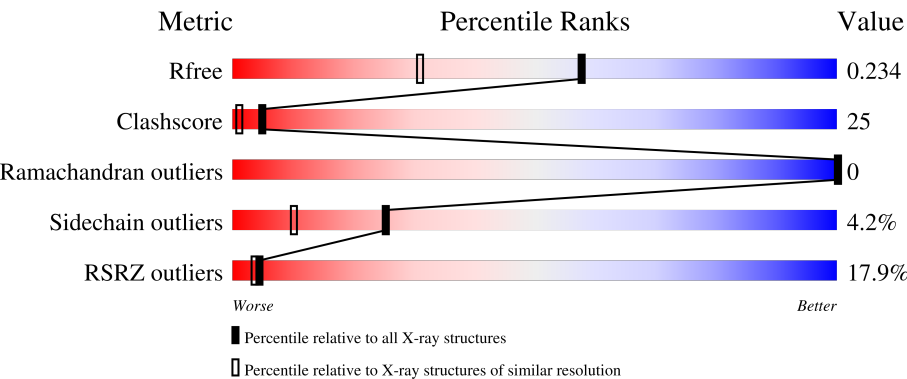
MolProbity : 4.02b-467
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 1.20.1
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.003 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	5161 (1.70-1.70)
Clashscore	180529	5671 (1.70-1.70)
Ramachandran outliers	177936	5594 (1.70-1.70)
Sidechain outliers	177891	5594 (1.70-1.70)
RSRZ outliers	164620	5159 (1.70-1.70)

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	190	<div><div>14%</div><div><div></div><div></div><div></div><div></div></div><div>70%</div><div>17%</div><div>•</div><div>12%</div></div>
1	C	190	<div><div>15%</div><div><div></div><div></div><div></div><div></div></div><div>66%</div><div>18%</div><div>•</div><div>15%</div></div>
2	B	186	<div><div>17%</div><div><div></div><div></div><div></div><div></div></div><div>73%</div><div>22%</div><div>•••</div></div>
2	D	186	<div><div>20%</div><div><div></div><div></div><div></div><div></div></div><div>73%</div><div>20%</div><div>••</div></div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	GOL	B	188	-	-	X	-
3	GOL	B	189	-	-	X	-
3	GOL	B	190	-	-	X	-
3	GOL	D	187	-	-	X	-
3	GOL	D	188	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6153 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 Putative uncharacterized protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	168	Total	C	N	O	S	0	6	0
			1343	848	247	241	7			
1	C	161	Total	C	N	O	S	0	6	0
			1295	818	241	229	7			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP Q9YE85
A	-18	GLY	-	expression tag	UNP Q9YE85
A	-17	SER	-	expression tag	UNP Q9YE85
A	-16	SER	-	expression tag	UNP Q9YE85
A	-15	HIS	-	expression tag	UNP Q9YE85
A	-14	HIS	-	expression tag	UNP Q9YE85
A	-13	HIS	-	expression tag	UNP Q9YE85
A	-12	HIS	-	expression tag	UNP Q9YE85
A	-11	HIS	-	expression tag	UNP Q9YE85
A	-10	HIS	-	expression tag	UNP Q9YE85
A	-9	SER	-	expression tag	UNP Q9YE85
A	-8	SER	-	expression tag	UNP Q9YE85
A	-7	GLY	-	expression tag	UNP Q9YE85
A	-6	LEU	-	expression tag	UNP Q9YE85
A	-5	VAL	-	expression tag	UNP Q9YE85
A	-4	PRO	-	expression tag	UNP Q9YE85
A	-3	ARG	-	expression tag	UNP Q9YE85
A	-2	GLY	-	expression tag	UNP Q9YE85
A	-1	SER	-	expression tag	UNP Q9YE85
A	0	HIS	-	expression tag	UNP Q9YE85
C	-19	MET	-	expression tag	UNP Q9YE85
C	-18	GLY	-	expression tag	UNP Q9YE85
C	-17	SER	-	expression tag	UNP Q9YE85
C	-16	SER	-	expression tag	UNP Q9YE85
C	-15	HIS	-	expression tag	UNP Q9YE85

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-14	HIS	-	expression tag	UNP Q9YE85
C	-13	HIS	-	expression tag	UNP Q9YE85
C	-12	HIS	-	expression tag	UNP Q9YE85
C	-11	HIS	-	expression tag	UNP Q9YE85
C	-10	HIS	-	expression tag	UNP Q9YE85
C	-9	SER	-	expression tag	UNP Q9YE85
C	-8	SER	-	expression tag	UNP Q9YE85
C	-7	GLY	-	expression tag	UNP Q9YE85
C	-6	LEU	-	expression tag	UNP Q9YE85
C	-5	VAL	-	expression tag	UNP Q9YE85
C	-4	PRO	-	expression tag	UNP Q9YE85
C	-3	ARG	-	expression tag	UNP Q9YE85
C	-2	GLY	-	expression tag	UNP Q9YE85
C	-1	SER	-	expression tag	UNP Q9YE85
C	0	HIS	-	expression tag	UNP Q9YE85

- Molecule 2 is a protein called tRNA-splicing endonuclease.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	180	Total	C	N	O	S	0	8	0
			1461	935	256	267	3			
2	D	178	Total	C	N	O	S	5	9	0
			1443	927	249	263	4			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	133	ALA	HIS	engineered mutation	UNP Q9YBF1
D	133	ALA	HIS	engineered mutation	UNP Q9YBF1

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Cl	0	0
			1	1		
4	D	1	Total	Cl	0	0
			1	1		

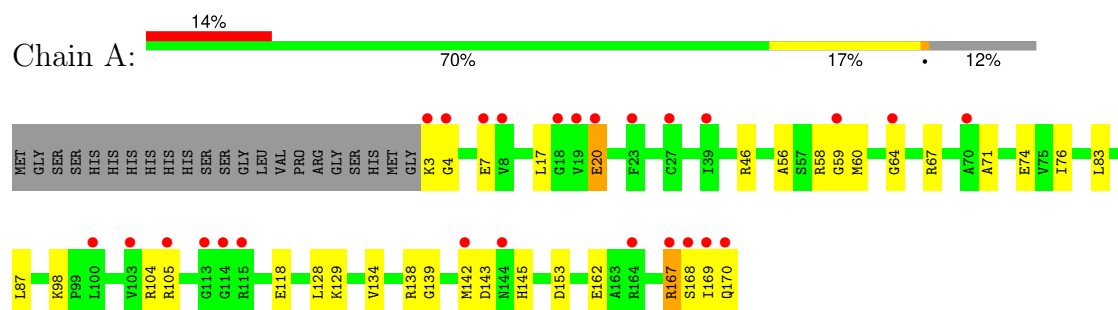
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	141	Total 141	O 141	0	0
5	B	143	Total 143	O 143	0	0
5	C	107	Total 107	O 107	0	0
5	D	158	Total 158	O 158	0	0

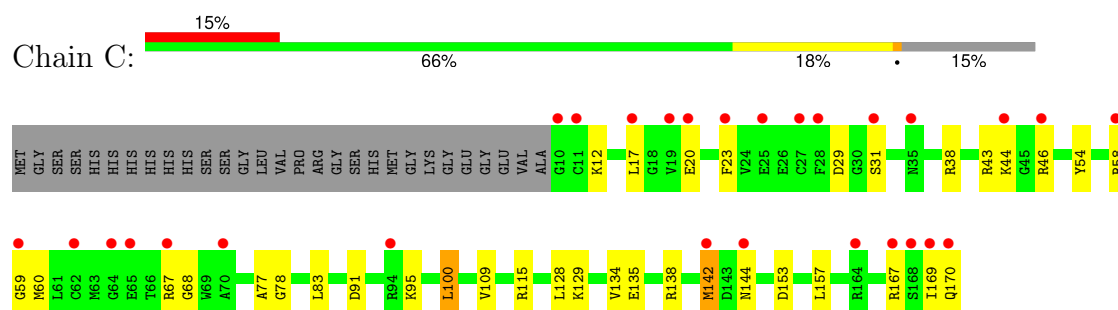
3 Residue-property plots [i](#)

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.

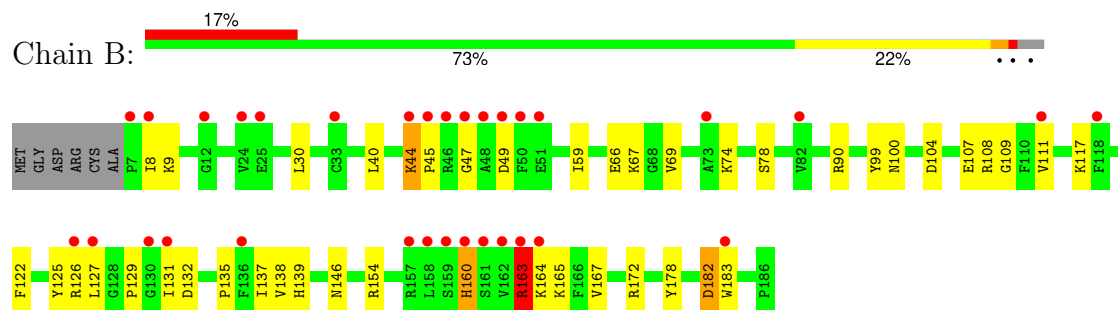
• Molecule 1: Putative uncharacterized protein



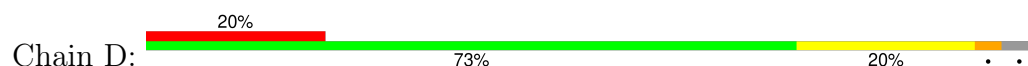
• Molecule 1: Putative uncharacterized protein

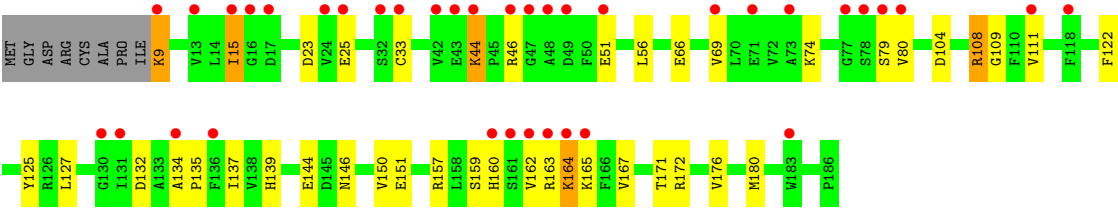


• Molecule 2: tRNA-splicing endonuclease



• Molecule 2: tRNA-splicing endonuclease





4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	95.33Å 95.33Å 253.82Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 1.70 30.00 – 1.70	Depositor EDS
% Data completeness (in resolution range)	98.3 (30.00-1.70) 93.9 (30.00-1.70)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.59 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.5.0066	Depositor
R, R_{free}	0.218 , 0.229 0.239 , 0.234	Depositor DCC
R_{free} test set	4436 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	21.2	Xtriage
Anisotropy	0.134	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 44.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	0.000 for -h-k,k,-l	Xtriage
Reported twinning fraction	0.946 for H, K, L 0.054 for K, H, -L	Depositor
Outliers	0 of 88644 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6153	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 22.59 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.5291e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.63	0/1374	0.69	0/1848
1	C	0.65	0/1322	0.70	0/1778
2	B	0.77	0/1502	0.82	3/2030 (0.1%)
2	D	0.73	0/1492	0.84	1/2018 (0.0%)
All	All	0.70	0/5690	0.77	4/7674 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	163	ARG	N-CA-C	-5.78	95.40	111.00
2	D	122	PHE	CB-CG-CD2	-5.19	117.17	120.80
2	B	122	PHE	CB-CG-CD2	-5.13	117.21	120.80
2	B	178	TYR	CB-CG-CD1	-5.06	117.96	121.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	1343	0	1363	58	0
1	C	1295	0	1324	71	0
2	B	1461	0	1475	73	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	1443	0	1463	98	0
3	A	12	0	16	2	0
3	B	24	0	32	23	0
3	C	6	0	8	1	0
3	D	18	0	24	20	0
4	B	1	0	0	0	0
4	D	1	0	0	0	0
5	A	141	0	0	17	0
5	B	143	0	0	18	0
5	C	107	0	0	12	0
5	D	158	0	0	17	0
All	All	6153	0	5705	280	0

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 25.

All (280) 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:C:43:ARG:HH22	1:C:44:LYS:NZ	0.99	1.42
1:C:43:ARG:HH22	1:C:44:LYS:CE	1.32	1.41
1:C:43:ARG:NH2	1:C:44:LYS:NZ	1.75	1.30
1:C:43:ARG:NH2	1:C:44:LYS:CE	1.88	1.29
1:A:7:GLU:CG	1:A:67:ARG:HH21	1.49	1.26
2:D:164:LYS:HD3	2:D:164:LYS:N	1.46	1.23
2:D:162:VAL:CG2	2:D:163:ARG:H	1.48	1.21
2:D:111[A]:VAL:CG1	2:D:125:TYR:HB2	1.71	1.19
1:C:43:ARG:HH21	1:C:44:LYS:CD	1.55	1.19
2:D:163:ARG:CB	3:D:187:GOL:H32	1.72	1.18
2:D:164:LYS:H	2:D:164:LYS:CD	1.57	1.16
1:C:43:ARG:NH2	1:C:44:LYS:CD	2.12	1.12
1:A:7:GLU:HG2	1:A:67:ARG:NH2	1.67	1.10
1:A:3:LYS:HG2	1:A:4:GLY:N	1.65	1.10
1:A:3:LYS:HG2	1:A:4:GLY:H	0.94	1.08
2:B:111[A]:VAL:CG1	2:B:125:TYR:HB2	1.84	1.07
2:D:162:VAL:HG23	2:D:163:ARG:N	1.58	1.07
1:C:169:ILE:HD11	2:D:167:VAL:HG11	1.37	1.06
1:C:43:ARG:HH21	1:C:44:LYS:HD2	0.90	1.05
2:D:111[A]:VAL:HG11	2:D:125:TYR:HB2	1.32	1.05
2:D:162:VAL:HG23	2:D:163:ARG:H	1.07	1.04
2:D:164:LYS:HD3	2:D:164:LYS:H	0.88	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:46:ARG:NH2	1:A:46:ARG:HB3	1.72	1.03
2:D:163:ARG:HB2	3:D:187:GOL:H32	1.40	1.03
1:C:12:LYS:HE2	1:C:60:MET:SD	2.00	1.02
1:A:20:GLU:OE2	1:A:20:GLU:C	1.99	1.01
1:C:43:ARG:NH2	1:C:44:LYS:HD2	1.72	1.01
1:A:46:ARG:CB	1:A:46:ARG:HH21	1.75	1.00
1:C:43:ARG:NH2	1:C:44:LYS:HZ3	1.52	0.99
1:A:7:GLU:HG2	1:A:67:ARG:HH21	0.84	0.97
2:B:66:GLU:HG2	5:B:463:HOH:O	1.64	0.97
2:B:104:ASP:O	2:B:108:ARG:HG2	1.66	0.96
2:D:150:VAL:HG23	3:D:188:GOL:C3	1.96	0.96
1:A:20:GLU:OE2	1:A:20:GLU:O	1.82	0.96
1:C:144:ASN:HB3	5:C:471:HOH:O	1.66	0.96
2:B:40:LEU:O	3:B:190:GOL:H11	1.66	0.96
1:A:87:LEU:HD13	5:A:194:HOH:O	1.66	0.95
1:A:58[B]:ARG:HD3	5:A:547:HOH:O	1.65	0.95
2:D:150:VAL:HG23	3:D:188:GOL:H31	1.46	0.95
2:D:164:LYS:HE2	5:D:308:HOH:O	1.65	0.94
2:B:90:ARG:HH22	2:B:100:ASN:HD21	1.14	0.93
2:B:111[A]:VAL:HG11	2:B:125:TYR:HB2	1.51	0.93
2:D:134:ALA:HB3	3:D:187:GOL:H11	1.49	0.93
2:B:44:LYS:HG2	3:B:189:GOL:O2	1.70	0.92
2:D:51:GLU:HG2	5:D:257:HOH:O	1.69	0.92
1:C:43:ARG:HH22	1:C:44:LYS:HZ1	1.13	0.90
1:A:3:LYS:CG	1:A:4:GLY:H	1.82	0.90
1:A:64:GLY:HA3	5:A:299:HOH:O	1.70	0.90
1:A:129:LYS:HG3	2:B:146:ASN:HD21	1.35	0.90
2:D:135:PRO:HG2	5:D:330:HOH:O	1.74	0.87
2:B:164:LYS:HD2	2:B:183:TRP:HB3	1.56	0.87
2:D:162:VAL:CG2	2:D:163:ARG:N	2.17	0.86
1:A:17:LEU:HD23	5:A:248:HOH:O	1.76	0.85
1:A:7:GLU:CG	1:A:67:ARG:NH2	2.32	0.84
2:B:154:ARG:NH1	3:B:188:GOL:H11	1.90	0.84
2:B:154:ARG:NH1	3:B:188:GOL:C1	2.41	0.84
2:B:44:LYS:HB3	3:B:189:GOL:H2	1.57	0.84
1:A:83:LEU:HD22	2:D:15:ILE:HG23	1.60	0.83
2:B:47:GLY:HA2	5:B:423:HOH:O	1.75	0.83
2:D:134:ALA:O	3:D:187:GOL:H12	1.79	0.83
2:D:163:ARG:CG	3:D:187:GOL:H32	2.08	0.82
3:B:189:GOL:H12	5:B:354:HOH:O	1.78	0.82
1:C:43:ARG:NH2	1:C:44:LYS:HE2	1.94	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:163:ARG:HD3	2:B:165:LYS:HB3	1.59	0.82
2:D:134:ALA:HB3	3:D:187:GOL:C1	2.09	0.82
2:D:163:ARG:CB	3:D:187:GOL:C3	2.57	0.81
1:A:46:ARG:NH2	1:A:46:ARG:CB	2.37	0.81
2:D:108:ARG:HG2	2:D:108:ARG:HH11	1.44	0.81
2:D:162:VAL:HG22	2:D:163:ARG:H	1.42	0.80
2:D:137:ILE:HD11	5:D:330:HOH:O	1.81	0.80
1:A:58[B]:ARG:CD	5:A:547:HOH:O	2.24	0.79
1:A:129:LYS:HG3	2:B:146:ASN:ND2	1.97	0.79
2:B:163:ARG:NH1	2:B:163:ARG:HG2	1.99	0.78
2:D:162:VAL:O	2:D:163:ARG:HD2	1.84	0.78
2:D:163:ARG:HB2	3:D:187:GOL:C3	2.13	0.78
2:D:111[A]:VAL:HG12	2:D:125:TYR:HB2	1.66	0.78
1:A:46:ARG:HH21	1:A:46:ARG:HB2	1.47	0.77
1:A:59:GLY:C	1:A:60:MET:HE2	2.05	0.77
2:B:163:ARG:HH11	2:B:163:ARG:CG	1.98	0.76
2:D:151[A]:GLU:HG2	3:D:188:GOL:H2	1.67	0.76
2:B:44:LYS:HB3	3:B:189:GOL:C2	2.15	0.76
2:D:66:GLU:HG2	5:D:456:HOH:O	1.86	0.76
1:C:129[A]:LYS:HG3	2:D:146:ASN:HD21	1.51	0.75
1:C:43:ARG:HD2	5:C:247:HOH:O	1.87	0.75
1:A:142:MET:HG2	5:A:390:HOH:O	1.86	0.74
2:B:117:LYS:HE2	1:C:157:LEU:HD13	1.69	0.73
2:D:108:ARG:HH11	2:D:108:ARG:CG	2.02	0.72
3:C:171:GOL:H11	5:C:211:HOH:O	1.90	0.72
1:C:169:ILE:HD12	2:D:167:VAL:HG21	1.73	0.71
1:C:142:MET:HE2	5:C:533:HOH:O	1.91	0.70
2:B:135:PRO:O	3:B:187:GOL:H11	1.91	0.70
2:D:150:VAL:HG23	3:D:188:GOL:H32	1.72	0.69
1:A:83:LEU:HD13	2:D:15:ILE:HD13	1.74	0.69
1:C:129[A]:LYS:CG	2:D:146:ASN:ND2	2.56	0.69
2:B:44:LYS:CG	3:B:189:GOL:O2	2.40	0.69
2:B:163:ARG:HD3	2:B:165:LYS:CB	2.23	0.68
2:D:165:LYS:HZ1	2:D:180:MET:HB3	1.57	0.68
1:C:129[A]:LYS:CG	2:D:146:ASN:HD21	2.07	0.67
2:D:163:ARG:HG2	3:D:187:GOL:H32	1.75	0.67
1:C:167:ARG:NH2	2:D:108:ARG:HH22	1.93	0.67
5:A:324:HOH:O	2:B:160:HIS:HE1	1.76	0.67
2:B:163:ARG:HG2	2:B:163:ARG:HH11	1.55	0.67
2:D:163:ARG:HB3	3:D:187:GOL:H32	1.74	0.67
2:B:154:ARG:HD3	3:B:188:GOL:H12	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:324:HOH:O	2:B:160:HIS:CE1	2.48	0.66
2:D:111[A]:VAL:CG1	2:D:125:TYR:CB	2.64	0.66
2:B:8:ILE:HG13	2:B:69:VAL:HG13	1.78	0.66
2:B:47:GLY:CA	5:B:423:HOH:O	2.37	0.66
2:D:150:VAL:CG2	3:D:188:GOL:H31	2.24	0.66
2:B:154:ARG:HH11	3:B:188:GOL:C1	2.06	0.65
2:D:172:ARG:HD2	5:D:417:HOH:O	1.95	0.65
1:C:142:MET:HB3	5:C:533:HOH:O	1.94	0.65
2:D:139:HIS:HE1	5:D:216:HOH:O	1.80	0.65
2:D:46:ARG:HH21	2:D:46:ARG:HB3	1.62	0.65
1:C:129[A]:LYS:HG2	2:D:146:ASN:ND2	2.11	0.64
1:C:167:ARG:CZ	2:D:108:ARG:NH2	2.60	0.64
2:B:129:PRO:HB2	3:B:189:GOL:C3	2.29	0.63
2:B:111[A]:VAL:O	2:B:111[A]:VAL:HG13	1.99	0.63
2:B:44:LYS:HG2	3:B:189:GOL:HO2	1.65	0.62
1:C:100:LEU:N	1:C:100:LEU:HD23	2.15	0.62
1:C:38:ARG:HG2	1:C:38:ARG:HH11	1.65	0.61
2:B:111[A]:VAL:HG12	2:B:125:TYR:O	2.00	0.61
2:D:164:LYS:H	2:D:164:LYS:CE	2.11	0.61
3:A:171:GOL:H31	5:D:255:HOH:O	2.01	0.61
1:A:59:GLY:C	1:A:60:MET:CE	2.70	0.61
2:B:67:LYS:CE	2:B:107:GLU:OE2	2.49	0.60
2:D:109:GLY:C	5:D:541:HOH:O	2.38	0.60
2:D:111[A]:VAL:HG13	2:D:111[A]:VAL:O	2.02	0.60
1:C:170:GLN:HG3	1:C:170:GLN:OXT	2.00	0.60
1:A:143:ASP:HB3	5:A:348:HOH:O	2.01	0.59
1:C:17:LEU:HD21	1:C:78:GLY:HA3	1.82	0.59
1:A:59:GLY:O	1:A:60:MET:HE1	2.03	0.59
2:D:108:ARG:CG	2:D:108:ARG:NH1	2.65	0.59
1:A:118:GLU:OE2	1:A:145:HIS:HD2	1.85	0.59
1:C:67[A]:ARG:HB3	5:C:464:HOH:O	2.01	0.59
2:B:49:ASP:OD1	2:B:49:ASP:O	2.20	0.59
2:B:40:LEU:O	3:B:190:GOL:C1	2.48	0.59
1:C:144:ASN:CB	5:C:471:HOH:O	2.38	0.59
2:B:117:LYS:CD	5:B:347:HOH:O	2.52	0.58
3:D:188:GOL:H11	5:D:452:HOH:O	2.04	0.58
1:C:43:ARG:HG2	1:C:44:LYS:HD2	1.85	0.58
1:C:169:ILE:CD1	2:D:167:VAL:HG11	2.22	0.58
2:D:111[A]:VAL:HG12	2:D:125:TYR:O	2.02	0.58
2:D:74:LYS:HD2	5:D:236:HOH:O	2.05	0.57
2:D:160:HIS:CD2	5:D:381:HOH:O	2.56	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:60:MET:HE2	1:A:60:MET:N	2.18	0.57
1:A:76:ILE:HG21	2:D:15:ILE:HD11	1.85	0.57
1:C:167:ARG:NH2	2:D:108:ARG:NH2	2.52	0.57
1:C:134:VAL:O	1:C:138[A]:ARG:HG3	2.06	0.56
1:A:128:LEU:HD23	1:A:128:LEU:H	1.71	0.56
2:B:154:ARG:NH1	3:B:188:GOL:O1	2.39	0.56
1:A:169:ILE:O	1:A:170:GLN:HB3	2.04	0.56
1:C:100:LEU:HD23	1:C:109[A]:VAL:O	2.07	0.55
1:A:20:GLU:OE2	1:A:20:GLU:CA	2.53	0.55
2:B:90:ARG:HH22	2:B:100:ASN:ND2	1.94	0.55
1:C:67[B]:ARG:HG2	1:C:68:GLY:N	2.21	0.55
2:B:109:GLY:C	5:B:542:HOH:O	2.44	0.55
2:B:127[A]:LEU:HD12	2:B:131:ILE:HG22	1.89	0.55
1:A:104:ARG:NH2	1:A:139:GLY:O	2.39	0.55
1:C:38:ARG:HG2	1:C:38:ARG:NH1	2.22	0.55
2:D:46:ARG:HH21	2:D:46:ARG:CB	2.19	0.54
1:A:128:LEU:HD23	1:A:128:LEU:N	2.22	0.54
1:C:169:ILE:HD11	2:D:167:VAL:CG1	2.24	0.54
1:A:129:LYS:CG	2:B:146:ASN:ND2	2.71	0.54
1:C:67[A]:ARG:HG2	1:C:68:GLY:N	2.23	0.54
1:A:98:LYS:CE	5:A:363:HOH:O	2.55	0.54
1:A:128:LEU:HB3	5:A:230:HOH:O	2.07	0.53
2:D:46:ARG:CB	2:D:46:ARG:NH2	2.71	0.53
1:C:144:ASN:HB3	5:C:524:HOH:O	2.07	0.53
2:B:117:LYS:HE2	1:C:157:LEU:CD1	2.35	0.53
2:B:165:LYS:CG	2:B:165:LYS:O	2.57	0.53
2:D:9:LYS:HB3	2:D:69:VAL:O	2.09	0.53
1:A:3:LYS:CG	1:A:4:GLY:N	2.45	0.53
1:A:46:ARG:HB3	1:A:46:ARG:CZ	2.37	0.53
1:C:54:TYR:O	1:C:58:ARG:HG3	2.08	0.53
1:C:167:ARG:CZ	2:D:108:ARG:HH22	2.21	0.52
2:B:109:GLY:HA2	5:B:542:HOH:O	2.09	0.52
1:C:128:LEU:HD23	1:C:128:LEU:H	1.72	0.52
2:B:139:HIS:HE1	5:B:207:HOH:O	1.93	0.52
1:C:100:LEU:HD23	1:C:100:LEU:H	1.73	0.51
2:B:67:LYS:HE3	2:B:107:GLU:OE2	2.10	0.51
1:A:104:ARG:HD2	1:A:118:GLU:OE1	2.11	0.51
1:C:60:MET:HE2	1:C:60:MET:HA	1.92	0.51
1:C:129[A]:LYS:HG3	2:D:146:ASN:ND2	2.17	0.51
2:D:159:SER:HB3	2:D:163:ARG:O	2.11	0.51
1:C:129[A]:LYS:HD2	2:D:144:GLU:HA	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:117:LYS:HD3	5:B:347:HOH:O	2.11	0.50
2:D:163:ARG:HB3	3:D:187:GOL:C3	2.36	0.50
1:C:43:ARG:NH2	1:C:44:LYS:HZ1	1.84	0.50
1:C:67[A]:ARG:CG	1:C:68:GLY:N	2.74	0.50
5:B:248:HOH:O	1:C:83:LEU:HD23	2.11	0.50
2:D:134:ALA:CB	3:D:187:GOL:H11	2.31	0.50
2:D:159:SER:O	2:D:163:ARG:O	2.29	0.50
2:D:171:THR:HB	2:D:176[B]:VAL:HG12	1.92	0.50
2:B:44:LYS:HB3	3:B:189:GOL:O2	2.11	0.50
1:A:7:GLU:CD	1:A:67:ARG:HH21	2.12	0.50
1:C:43:ARG:CZ	1:C:44:LYS:NZ	2.64	0.49
1:C:135:GLU:HG3	5:C:277:HOH:O	2.12	0.49
2:D:23:ASP:OD2	2:D:25:GLU:HG2	2.13	0.49
2:D:172:ARG:CD	5:D:417:HOH:O	2.59	0.49
2:D:9:LYS:HG3	2:D:69:VAL:HG13	1.95	0.49
2:D:111[A]:VAL:CG1	2:D:111[A]:VAL:O	2.60	0.49
2:D:163:ARG:C	2:D:165:LYS:H	2.16	0.49
1:A:145:HIS:HE1	5:A:195:HOH:O	1.96	0.48
1:C:77:ALA:HA	5:C:453:HOH:O	2.12	0.48
2:B:59[B]:ILE:HG23	2:B:99:TYR:HD1	1.79	0.48
2:D:164:LYS:HB3	5:D:432:HOH:O	2.14	0.48
2:B:127[A]:LEU:CD1	2:B:131:ILE:HG22	2.44	0.47
2:B:90:ARG:NH2	2:B:100:ASN:HD21	1.97	0.47
1:C:138[A]:ARG:NE	5:C:369:HOH:O	2.34	0.47
2:B:109:GLY:CA	5:B:542:HOH:O	2.62	0.47
2:B:49:ASP:HB3	5:B:465:HOH:O	2.13	0.47
1:C:29:ASP:OD1	1:C:29:ASP:C	2.52	0.47
1:C:169:ILE:HD13	2:D:180:MET:SD	2.55	0.47
1:A:59:GLY:O	1:A:60:MET:CE	2.62	0.47
1:C:23:PHE:CE1	1:C:46:ARG:HG2	2.50	0.46
1:C:12:LYS:CE	1:C:60:MET:SD	2.90	0.46
2:B:129:PRO:HB2	3:B:189:GOL:H31	1.96	0.46
2:D:159:SER:O	2:D:162:VAL:HG22	2.16	0.46
1:A:167:ARG:O	1:A:167:ARG:NE	2.49	0.46
2:D:165:LYS:HZ1	2:D:180:MET:HE2	1.79	0.46
1:C:60:MET:HA	1:C:60:MET:CE	2.46	0.46
1:C:43:ARG:O	1:C:44:LYS:HB2	2.16	0.45
1:C:128:LEU:HD23	1:C:128:LEU:N	2.30	0.45
1:C:167:ARG:HH21	2:D:108:ARG:HH22	1.64	0.45
2:D:46:ARG:NH2	2:D:46:ARG:HB2	2.30	0.45
2:B:111[A]:VAL:HG12	2:B:125:TYR:HB2	1.85	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:59:GLY:O	1:C:67[B]:ARG:NH2	2.49	0.45
2:B:44:LYS:CB	3:B:189:GOL:C2	2.92	0.45
1:A:143:ASP:CB	5:A:348:HOH:O	2.63	0.45
2:B:111[A]:VAL:CG1	2:B:111[A]:VAL:O	2.63	0.45
1:C:169:ILE:O	1:C:170:GLN:HB3	2.16	0.45
2:D:44:LYS:HE2	2:D:44:LYS:HB2	1.54	0.45
2:B:44:LYS:CB	3:B:189:GOL:O2	2.65	0.45
2:B:154:ARG:CZ	3:B:188:GOL:H11	2.44	0.45
2:D:165:LYS:HZ1	2:D:180:MET:CE	2.30	0.45
1:C:115:ARG:HD3	5:C:196:HOH:O	2.16	0.44
2:D:134:ALA:C	3:D:187:GOL:H12	2.36	0.44
2:D:135:PRO:HG2	2:D:137:ILE:HD11	1.99	0.44
2:B:126[A]:ARG:HD2	5:B:212:HOH:O	2.16	0.44
2:B:125:TYR:CE1	2:B:129:PRO:HA	2.53	0.44
1:C:167:ARG:NE	2:D:108:ARG:NH2	2.65	0.44
2:D:151[A]:GLU:HG2	3:D:188:GOL:C2	2.44	0.43
1:A:104:ARG:NH2	1:A:139:GLY:C	2.72	0.43
2:B:117:LYS:NZ	5:B:379:HOH:O	2.49	0.43
1:A:74:GLU:HA	5:A:255:HOH:O	2.18	0.43
2:D:165:LYS:NZ	2:D:180:MET:CE	2.81	0.43
2:B:8:ILE:HD12	2:B:30:LEU:HD23	2.00	0.43
2:D:9:LYS:HD2	2:D:9:LYS:HA	1.71	0.43
2:D:109:GLY:CA	5:D:541:HOH:O	2.66	0.43
1:A:56:ALA:HB1	1:A:71:ALA:HB3	2.00	0.43
2:B:135:PRO:HG2	2:B:137:ILE:HD11	2.01	0.42
1:A:60:MET:CE	1:A:60:MET:HA	2.50	0.42
1:A:98:LYS:NZ	5:A:363:HOH:O	2.30	0.42
1:A:167:ARG:HG3	1:A:167:ARG:HH21	1.84	0.42
2:B:172:ARG:HD2	5:B:282:HOH:O	2.18	0.42
1:C:29:ASP:OD1	1:C:31:SER:HB3	2.19	0.42
2:B:74:LYS:HE3	2:B:78:SER:OG	2.20	0.42
2:B:135:PRO:O	3:B:187:GOL:C1	2.63	0.42
1:A:167:ARG:HA	1:A:167:ARG:HD2	1.56	0.42
2:D:79:SER:HB3	5:D:273:HOH:O	2.20	0.42
3:B:190:GOL:H2	5:B:401:HOH:O	2.19	0.42
5:B:231:HOH:O	2:D:139:HIS:HD2	2.02	0.41
1:A:162:GLU:HB3	2:B:182:ASP:OD1	2.20	0.41
1:C:91:ASP:OD2	1:C:95:LYS:HE2	2.20	0.41
2:B:44:LYS:HA	2:B:45:PRO:HD2	1.90	0.41
1:A:128:LEU:CB	5:A:230:HOH:O	2.66	0.41
2:D:104:ASP:CG	2:D:176[B]:VAL:CG2	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:111[A]:VAL:HG12	2:D:125:TYR:CB	2.42	0.41
1:A:134:VAL:O	1:A:138[A]:ARG:HG3	2.20	0.41
1:A:129:LYS:NZ	1:A:129:LYS:CB	2.84	0.40
1:A:168:SER:HB2	2:B:108:ARG:NH1	2.35	0.40
2:D:162:VAL:O	2:D:163:ARG:CD	2.62	0.40
3:A:171:GOL:H32	5:A:548:HOH:O	2.22	0.40
2:D:80:VAL:O	5:D:440:HOH:O	2.22	0.40
2:B:138:VAL:HG22	2:B:167:VAL:HB	2.03	0.40
2:B:104:ASP:O	2:B:108:ARG:CG	2.53	0.40
3:B:190:GOL:C2	5:B:401:HOH:O	2.69	0.40
1:C:100:LEU:N	1:C:100:LEU:CD2	2.84	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	172/190 (90%)	169 (98%)	3 (2%)	0	100	100
1	C	165/190 (87%)	164 (99%)	1 (1%)	0	100	100
2	B	186/186 (100%)	180 (97%)	6 (3%)	0	100	100
2	D	185/186 (100%)	179 (97%)	6 (3%)	0	100	100
All	All	708/752 (94%)	692 (98%)	16 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	136/148 (92%)	132 (97%)	4 (3%)	37	20
1	C	132/148 (89%)	128 (97%)	4 (3%)	36	19
2	B	158/154 (103%)	152 (96%)	6 (4%)	28	12
2	D	157/154 (102%)	145 (92%)	12 (8%)	11	2
All	All	583/604 (96%)	557 (96%)	26 (4%)	25	9

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	GLU
1	A	105	ARG
1	A	153	ASP
1	A	167	ARG
2	B	9	LYS
2	B	44	LYS
2	B	132	ASP
2	B	160	HIS
2	B	163	ARG
2	B	182	ASP
1	C	20	GLU
1	C	100	LEU
1	C	142	MET
1	C	153	ASP
2	D	9	LYS
2	D	15	ILE
2	D	44	LYS
2	D	56[A]	LEU
2	D	56[B]	LEU
2	D	108	ARG
2	D	127[A]	LEU
2	D	127[B]	LEU
2	D	132	ASP
2	D	157[A]	ARG
2	D	157[B]	ARG
2	D	164	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	144	ASN
1	A	145	HIS
2	B	100	ASN
2	B	139	HIS
2	B	146	ASN
2	B	160	HIS
1	C	144	ASN
2	D	139	HIS
2	D	146	ASN
2	D	160	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 2 are monoatomic - leaving 10 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	GOL	A	172	-	5,5,5	0.42	0	5,5,5	0.29	0
3	GOL	D	188	-	5,5,5	0.27	0	5,5,5	0.75	0
3	GOL	A	171	-	5,5,5	0.22	0	5,5,5	0.66	0
3	GOL	B	189	-	5,5,5	0.41	0	5,5,5	0.59	0
3	GOL	B	187	-	5,5,5	0.33	0	5,5,5	0.68	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GOL	D	187	-	5,5,5	0.41	0	5,5,5	0.66	0
3	GOL	B	190	-	5,5,5	0.80	0	5,5,5	1.36	0
3	GOL	D	189	-	5,5,5	0.34	0	5,5,5	0.41	0
3	GOL	B	188	-	5,5,5	0.44	0	5,5,5	0.88	0
3	GOL	C	171	-	5,5,5	0.34	0	5,5,5	1.39	2 (40%)

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	GOL	A	172	-	-	2/4/4/4	-
3	GOL	D	188	-	-	2/4/4/4	-
3	GOL	A	171	-	-	3/4/4/4	-
3	GOL	B	189	-	-	2/4/4/4	-
3	GOL	B	187	-	-	2/4/4/4	-
3	GOL	D	187	-	-	2/4/4/4	-
3	GOL	B	190	-	-	4/4/4/4	-
3	GOL	D	189	-	-	2/4/4/4	-
3	GOL	B	188	-	-	2/4/4/4	-
3	GOL	C	171	-	-	0/4/4/4	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	171	GOL	O1-C1-C2	-2.08	101.02	110.38
3	C	171	GOL	C3-C2-C1	-2.03	104.36	111.80

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	172	GOL	C1-C2-C3-O3
3	B	188	GOL	O1-C1-C2-C3
3	B	189	GOL	O1-C1-C2-C3
3	B	190	GOL	C1-C2-C3-O3
3	D	187	GOL	O1-C1-C2-C3

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Mol	Chain	Res	Type	Atoms
3	D	188	GOL	O1-C1-C2-C3
3	D	189	GOL	C1-C2-C3-O3
3	B	188	GOL	O1-C1-C2-O2
3	B	189	GOL	O1-C1-C2-O2
3	A	171	GOL	C1-C2-C3-O3
3	B	187	GOL	C1-C2-C3-O3
3	B	190	GOL	O1-C1-C2-C3
3	A	171	GOL	O2-C2-C3-O3
3	B	190	GOL	O1-C1-C2-O2
3	B	190	GOL	O2-C2-C3-O3
3	D	187	GOL	O1-C1-C2-O2
3	A	172	GOL	O2-C2-C3-O3
3	B	187	GOL	O2-C2-C3-O3
3	D	188	GOL	O1-C1-C2-O2
3	D	189	GOL	O2-C2-C3-O3
3	A	171	GOL	O1-C1-C2-C3

There are no ring outliers.

8 monomers are involved in 46 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	188	GOL	7	0
3	A	171	GOL	2	0
3	B	189	GOL	11	0
3	B	187	GOL	2	0
3	D	187	GOL	13	0
3	B	190	GOL	4	0
3	B	188	GOL	6	0
3	C	171	GOL	1	0

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	168/190 (88%)	1.05	26 (15%) 6 5	6, 23, 38, 46	6 (3%)
1	C	161/190 (84%)	0.96	28 (17%) 5 4	6, 23, 39, 47	6 (3%)
2	B	180/186 (96%)	1.08	32 (17%) 4 4	7, 19, 42, 49	8 (4%)
2	D	178/186 (95%)	1.14	37 (20%) 3 2	7, 20, 41, 51	9 (5%)
All	All	687/752 (91%)	1.06	123 (17%) 4 4	6, 21, 40, 51	29 (4%)

All (123) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	8	ILE	6.9
2	B	127[A]	LEU	6.1
2	B	160	HIS	5.5
1	C	19	VAL	5.5
2	D	162	VAL	5.4
2	D	183	TRP	5.2
1	A	19	VAL	5.0
1	C	11	CYS	5.0
2	D	160	HIS	4.7
2	B	163	ARG	4.5
2	B	46	ARG	4.3
1	A	23[A]	PHE	4.3
2	B	7	PRO	4.1
1	A	170	GLN	4.1
2	B	49	ASP	4.1
1	C	167	ARG	4.1
2	D	161	SER	4.0
1	C	27	CYS	4.0
1	A	3	LYS	4.0
2	B	136	PHE	4.0
1	C	20	GLU	3.9

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Mol	Chain	Res	Type	RSRZ
2	B	48	ALA	3.9
1	A	7	GLU	3.8
2	D	164	LYS	3.8
1	A	169	ILE	3.6
1	C	62	CYS	3.6
1	A	167	ARG	3.6
2	D	165	LYS	3.5
1	A	114	GLY	3.5
2	B	159	SER	3.5
1	A	168	SER	3.4
2	D	24	VAL	3.4
1	C	10	GLY	3.4
1	C	169	ILE	3.4
2	D	163	ARG	3.4
1	C	28	PHE	3.4
2	B	50	PHE	3.4
1	A	113	GLY	3.4
2	B	161	SER	3.3
1	A	115	ARG	3.3
1	A	27	CYS	3.2
1	A	103	VAL	3.2
2	D	51	GLU	3.2
2	D	130	GLY	3.2
2	B	73	ALA	3.1
1	A	20	GLU	3.1
2	B	24	VAL	3.1
2	D	15	ILE	3.0
2	B	82	VAL	3.0
1	C	44	LYS	3.0
2	B	183	TRP	3.0
2	D	9	LYS	3.0
1	C	142	MET	3.0
2	D	46	ARG	2.9
2	D	78	SER	2.9
1	C	17	LEU	2.8
2	B	162	VAL	2.8
1	C	170	GLN	2.8
1	A	142	MET	2.8
2	B	45	PRO	2.8
2	B	47	GLY	2.8
1	A	144	ASN	2.7
2	D	118	PHE	2.7

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Mol	Chain	Res	Type	RSRZ
2	B	131	ILE	2.7
2	D	42[A]	VAL	2.7
2	B	130	GLY	2.7
2	D	47	GLY	2.7
2	D	25	GLU	2.7
2	D	111[A]	VAL	2.7
2	D	48	ALA	2.6
1	C	58	ARG	2.6
1	C	94[A]	ARG	2.6
2	B	118	PHE	2.5
2	D	32	SER	2.6
1	A	64	GLY	2.5
2	D	77	GLY	2.5
1	C	23	PHE	2.5
2	B	12	GLY	2.5
2	B	126[A]	ARG	2.5
2	B	158	LEU	2.4
2	B	33	CYS	2.4
1	C	31	SER	2.4
1	A	8	VAL	2.4
2	D	43	GLU	2.4
2	D	69	VAL	2.4
1	C	67[A]	ARG	2.4
1	C	70	ALA	2.4
2	D	79	SER	2.4
2	D	136	PHE	2.4
1	A	4	GLY	2.4
1	C	25	GLU	2.3
1	A	70	ALA	2.3
2	D	71	GLU	2.3
2	D	134	ALA	2.3
1	C	59	GLY	2.3
1	C	164	ARG	2.3
2	D	131	ILE	2.3
2	D	17	ASP	2.3
2	B	44	LYS	2.2
1	A	18	GLY	2.2
2	D	33[A]	CYS	2.2
2	D	44	LYS	2.2
2	D	16	GLY	2.2
1	C	46	ARG	2.2
2	B	157[A]	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
2	D	49	ASP	2.2
1	A	59	GLY	2.1
1	A	100	LEU	2.1
1	C	64	GLY	2.1
1	C	65	GLU	2.1
2	B	25	GLU	2.1
1	C	35	ASN	2.1
1	C	144	ASN	2.1
2	D	73	ALA	2.1
2	B	164	LYS	2.1
2	B	111[A]	VAL	2.1
2	D	13	VAL	2.1
1	A	105	ARG	2.0
1	A	164	ARG	2.0
2	D	80	VAL	2.0
2	B	51	GLU	2.0
1	C	168	SER	2.0
1	A	39	ILE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

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(Å ²)	Q<0.9
3	GOL	A	172	6/6	0.61	0.20	39,40,41,42	0
3	GOL	B	187	6/6	0.73	0.24	42,45,46,47	0
3	GOL	D	188	6/6	0.73	0.20	36,39,40,41	0
3	GOL	B	189	6/6	0.76	0.16	33,37,38,40	0
3	GOL	B	188	6/6	0.76	0.19	37,38,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	GOL	B	190	6/6	0.77	0.21	24,29,31,32	0
3	GOL	D	189	6/6	0.77	0.15	41,43,44,45	0
3	GOL	C	171	6/6	0.80	0.16	24,34,35,36	0
3	GOL	D	187	6/6	0.82	0.17	38,39,41,41	0
3	GOL	A	171	6/6	0.85	0.14	26,35,36,38	0
4	CL	B	191	1/1	0.94	0.08	26,26,26,26	0
4	CL	D	190	1/1	0.96	0.07	26,26,26,26	0

6.5 Other polymers [i](#)

There are no such residues in this entry.