Full wwPDB X-ray Structure Validation Report ⓘ

Jun 24, 2024 – 02:08 PM EDT

PDB ID	:	6EY0
Title	:	N-terminal part (residues 30-212) of PorM with the llama nanobody nb01
Authors	:	Leone, P.; Roche, J.; Cambillau, C.; Roussel, A.
Deposited on	:	2017-11-10
Resolution	:	2.40 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:

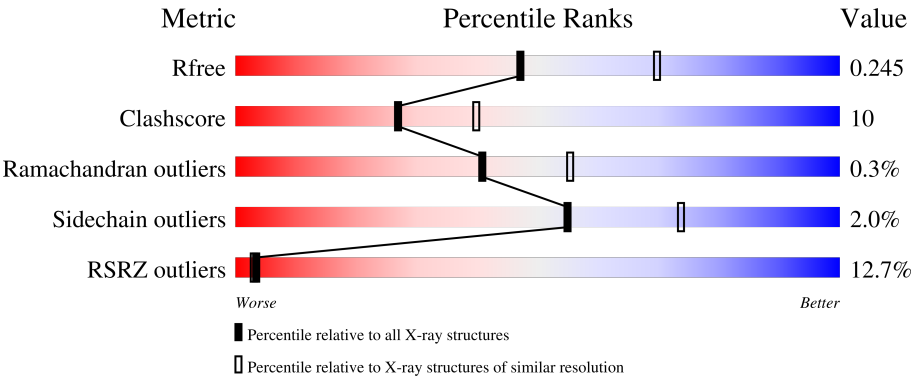
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 2.40 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}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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 <=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	197	3% 56% 16% · 25%
1	B	197	6% 61% 14% · 25%
1	C	197	5% 65% 9% · 25%
1	D	197	4% 57% 15% · 27%
2	E	134	34% 71% 22% · 7%

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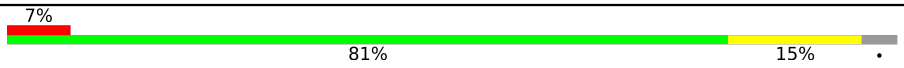
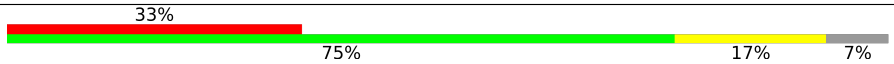
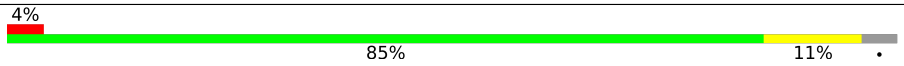
Mol	Chain	Length	Quality of chain
2	G	134	
2	H	134	
3	F	136	

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 8729 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 T9SS component cytoplasmic membrane protein PorM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	147	Total	C	N	O	S	0	0	0
			1150	722	198	226	4			
1	B	148	Total	C	N	O	S	0	0	0
			1157	726	199	228	4			
1	C	147	Total	C	N	O	S	0	0	0
			1150	722	198	226	4			
1	D	144	Total	C	N	O	S	0	0	0
			1126	708	194	220	4			

There are 92 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	21	MET	-	initiating methionine	UNP A0A1R4DSC1
A	22	GLY	-	expression tag	UNP A0A1R4DSC1
A	23	HIS	-	expression tag	UNP A0A1R4DSC1
A	24	HIS	-	expression tag	UNP A0A1R4DSC1
A	25	HIS	-	expression tag	UNP A0A1R4DSC1
A	26	HIS	-	expression tag	UNP A0A1R4DSC1
A	27	HIS	-	expression tag	UNP A0A1R4DSC1
A	28	HIS	-	expression tag	UNP A0A1R4DSC1
A	29	SER	-	expression tag	UNP A0A1R4DSC1
A	30	SER	-	expression tag	UNP A0A1R4DSC1
A	31	GLY	-	expression tag	UNP A0A1R4DSC1
A	32	VAL	-	expression tag	UNP A0A1R4DSC1
A	33	ASP	-	expression tag	UNP A0A1R4DSC1
A	34	LEU	-	expression tag	UNP A0A1R4DSC1
A	35	GLY	-	expression tag	UNP A0A1R4DSC1
A	36	THR	-	expression tag	UNP A0A1R4DSC1
A	37	GLU	-	expression tag	UNP A0A1R4DSC1
A	38	ASN	-	expression tag	UNP A0A1R4DSC1
A	39	LEU	-	expression tag	UNP A0A1R4DSC1
A	40	TYR	-	expression tag	UNP A0A1R4DSC1
A	41	PHE	-	expression tag	UNP A0A1R4DSC1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	42	GLN	-	expression tag	UNP A0A1R4DSC1
A	43	SER	-	expression tag	UNP A0A1R4DSC1
B	21	MET	-	initiating methionine	UNP A0A1R4DSC1
B	22	GLY	-	expression tag	UNP A0A1R4DSC1
B	23	HIS	-	expression tag	UNP A0A1R4DSC1
B	24	HIS	-	expression tag	UNP A0A1R4DSC1
B	25	HIS	-	expression tag	UNP A0A1R4DSC1
B	26	HIS	-	expression tag	UNP A0A1R4DSC1
B	27	HIS	-	expression tag	UNP A0A1R4DSC1
B	28	HIS	-	expression tag	UNP A0A1R4DSC1
B	29	SER	-	expression tag	UNP A0A1R4DSC1
B	30	SER	-	expression tag	UNP A0A1R4DSC1
B	31	GLY	-	expression tag	UNP A0A1R4DSC1
B	32	VAL	-	expression tag	UNP A0A1R4DSC1
B	33	ASP	-	expression tag	UNP A0A1R4DSC1
B	34	LEU	-	expression tag	UNP A0A1R4DSC1
B	35	GLY	-	expression tag	UNP A0A1R4DSC1
B	36	THR	-	expression tag	UNP A0A1R4DSC1
B	37	GLU	-	expression tag	UNP A0A1R4DSC1
B	38	ASN	-	expression tag	UNP A0A1R4DSC1
B	39	LEU	-	expression tag	UNP A0A1R4DSC1
B	40	TYR	-	expression tag	UNP A0A1R4DSC1
B	41	PHE	-	expression tag	UNP A0A1R4DSC1
B	42	GLN	-	expression tag	UNP A0A1R4DSC1
B	43	SER	-	expression tag	UNP A0A1R4DSC1
C	21	MET	-	initiating methionine	UNP A0A1R4DSC1
C	22	GLY	-	expression tag	UNP A0A1R4DSC1
C	23	HIS	-	expression tag	UNP A0A1R4DSC1
C	24	HIS	-	expression tag	UNP A0A1R4DSC1
C	25	HIS	-	expression tag	UNP A0A1R4DSC1
C	26	HIS	-	expression tag	UNP A0A1R4DSC1
C	27	HIS	-	expression tag	UNP A0A1R4DSC1
C	28	HIS	-	expression tag	UNP A0A1R4DSC1
C	29	SER	-	expression tag	UNP A0A1R4DSC1
C	30	SER	-	expression tag	UNP A0A1R4DSC1
C	31	GLY	-	expression tag	UNP A0A1R4DSC1
C	32	VAL	-	expression tag	UNP A0A1R4DSC1
C	33	ASP	-	expression tag	UNP A0A1R4DSC1
C	34	LEU	-	expression tag	UNP A0A1R4DSC1
C	35	GLY	-	expression tag	UNP A0A1R4DSC1
C	36	THR	-	expression tag	UNP A0A1R4DSC1
C	37	GLU	-	expression tag	UNP A0A1R4DSC1

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Chain	Residue	Modelled	Actual	Comment	Reference
C	38	ASN	-	expression tag	UNP A0A1R4DSC1
C	39	LEU	-	expression tag	UNP A0A1R4DSC1
C	40	TYR	-	expression tag	UNP A0A1R4DSC1
C	41	PHE	-	expression tag	UNP A0A1R4DSC1
C	42	GLN	-	expression tag	UNP A0A1R4DSC1
C	43	SER	-	expression tag	UNP A0A1R4DSC1
D	21	MET	-	initiating methionine	UNP A0A1R4DSC1
D	22	GLY	-	expression tag	UNP A0A1R4DSC1
D	23	HIS	-	expression tag	UNP A0A1R4DSC1
D	24	HIS	-	expression tag	UNP A0A1R4DSC1
D	25	HIS	-	expression tag	UNP A0A1R4DSC1
D	26	HIS	-	expression tag	UNP A0A1R4DSC1
D	27	HIS	-	expression tag	UNP A0A1R4DSC1
D	28	HIS	-	expression tag	UNP A0A1R4DSC1
D	29	SER	-	expression tag	UNP A0A1R4DSC1
D	30	SER	-	expression tag	UNP A0A1R4DSC1
D	31	GLY	-	expression tag	UNP A0A1R4DSC1
D	32	VAL	-	expression tag	UNP A0A1R4DSC1
D	33	ASP	-	expression tag	UNP A0A1R4DSC1
D	34	LEU	-	expression tag	UNP A0A1R4DSC1
D	35	GLY	-	expression tag	UNP A0A1R4DSC1
D	36	THR	-	expression tag	UNP A0A1R4DSC1
D	37	GLU	-	expression tag	UNP A0A1R4DSC1
D	38	ASN	-	expression tag	UNP A0A1R4DSC1
D	39	LEU	-	expression tag	UNP A0A1R4DSC1
D	40	TYR	-	expression tag	UNP A0A1R4DSC1
D	41	PHE	-	expression tag	UNP A0A1R4DSC1
D	42	GLN	-	expression tag	UNP A0A1R4DSC1
D	43	SER	-	expression tag	UNP A0A1R4DSC1

- Molecule 2 is a protein called llama nanobody nb01.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	125	Total	C	N	O	S	0	0	0
			976	609	170	193	4			
2	G	129	Total	C	N	O	S	0	0	0
			1012	630	180	198	4			
2	H	124	Total	C	N	O	S	0	0	0
			968	605	169	190	4			

- Molecule 3 is a protein called llama nanobody nb01.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	F	131	Total	C	N	O	S	0	0	0
			1032	642	186	200	4			

- Molecule 4 is water.

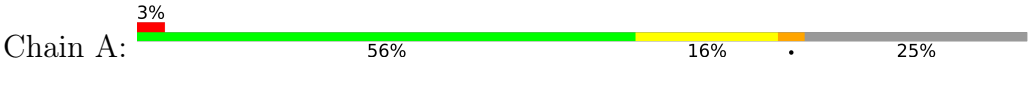
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	23	Total	O	0	0
			23	23		
4	B	14	Total	O	0	0
			14	14		
4	C	24	Total	O	0	0
			24	24		
4	D	28	Total	O	0	0
			28	28		
4	E	5	Total	O	0	0
			5	5		
4	F	31	Total	O	0	0
			31	31		
4	G	25	Total	O	0	0
			25	25		
4	H	8	Total	O	0	0
			8	8		

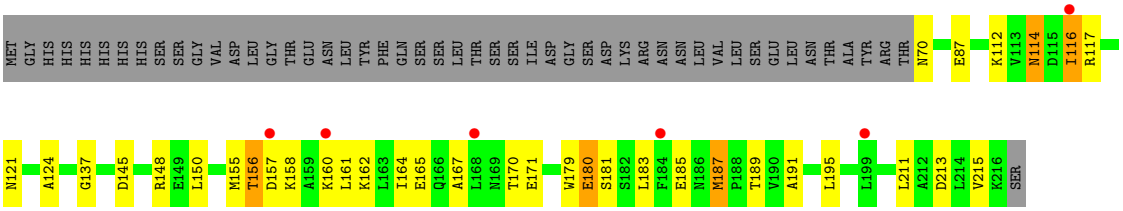
3 Residue-property plots (i)

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: T9SS component cytoplasmic membrane protein PorM

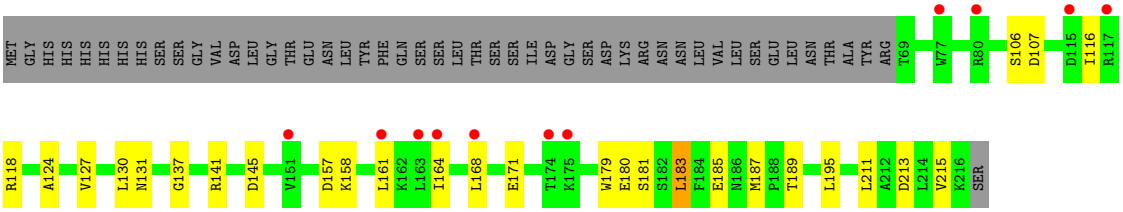
Chain A:





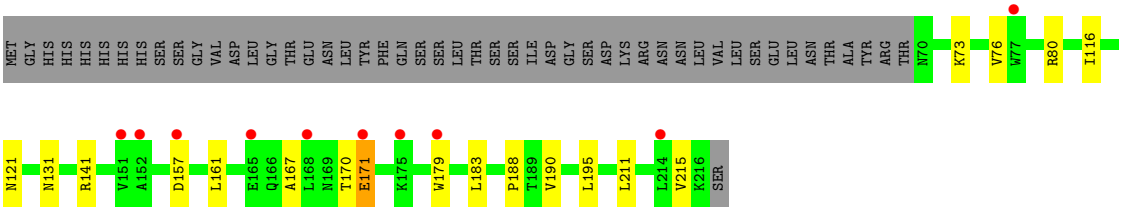
• Molecule 1: T9SS component cytoplasmic membrane protein PorM

Chain B:



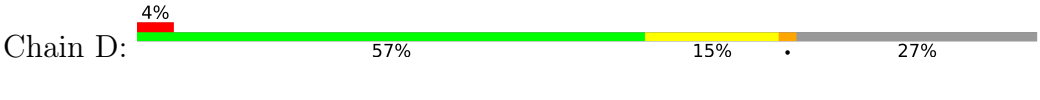
• Molecule 1: T9SS component cytoplasmic membrane protein PorM

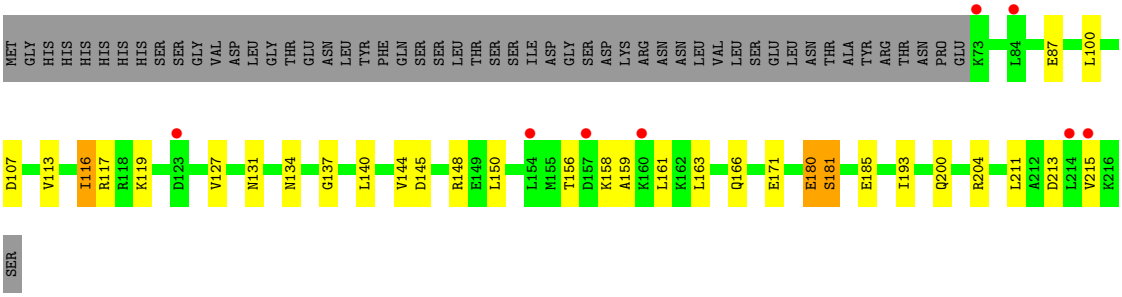
Chain C:



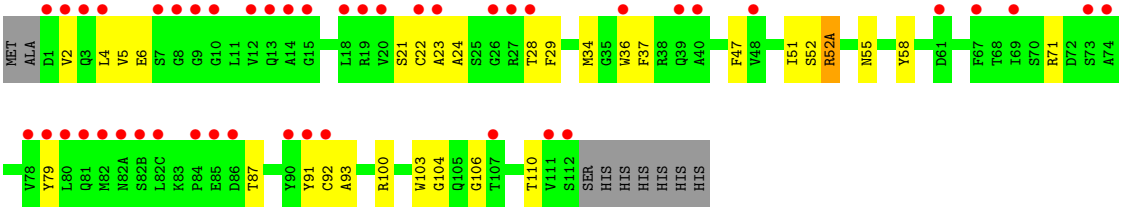
• Molecule 1: T9SS component cytoplasmic membrane protein PorM

Chain D:

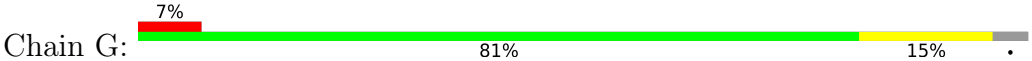


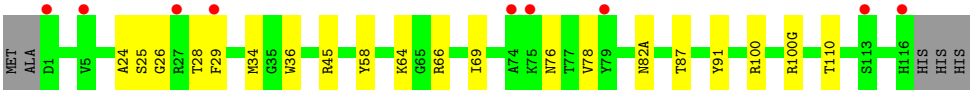


• Molecule 2: llama nanobody nb01

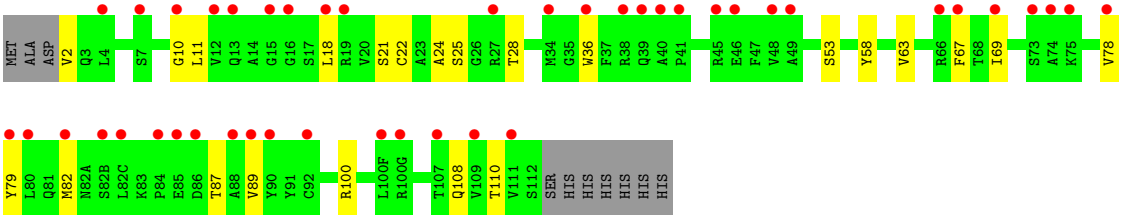


• Molecule 2: llama nanobody nb01

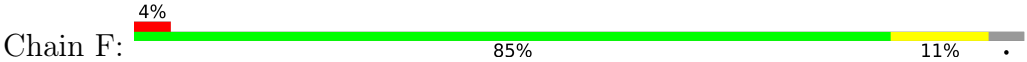


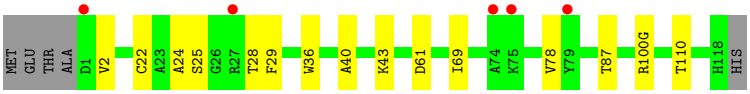


• Molecule 2: llama nanobody nb01



• Molecule 3: llama nanobody nb01





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	80.28Å 99.92Å 80.29Å 90.00° 93.83° 90.00°	Depositor
Resolution (Å)	40.00 – 2.40 42.39 – 2.24	Depositor EDS
% Data completeness (in resolution range)	98.5 (40.00-2.40) 96.6 (42.39-2.24)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.21 (at 2.24Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.213 , 0.242 0.223 , 0.245	Depositor DCC
R_{free} test set	2976 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	58.3	Xtriage
Anisotropy	0.211	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 81.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.017 for l,-k,h	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	8729	wwPDB-VP
Average B, all atoms (Å^2)	119.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.68% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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

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	0.49	0/1161	0.70	0/1562
1	B	0.49	0/1168	0.69	0/1572
1	C	0.48	0/1161	0.72	0/1562
1	D	0.50	0/1136	0.70	0/1527
2	E	0.43	0/997	0.67	0/1348
2	G	0.48	0/1036	0.68	0/1401
2	H	0.41	0/989	0.65	0/1337
3	F	0.44	0/1058	0.66	0/1431
All	All	0.47	0/8706	0.69	0/11740

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	1150	0	1196	28	0
1	B	1157	0	1203	28	0
1	C	1150	0	1196	17	0
1	D	1126	0	1177	20	0
2	E	976	0	928	41	0
2	G	1012	0	954	14	0
2	H	968	0	921	19	0
3	F	1032	0	968	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	23	0	0	0	0
4	B	14	0	0	0	0
4	C	24	0	0	1	0
4	D	28	0	0	0	0
4	E	5	0	0	2	0
4	F	31	0	0	0	0
4	G	25	0	0	0	0
4	H	8	0	0	0	0
All	All	8729	0	8543	175	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 10.

All (175) 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:B:183:LEU:CD2	1:B:195:LEU:HD21	1.74	1.16
1:B:183:LEU:HD23	1:B:195:LEU:HD21	1.20	1.11
1:D:117:ARG:HH21	1:D:193:ILE:HG21	1.14	1.10
1:A:145:ASP:OD1	1:A:171:GLU:HG3	1.49	1.09
2:H:63:VAL:HB	2:H:67:PHE:HD2	1.15	1.07
1:B:141:ARG:HB2	1:B:180:GLU:OE1	1.55	1.05
1:D:117:ARG:NH2	1:D:193:ILE:HG21	1.71	1.04
2:H:63:VAL:HB	2:H:67:PHE:CD2	1.95	1.00
2:E:22:CYS:HB2	2:E:36:TRP:CZ2	2.07	0.90
2:E:5:VAL:HB	2:E:23:ALA:HB3	1.52	0.89
2:H:67:PHE:HD1	2:H:82:MET:HA	1.42	0.84
2:E:24:ALA:CB	2:E:29:PHE:CE1	2.62	0.83
2:E:24:ALA:HB2	2:E:29:PHE:HE1	1.41	0.83
2:E:24:ALA:CB	2:E:29:PHE:HE1	1.91	0.83
2:E:22:CYS:HB2	2:E:36:TRP:HZ2	1.42	0.82
1:A:116:ILE:HG22	1:A:117:ARG:HH21	1.46	0.80
2:H:67:PHE:CD1	2:H:82:MET:HA	2.16	0.80
1:B:181:SER:O	1:B:185:GLU:HB2	1.82	0.80
3:F:22:CYS:HB3	3:F:78:VAL:HG22	1.63	0.78
1:B:141:ARG:CB	1:B:180:GLU:OE1	2.33	0.77
1:B:183:LEU:HD22	1:B:195:LEU:HD21	1.67	0.77
2:E:51:ILE:CD1	2:E:71:ARG:HB2	2.15	0.76
1:A:114:ASN:O	1:A:117:ARG:HG2	1.85	0.76
1:B:181:SER:O	1:B:185:GLU:CB	2.33	0.76
1:C:141:ARG:HG2	1:C:171:GLU:CG	2.17	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:52:SER:O	2:E:55:ASN:HA	1.89	0.73
1:C:141:ARG:HG2	1:C:171:GLU:OE2	1.90	0.72
2:E:106:GLY:HA2	4:E:201:HOH:O	1.89	0.71
1:A:155:MET:HB3	1:A:162:LYS:HE2	1.73	0.71
1:A:155:MET:CE	1:A:165:GLU:OE1	2.39	0.71
2:E:6:GLU:OE1	2:E:104:GLY:HA3	1.91	0.71
2:G:29:PHE:HE1	2:G:78:VAL:HG23	1.54	0.70
1:C:157:ASP:HB3	1:C:161:LEU:HD13	1.74	0.70
1:D:145:ASP:OD1	1:D:171:GLU:HG3	1.91	0.70
2:E:36:TRP:HE3	2:E:91:TYR:O	1.75	0.69
1:B:158:LYS:HB3	1:B:161:LEU:HD13	1.73	0.69
1:B:145:ASP:OD1	1:B:171:GLU:HG3	1.93	0.69
2:E:51:ILE:HD13	2:E:71:ARG:HB2	1.76	0.68
1:D:113:VAL:O	1:D:117:ARG:CZ	2.42	0.68
2:E:36:TRP:CE3	2:E:91:TYR:O	2.46	0.68
3:F:22:CYS:HB3	3:F:78:VAL:CG2	2.23	0.67
2:E:2:VAL:HG13	2:E:28:THR:HG21	1.75	0.67
1:B:183:LEU:HD23	1:B:195:LEU:CD2	2.14	0.67
2:E:36:TRP:CH2	2:E:92:CYS:HB2	2.30	0.67
2:E:4:LEU:HD23	2:E:92:CYS:SG	2.36	0.65
1:C:171:GLU:HA	1:C:179:TRP:CD1	2.31	0.64
2:H:2:VAL:HG13	2:H:28:THR:HG21	1.79	0.64
1:A:156:THR:CG2	1:A:213:ASP:OD1	2.46	0.64
1:D:181:SER:O	1:D:185:GLU:HB2	1.98	0.63
2:E:24:ALA:HB3	2:E:29:PHE:CE1	2.34	0.62
1:A:116:ILE:HG22	1:A:117:ARG:NH2	2.14	0.61
2:E:36:TRP:CZ3	2:E:91:TYR:C	2.74	0.61
1:A:148:ARG:HH21	1:A:171:GLU:HG2	1.65	0.61
2:H:25:SER:O	2:H:28:THR:HG23	2.01	0.61
2:E:36:TRP:CZ3	2:E:92:CYS:CA	2.83	0.60
1:B:137:GLY:C	1:B:180:GLU:HG2	2.21	0.60
1:A:121:ASN:O	1:A:189:THR:HG23	2.02	0.60
1:A:156:THR:HG23	1:A:213:ASP:OD1	2.02	0.59
1:B:157:ASP:HB2	1:B:213:ASP:OD2	2.01	0.59
1:C:167:ALA:HA	1:C:170:THR:HG23	1.85	0.58
1:A:158:LYS:HD3	1:A:161:LEU:HD22	1.85	0.58
2:G:26:GLY:HA2	2:G:76:ASN:CG	2.24	0.58
2:G:24:ALA:HB3	2:G:29:PHE:CZ	2.38	0.58
1:B:130:LEU:HD11	1:B:185:GLU:HA	1.86	0.57
2:E:36:TRP:CZ3	2:E:92:CYS:N	2.73	0.57
1:A:137:GLY:C	1:A:180:GLU:HG2	2.25	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:6:GLU:HG2	4:E:201:HOH:O	2.05	0.56
1:A:124:ALA:HB3	1:A:189:THR:HG22	1.88	0.56
1:B:130:LEU:CD1	1:B:185:GLU:HA	2.36	0.56
1:B:164:ILE:O	1:B:168:LEU:HD13	2.06	0.56
1:D:127:VAL:O	1:D:131:ASN:OD1	2.25	0.55
1:D:117:ARG:NH2	1:D:193:ILE:CG2	2.57	0.55
2:H:89:VAL:HG22	2:H:108:GLN:HG2	1.88	0.55
1:D:137:GLY:C	1:D:180:GLU:HG2	2.27	0.55
1:B:106:SER:OG	1:B:189:THR:HG21	2.07	0.54
2:E:52(A):ARG:HD3	2:E:52(A):ARG:H	1.72	0.54
2:E:36:TRP:CZ3	2:E:92:CYS:HA	2.42	0.54
1:D:156:THR:HG22	1:D:213:ASP:OD2	2.08	0.54
2:E:52(A):ARG:HH11	2:E:52(A):ARG:HG3	1.72	0.54
1:B:107:ASP:OD1	1:B:118:ARG:HB2	2.08	0.53
3:F:2:VAL:HG13	3:F:28:THR:HG21	1.89	0.53
2:E:37:PHE:HE1	2:E:93:ALA:HB3	1.74	0.53
2:E:36:TRP:HZ3	2:E:91:TYR:C	2.12	0.53
1:C:116:ILE:HD13	1:C:190:VAL:HG12	1.90	0.52
2:H:11:LEU:HA	2:H:110:THR:O	2.09	0.52
1:B:179:TRP:CE2	1:B:183:LEU:HD13	2.44	0.52
2:G:24:ALA:HB3	2:G:29:PHE:CE2	2.45	0.52
2:G:25:SER:HB2	2:G:28:THR:HG23	1.92	0.52
1:A:155:MET:CB	1:A:162:LYS:HE2	2.39	0.51
1:D:131:ASN:HD21	1:D:134:ASN:HB2	1.75	0.51
2:H:10:GLY:H	2:H:18:LEU:HD21	1.76	0.51
2:H:67:PHE:CE1	2:H:82:MET:HB3	2.45	0.51
1:A:155:MET:HB3	1:A:162:LYS:CE	2.39	0.51
1:C:121:ASN:O	1:C:188:PRO:HA	2.11	0.51
1:B:179:TRP:CE2	1:B:183:LEU:CD1	2.94	0.50
1:C:141:ARG:CD	1:C:171:GLU:OE2	2.58	0.50
2:G:45:ARG:HD2	2:G:91:TYR:CD2	2.47	0.50
1:A:160:LYS:O	1:A:164:ILE:HG13	2.12	0.50
1:A:181:SER:O	1:A:185:GLU:HB3	2.11	0.50
2:G:29:PHE:CE1	2:G:78:VAL:HG23	2.42	0.50
1:A:167:ALA:O	1:A:170:THR:HG23	2.12	0.50
2:H:36:TRP:HD1	2:H:69:ILE:HD12	1.76	0.49
1:C:171:GLU:HA	1:C:179:TRP:NE1	2.26	0.49
1:C:141:ARG:HG2	1:C:171:GLU:CD	2.33	0.49
1:A:116:ILE:CG2	1:A:117:ARG:NH2	2.75	0.49
1:C:76:VAL:HG12	1:C:80:ARG:HD2	1.94	0.49
3:F:36:TRP:HD1	3:F:69:ILE:HD12	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:51:ILE:HD11	2:E:71:ARG:HB2	1.93	0.49
2:G:87:THR:HG23	2:G:110:THR:HA	1.94	0.49
1:C:141:ARG:HG2	1:C:171:GLU:HG3	1.91	0.48
1:C:73:LYS:HE3	4:C:302:HOH:O	2.12	0.48
1:A:183:LEU:HD13	1:A:195:LEU:HD21	1.95	0.48
1:D:159:ALA:O	1:D:163:LEU:HB2	2.13	0.48
3:F:24:ALA:HB3	3:F:29:PHE:CE1	2.49	0.48
2:H:58:TYR:CE1	2:H:100:ARG:HB3	2.49	0.48
1:C:141:ARG:CG	1:C:171:GLU:OE2	2.59	0.48
2:E:36:TRP:CE3	2:E:92:CYS:HA	2.48	0.48
2:H:11:LEU:HB2	2:H:110:THR:HB	1.95	0.48
1:D:117:ARG:HE	1:D:193:ILE:HD13	1.79	0.47
2:E:36:TRP:CH2	2:E:92:CYS:CB	2.97	0.47
2:E:36:TRP:HZ3	2:E:92:CYS:N	2.12	0.47
1:B:107:ASP:OD1	1:B:118:ARG:CB	2.62	0.47
1:B:179:TRP:NE1	1:B:183:LEU:HD11	2.29	0.47
2:G:34:MET:HG3	2:G:78:VAL:HG21	1.96	0.47
2:H:87:THR:HG23	2:H:110:THR:HA	1.96	0.47
2:H:2:VAL:HG22	2:H:28:THR:HG22	1.96	0.47
1:A:171:GLU:O	1:A:179:TRP:HB2	2.15	0.47
2:E:5:VAL:HB	2:E:23:ALA:CB	2.34	0.47
2:E:37:PHE:CE1	2:E:93:ALA:HB3	2.50	0.47
2:E:58:TYR:CE1	2:E:100:ARG:HB3	2.50	0.46
3:F:87:THR:HG23	3:F:110:THR:HA	1.97	0.46
1:B:179:TRP:NE1	1:B:183:LEU:CD1	2.79	0.46
2:E:92:CYS:O	2:E:103:TRP:HA	2.16	0.46
2:E:87:THR:HG23	2:E:110:THR:HA	1.98	0.46
1:D:100:LEU:HA	1:D:113:VAL:CG2	2.46	0.46
1:A:187:MET:HE1	1:A:191:ALA:HB1	1.97	0.46
1:C:116:ILE:HD12	1:C:116:ILE:H	1.81	0.45
2:H:22:CYS:HB3	2:H:78:VAL:HG12	1.98	0.45
1:B:107:ASP:CG	1:B:118:ARG:HB2	2.37	0.45
2:G:29:PHE:HE2	2:G:76:ASN:HB3	1.81	0.45
1:B:116:ILE:HG22	1:B:118:ARG:HG2	1.98	0.45
2:E:36:TRP:CZ3	2:E:92:CYS:HB2	2.52	0.45
3:F:40:ALA:HB3	3:F:43:LYS:HD3	1.99	0.45
2:E:36:TRP:CE3	2:E:91:TYR:C	2.90	0.44
1:A:211:LEU:O	1:A:215:VAL:HG23	2.18	0.44
1:C:183:LEU:HB3	1:C:195:LEU:HD21	1.99	0.44
2:E:34:MET:HB2	2:E:51:ILE:CG2	2.48	0.44
1:A:158:LYS:HB3	1:A:161:LEU:HB2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:181:SER:O	1:B:185:GLU:N	2.45	0.43
1:C:211:LEU:O	1:C:215:VAL:HG23	2.17	0.43
2:E:36:TRP:CZ3	2:E:92:CYS:CB	3.02	0.43
1:D:200:GLN:O	1:D:204:ARG:HG2	2.19	0.43
2:E:21:SER:HB3	2:E:79:TYR:CE1	2.54	0.42
1:A:87:GLU:HG3	1:A:150:LEU:HD22	2.00	0.42
1:D:140:LEU:O	1:D:144:VAL:HG23	2.18	0.42
1:D:211:LEU:O	1:D:215:VAL:HG23	2.19	0.42
2:G:58:TYR:CE1	2:G:100:ARG:HB3	2.54	0.42
1:D:158:LYS:HB3	1:D:161:LEU:HB2	2.00	0.42
2:G:66:ARG:HB3	2:G:82(A):ASN:O	2.20	0.42
1:A:155:MET:HE3	1:A:165:GLU:OE1	2.20	0.42
3:F:25:SER:O	3:F:28:THR:HG23	2.20	0.42
2:H:24:ALA:HB1	2:H:28:THR:OG1	2.19	0.42
1:B:127:VAL:O	1:B:131:ASN:HB2	2.19	0.42
2:H:67:PHE:HE1	2:H:82:MET:HB3	1.82	0.42
1:D:87:GLU:HG3	1:D:150:LEU:HD22	2.02	0.41
1:A:112:LYS:O	1:A:117:ARG:HG3	2.20	0.41
1:A:112:LYS:HB2	1:A:117:ARG:HD2	2.02	0.41
1:D:107:ASP:OD1	1:D:119:LYS:HB2	2.21	0.41
1:D:148:ARG:HD3	1:D:166:GLN:HG3	2.02	0.41
1:B:124:ALA:HB3	1:B:189:THR:HG22	2.02	0.41
2:E:34:MET:O	2:E:51:ILE:HG22	2.20	0.41
2:G:36:TRP:HD1	2:G:69:ILE:HD12	1.86	0.41
2:G:29:PHE:CE2	2:G:76:ASN:HB3	2.56	0.40
2:H:21:SER:HB3	2:H:79:TYR:CD1	2.56	0.40
1:B:211:LEU:O	1:B:215:VAL:HG23	2.22	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	145/197 (74%)	136 (94%)	7 (5%)	2 (1%)	11 15
1	B	146/197 (74%)	136 (93%)	10 (7%)	0	100 100
1	C	145/197 (74%)	141 (97%)	4 (3%)	0	100 100
1	D	142/197 (72%)	135 (95%)	6 (4%)	1 (1%)	22 32
2	E	123/134 (92%)	122 (99%)	1 (1%)	0	100 100
2	G	127/134 (95%)	123 (97%)	4 (3%)	0	100 100
2	H	122/134 (91%)	119 (98%)	3 (2%)	0	100 100
3	F	129/136 (95%)	126 (98%)	3 (2%)	0	100 100
All	All	1079/1326 (81%)	1038 (96%)	38 (4%)	3 (0%)	41 55

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	114	ASN
1	A	156	THR
1	D	116	ILE

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	129/174 (74%)	124 (96%)	5 (4%)	32 50
1	B	130/174 (75%)	128 (98%)	2 (2%)	65 80
1	C	129/174 (74%)	127 (98%)	2 (2%)	62 79
1	D	126/174 (72%)	123 (98%)	3 (2%)	49 68
2	E	102/110 (93%)	100 (98%)	2 (2%)	55 74
2	G	106/110 (96%)	104 (98%)	2 (2%)	57 75
2	H	101/110 (92%)	100 (99%)	1 (1%)	76 88
3	F	108/112 (96%)	106 (98%)	2 (2%)	57 75
All	All	931/1138 (82%)	912 (98%)	19 (2%)	55 74

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	70	ASN
1	A	116	ILE
1	A	157	ASP
1	A	180	GLU
1	A	187	MET
1	B	183	LEU
1	B	187	MET
1	C	131	ASN
1	C	171	GLU
1	D	116	ILE
1	D	180	GLU
1	D	181	SER
2	E	47	PHE
2	E	52(A)	ARG
3	F	61	ASP
3	F	100(G)	ARG
2	G	64	LYS
2	G	100(G)	ARG
2	H	53	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	131	ASN
1	D	131	ASN
3	F	118	HIS
2	G	13	GLN
2	G	76	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

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, 95^{th} 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	147/197 (74%)	0.37	6 (4%) 37 36	87, 104, 139, 178	0
1	B	148/197 (75%)	0.54	11 (7%) 14 13	84, 107, 161, 186	0
1	C	147/197 (74%)	0.41	10 (6%) 17 15	80, 100, 130, 157	0
1	D	144/197 (73%)	0.41	8 (5%) 24 23	83, 100, 134, 174	0
2	E	125/134 (93%)	1.70	46 (36%) 0 0	126, 168, 237, 255	0
2	G	129/134 (96%)	0.29	9 (6%) 16 15	75, 89, 126, 188	0
2	H	124/134 (92%)	1.65	44 (35%) 0 0	116, 152, 234, 262	0
3	F	131/136 (96%)	0.23	5 (3%) 40 39	82, 96, 143, 181	0
All	All	1095/1326 (82%)	0.68	139 (12%) 3 3	75, 107, 201, 262	0

All (139) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	14	ALA	8.6
2	E	1	ASP	7.3
2	E	13	GLN	7.2
2	H	111	VAL	7.1
2	H	36	TRP	7.1
2	H	40	ALA	6.9
2	H	12	VAL	6.2
2	E	20	VAL	6.1
2	H	79	TYR	6.0
2	E	80	LEU	5.9
2	E	26	GLY	5.9
2	H	18	LEU	5.9
2	E	74	ALA	5.8
3	F	1	ASP	5.8
2	H	69	ILE	5.8
1	A	157	ASP	5.8

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Mol	Chain	Res	Type	RSRZ
2	H	10	GLY	5.5
2	H	90	TYR	5.4
2	H	82(C)	LEU	5.4
2	H	84	PRO	5.3
2	H	13	GLN	4.9
2	E	84	PRO	4.8
2	E	48	VAL	4.8
2	E	9	GLY	4.8
1	B	163	LEU	4.7
1	B	117	ARG	4.7
2	G	116	HIS	4.7
1	B	168	LEU	4.7
2	H	15	GLY	4.7
2	E	73	SER	4.5
2	G	74	ALA	4.4
2	H	19	ARG	4.3
1	A	160	LYS	4.3
2	G	75	LYS	4.0
1	C	168	LEU	4.0
1	D	215	VAL	3.9
2	H	48	VAL	3.8
2	H	45	ARG	3.7
2	E	40	ALA	3.7
1	A	168	LEU	3.7
2	E	27	ARG	3.7
2	E	61	ASP	3.7
2	E	3	GLN	3.6
2	E	22	CYS	3.6
2	E	112	SER	3.6
2	E	82(C)	LEU	3.6
2	H	74	ALA	3.6
2	H	78	VAL	3.6
2	E	82	MET	3.6
2	E	36	TRP	3.6
2	H	41	PRO	3.5
2	E	78	VAL	3.5
3	F	79	TYR	3.5
2	E	28	THR	3.4
1	C	77	TRP	3.4
1	C	151	VAL	3.4
2	H	109	VAL	3.4
2	E	81	GLN	3.3

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Mol	Chain	Res	Type	RSRZ
1	D	123	ASP	3.3
2	H	75	LYS	3.3
2	E	111	VAL	3.3
2	H	67	PHE	3.2
2	H	89	VAL	3.2
1	D	157	ASP	3.1
1	B	151	VAL	3.1
2	E	91	TYR	3.1
2	E	67	PHE	3.1
2	E	82(B)	SER	3.1
2	H	16	GLY	3.1
2	E	2	VAL	3.1
2	E	10	GLY	3.1
2	H	7	SER	3.1
1	B	164	ILE	3.1
2	E	15	GLY	3.1
1	B	161	LEU	3.0
2	H	82(B)	SER	2.9
3	F	74	ALA	2.9
3	F	27	ARG	2.8
3	F	75	LYS	2.8
1	B	80	ARG	2.8
2	E	90	TYR	2.8
2	H	27	ARG	2.8
2	E	18	LEU	2.8
2	G	113	SER	2.8
2	H	85	GLU	2.7
2	H	4	LEU	2.7
2	E	19	ARG	2.7
2	H	107	THR	2.7
2	H	86	ASP	2.7
1	B	174	THR	2.6
1	C	165	GLU	2.6
2	H	38	ARG	2.5
2	E	23	ALA	2.5
1	C	157	ASP	2.5
1	D	73	LYS	2.5
2	H	82	MET	2.5
2	G	1	ASP	2.5
2	H	80	LEU	2.4
1	A	116	ILE	2.4
1	B	77	TRP	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	175	LYS	2.4
2	E	12	VAL	2.4
2	H	73	SER	2.4
1	D	160	LYS	2.4
1	D	214	LEU	2.4
2	E	79	TYR	2.4
1	B	115	ASP	2.3
2	E	92	CYS	2.3
2	G	79	TYR	2.3
2	H	66	ARG	2.3
2	E	4	LEU	2.3
2	H	34	MET	2.2
1	C	179	TRP	2.2
2	E	69	ILE	2.2
2	G	27	ARG	2.2
2	G	5	VAL	2.2
2	E	85	GLU	2.2
2	G	29	PHE	2.2
1	C	214	LEU	2.2
1	D	84	LEU	2.2
1	D	154	LEU	2.2
2	H	39	GLN	2.1
2	E	107	THR	2.1
2	E	7	SER	2.1
1	C	152	ALA	2.1
2	E	86	ASP	2.1
2	H	46	GLU	2.1
2	E	39	GLN	2.1
2	H	49	ALA	2.1
2	H	100(F)	LEU	2.1
2	H	88	ALA	2.1
1	A	199	LEU	2.1
2	H	92	CYS	2.1
2	E	8	GLY	2.1
1	C	171	GLU	2.1
2	H	100(G)	ARG	2.1
2	E	82(A)	ASN	2.1
1	C	175	LYS	2.0
1	A	184	PHE	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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.