Full wwPDB X-ray Structure Validation Report ⓘ

Nov 20, 2023 – 07:17 PM JST

PDB ID	:	7DRO
Title	:	Structure of ATP-grasp ligase PsnB complexed with minimal precursor
Authors	:	Song, I.; Yu, J.; Song, W.; Kim, S.
Deposited on	:	2020-12-29
Resolution	:	3.25 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:

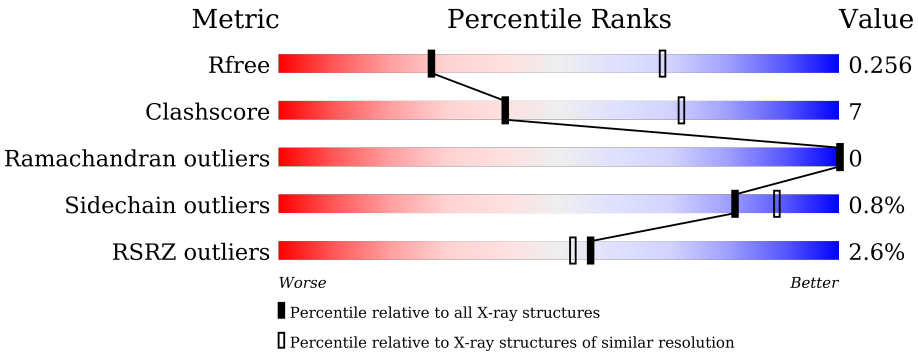
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 3.25 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	1191 (3.30-3.22)
Clashscore	141614	1251 (3.30-3.22)
Ramachandran outliers	138981	1229 (3.30-3.22)
Sidechain outliers	138945	1228 (3.30-3.22)
RSRZ outliers	127900	1154 (3.30-3.22)

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	334	76% 13% 10%
1	B	334	73% 16% 10%
1	C	334	74% 17% 9%
1	D	334	4% 75% 11% 13%
1	E	334	76% 13% 11%
1	F	334	4% 65% 21% 15%

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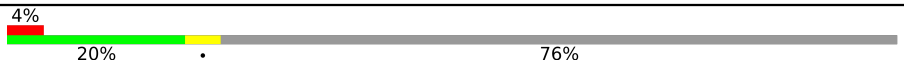
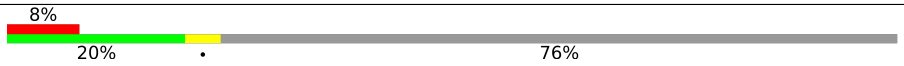
Mol	Chain	Length	Quality of chain
2	G	25	
2	H	25	
2	I	25	
2	J	25	

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 13250 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 ATP-grasp domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	299	Total	C	N	O	S	0	0	0
			2268	1424	408	425	11			
1	B	300	Total	C	N	O	S	0	0	0
			2217	1394	393	419	11			
1	C	303	Total	C	N	O	S	0	0	0
			2246	1407	402	427	10			
1	D	289	Total	C	N	O	S	0	0	0
			2084	1310	364	400	10			
1	E	296	Total	C	N	O	S	0	0	0
			2195	1377	400	409	9			
1	F	285	Total	C	N	O	S	0	0	0
			2062	1290	370	392	10			

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP A6G4D7
A	-18	GLY	-	expression tag	UNP A6G4D7
A	-17	SER	-	expression tag	UNP A6G4D7
A	-16	SER	-	expression tag	UNP A6G4D7
A	-15	HIS	-	expression tag	UNP A6G4D7
A	-14	HIS	-	expression tag	UNP A6G4D7
A	-13	HIS	-	expression tag	UNP A6G4D7
A	-12	HIS	-	expression tag	UNP A6G4D7
A	-11	HIS	-	expression tag	UNP A6G4D7
A	-10	HIS	-	expression tag	UNP A6G4D7
A	-9	SER	-	expression tag	UNP A6G4D7
A	-8	SER	-	expression tag	UNP A6G4D7
A	-7	GLY	-	expression tag	UNP A6G4D7
A	-6	LEU	-	expression tag	UNP A6G4D7
A	-5	VAL	-	expression tag	UNP A6G4D7
A	-4	PRO	-	expression tag	UNP A6G4D7
A	-3	ARG	-	expression tag	UNP A6G4D7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP A6G4D7
A	-1	SER	-	expression tag	UNP A6G4D7
A	0	HIS	-	expression tag	UNP A6G4D7
B	-19	MET	-	expression tag	UNP A6G4D7
B	-18	GLY	-	expression tag	UNP A6G4D7
B	-17	SER	-	expression tag	UNP A6G4D7
B	-16	SER	-	expression tag	UNP A6G4D7
B	-15	HIS	-	expression tag	UNP A6G4D7
B	-14	HIS	-	expression tag	UNP A6G4D7
B	-13	HIS	-	expression tag	UNP A6G4D7
B	-12	HIS	-	expression tag	UNP A6G4D7
B	-11	HIS	-	expression tag	UNP A6G4D7
B	-10	HIS	-	expression tag	UNP A6G4D7
B	-9	SER	-	expression tag	UNP A6G4D7
B	-8	SER	-	expression tag	UNP A6G4D7
B	-7	GLY	-	expression tag	UNP A6G4D7
B	-6	LEU	-	expression tag	UNP A6G4D7
B	-5	VAL	-	expression tag	UNP A6G4D7
B	-4	PRO	-	expression tag	UNP A6G4D7
B	-3	ARG	-	expression tag	UNP A6G4D7
B	-2	GLY	-	expression tag	UNP A6G4D7
B	-1	SER	-	expression tag	UNP A6G4D7
B	0	HIS	-	expression tag	UNP A6G4D7
C	-19	MET	-	expression tag	UNP A6G4D7
C	-18	GLY	-	expression tag	UNP A6G4D7
C	-17	SER	-	expression tag	UNP A6G4D7
C	-16	SER	-	expression tag	UNP A6G4D7
C	-15	HIS	-	expression tag	UNP A6G4D7
C	-14	HIS	-	expression tag	UNP A6G4D7
C	-13	HIS	-	expression tag	UNP A6G4D7
C	-12	HIS	-	expression tag	UNP A6G4D7
C	-11	HIS	-	expression tag	UNP A6G4D7
C	-10	HIS	-	expression tag	UNP A6G4D7
C	-9	SER	-	expression tag	UNP A6G4D7
C	-8	SER	-	expression tag	UNP A6G4D7
C	-7	GLY	-	expression tag	UNP A6G4D7
C	-6	LEU	-	expression tag	UNP A6G4D7
C	-5	VAL	-	expression tag	UNP A6G4D7
C	-4	PRO	-	expression tag	UNP A6G4D7
C	-3	ARG	-	expression tag	UNP A6G4D7
C	-2	GLY	-	expression tag	UNP A6G4D7
C	-1	SER	-	expression tag	UNP A6G4D7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	0	HIS	-	expression tag	UNP A6G4D7
D	-19	MET	-	expression tag	UNP A6G4D7
D	-18	GLY	-	expression tag	UNP A6G4D7
D	-17	SER	-	expression tag	UNP A6G4D7
D	-16	SER	-	expression tag	UNP A6G4D7
D	-15	HIS	-	expression tag	UNP A6G4D7
D	-14	HIS	-	expression tag	UNP A6G4D7
D	-13	HIS	-	expression tag	UNP A6G4D7
D	-12	HIS	-	expression tag	UNP A6G4D7
D	-11	HIS	-	expression tag	UNP A6G4D7
D	-10	HIS	-	expression tag	UNP A6G4D7
D	-9	SER	-	expression tag	UNP A6G4D7
D	-8	SER	-	expression tag	UNP A6G4D7
D	-7	GLY	-	expression tag	UNP A6G4D7
D	-6	LEU	-	expression tag	UNP A6G4D7
D	-5	VAL	-	expression tag	UNP A6G4D7
D	-4	PRO	-	expression tag	UNP A6G4D7
D	-3	ARG	-	expression tag	UNP A6G4D7
D	-2	GLY	-	expression tag	UNP A6G4D7
D	-1	SER	-	expression tag	UNP A6G4D7
D	0	HIS	-	expression tag	UNP A6G4D7
E	-19	MET	-	expression tag	UNP A6G4D7
E	-18	GLY	-	expression tag	UNP A6G4D7
E	-17	SER	-	expression tag	UNP A6G4D7
E	-16	SER	-	expression tag	UNP A6G4D7
E	-15	HIS	-	expression tag	UNP A6G4D7
E	-14	HIS	-	expression tag	UNP A6G4D7
E	-13	HIS	-	expression tag	UNP A6G4D7
E	-12	HIS	-	expression tag	UNP A6G4D7
E	-11	HIS	-	expression tag	UNP A6G4D7
E	-10	HIS	-	expression tag	UNP A6G4D7
E	-9	SER	-	expression tag	UNP A6G4D7
E	-8	SER	-	expression tag	UNP A6G4D7
E	-7	GLY	-	expression tag	UNP A6G4D7
E	-6	LEU	-	expression tag	UNP A6G4D7
E	-5	VAL	-	expression tag	UNP A6G4D7
E	-4	PRO	-	expression tag	UNP A6G4D7
E	-3	ARG	-	expression tag	UNP A6G4D7
E	-2	GLY	-	expression tag	UNP A6G4D7
E	-1	SER	-	expression tag	UNP A6G4D7
E	0	HIS	-	expression tag	UNP A6G4D7
F	-19	MET	-	expression tag	UNP A6G4D7

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-18	GLY	-	expression tag	UNP A6G4D7
F	-17	SER	-	expression tag	UNP A6G4D7
F	-16	SER	-	expression tag	UNP A6G4D7
F	-15	HIS	-	expression tag	UNP A6G4D7
F	-14	HIS	-	expression tag	UNP A6G4D7
F	-13	HIS	-	expression tag	UNP A6G4D7
F	-12	HIS	-	expression tag	UNP A6G4D7
F	-11	HIS	-	expression tag	UNP A6G4D7
F	-10	HIS	-	expression tag	UNP A6G4D7
F	-9	SER	-	expression tag	UNP A6G4D7
F	-8	SER	-	expression tag	UNP A6G4D7
F	-7	GLY	-	expression tag	UNP A6G4D7
F	-6	LEU	-	expression tag	UNP A6G4D7
F	-5	VAL	-	expression tag	UNP A6G4D7
F	-4	PRO	-	expression tag	UNP A6G4D7
F	-3	ARG	-	expression tag	UNP A6G4D7
F	-2	GLY	-	expression tag	UNP A6G4D7
F	-1	SER	-	expression tag	UNP A6G4D7
F	0	HIS	-	expression tag	UNP A6G4D7

- Molecule 2 is a protein called PsnA214-38, Precursor peptide.

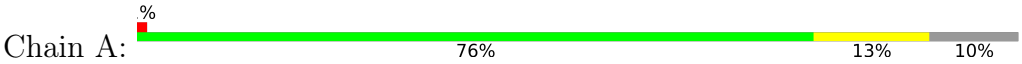
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	G	6	Total	C	N	O	0	0	0
			45	33	6	6			
2	H	5	Total	C	N	O	0	0	0
			37	27	5	5			
2	I	6	Total	C	N	O	0	0	0
			48	34	6	8			
2	J	6	Total	C	N	O	0	0	0
			48	34	6	8			

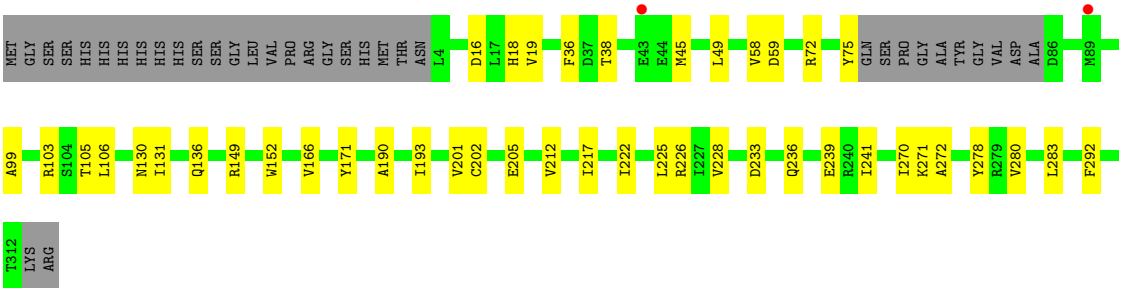
3 Residue-property plots (i)

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: ATP-grasp domain-containing protein

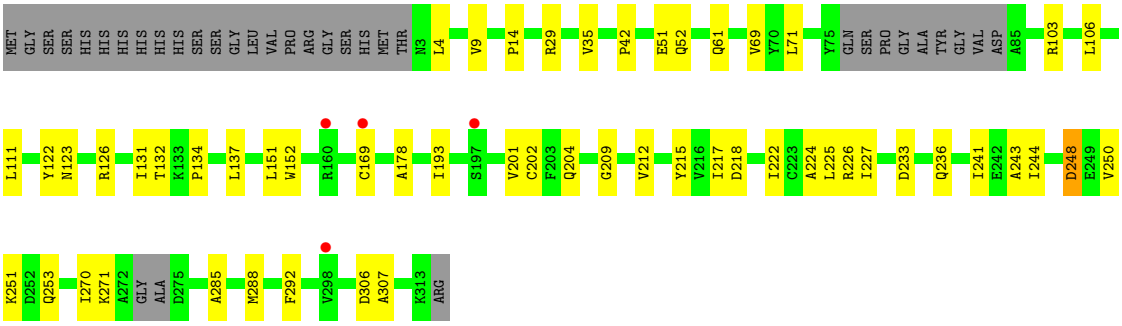
Chain A:





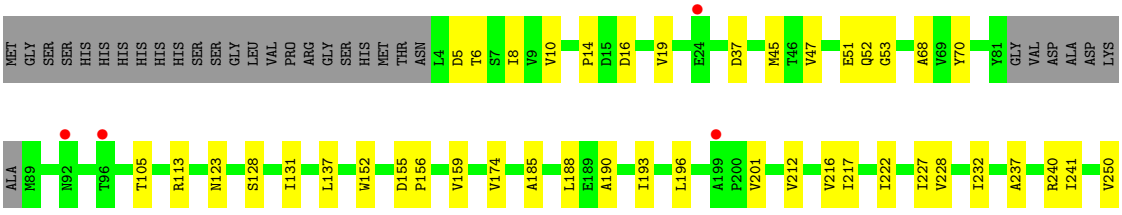
• Molecule 1: ATP-grasp domain-containing protein

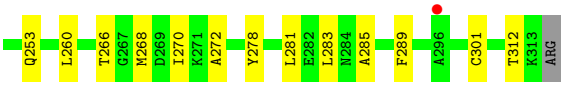
Chain B:



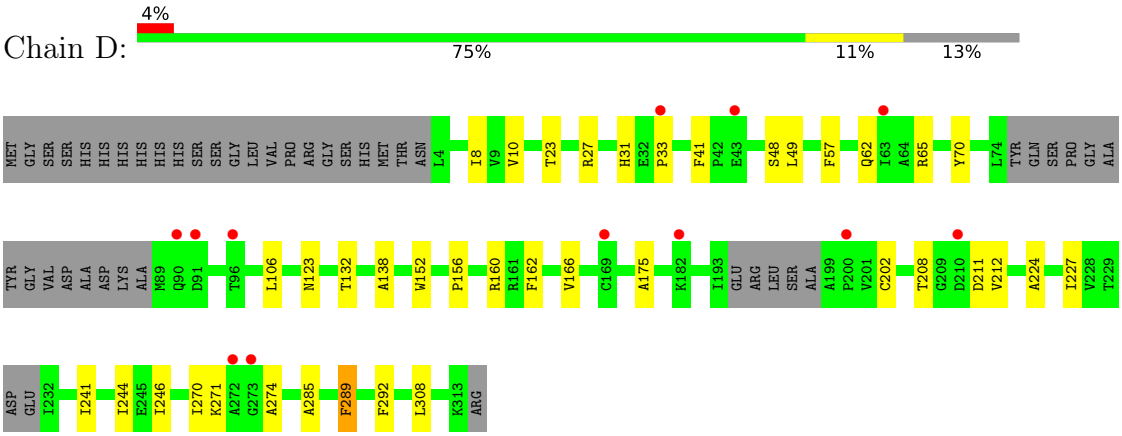
• Molecule 1: ATP-grasp domain-containing protein

Chain C:

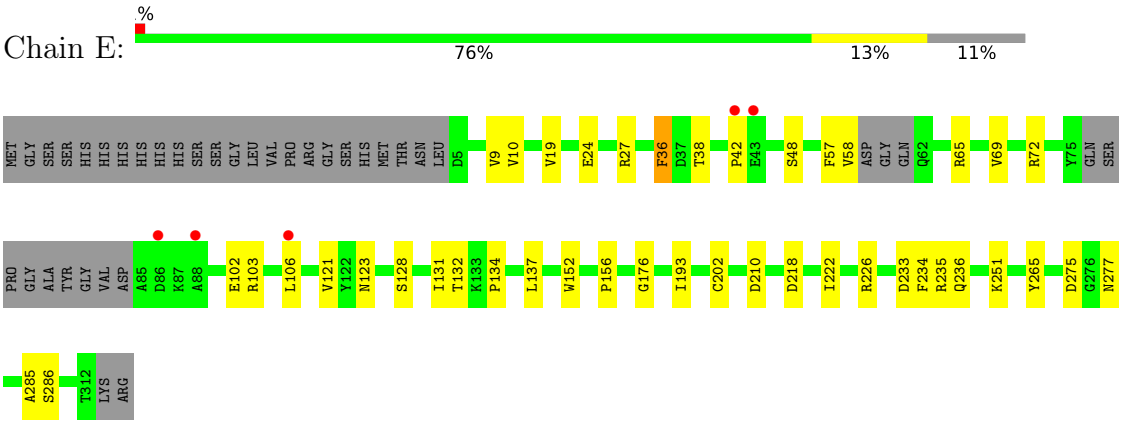




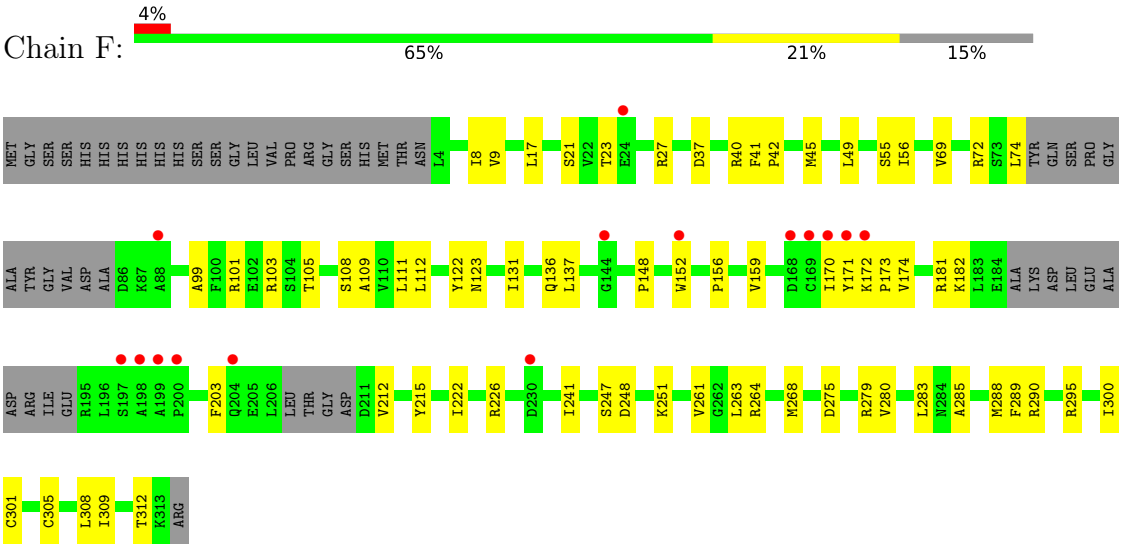
• Molecule 1: ATP-grasp domain-containing protein



• Molecule 1: ATP-grasp domain-containing protein

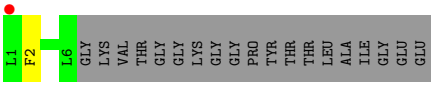


• Molecule 1: ATP-grasp domain-containing protein



• Molecule 2: PsnA214-38, Precursor peptide

Chain G:

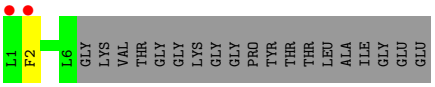


• Molecule 2: PsnA214-38, Precursor peptide

Chain H:

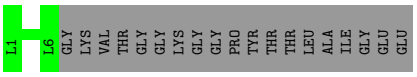
• Molecule 2: PsnA214-38, Precursor peptide

Chain I:



• Molecule 2: PsnA214-38, Precursor peptide

Chain J:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	86.89Å 146.94Å 167.83Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.04 – 3.25 47.04 – 3.25	Depositor EDS
% Data completeness (in resolution range)	99.4 (47.04-3.25) 99.5 (47.04-3.25)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	7.37 (at 3.25Å)	Xtriage
Refinement program	PHENIX 1.19.1_4122	Depositor
R, R_{free}	0.256 , 0.263 0.251 , 0.256	Depositor DCC
R_{free} test set	1729 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	80.6	Xtriage
Anisotropy	0.173	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 66.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.89	EDS
Total number of atoms	13250	wwPDB-VP
Average B, all atoms (Å^2)	79.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.34% 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	0.38	0/2305	0.55	0/3133
1	B	0.38	0/2251	0.57	0/3064
1	C	0.34	0/2284	0.51	0/3110
1	D	0.36	0/2115	0.56	0/2884
1	E	0.35	0/2230	0.52	0/3033
1	F	0.37	0/2095	0.55	0/2856
2	G	0.49	0/45	0.68	0/60
2	H	0.28	0/37	0.38	0/49
2	I	0.35	0/48	0.45	0/64
2	J	0.27	0/48	0.59	0/64
All	All	0.36	0/13458	0.54	0/18317

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	2268	0	2211	29	0
1	B	2217	0	2130	35	0
1	C	2246	0	2134	36	0
1	D	2084	0	1952	25	0
1	E	2195	0	2110	28	0
1	F	2062	0	1911	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	G	45	0	48	2	0
2	H	37	0	34	3	0
2	I	48	0	50	2	0
2	J	48	0	50	0	0
All	All	13250	0	12630	187	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 7.

All (187) 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:D:123:ASN:ND2	1:D:285:ALA:O	2.24	0.69
1:B:250:VAL:HA	1:B:253:GLN:HB2	1.76	0.67
1:B:42:PRO:HG3	1:B:103:ARG:HD2	1.79	0.63
1:F:123:ASN:ND2	1:F:285:ALA:O	2.32	0.63
1:C:190:ALA:HA	1:C:193:ILE:HG22	1.81	0.63
1:C:268:MET:HB3	1:C:283:LEU:HG	1.84	0.59
1:C:201:VAL:HG11	2:I:2:PHE:CD2	2.38	0.58
1:A:105:THR:HG23	1:B:132:THR:HG23	1.85	0.58
1:A:201:VAL:HG21	2:G:2:PHE:CD2	2.38	0.58
1:E:48:SER:HB3	1:E:57:PHE:HB2	1.85	0.58
1:C:216:VAL:HB	1:C:266:THR:HG22	1.85	0.58
1:F:312:THR:O	1:F:312:THR:HG22	2.03	0.58
1:A:190:ALA:HA	1:A:193:ILE:HG22	1.87	0.57
1:C:45:MET:HG2	1:C:47:VAL:HG23	1.86	0.57
1:B:9:VAL:HB	1:B:69:VAL:HG22	1.86	0.57
1:C:312:THR:HG22	1:C:312:THR:O	2.05	0.56
1:C:10:VAL:HG13	1:C:70:TYR:HD2	1.70	0.56
1:B:132:THR:HG22	1:B:134:PRO:HD2	1.87	0.55
1:E:132:THR:HG23	1:F:105:THR:HG23	1.88	0.55
1:D:224:ALA:HB2	1:D:246:ILE:HD13	1.89	0.55
1:A:270:ILE:HG22	1:A:280:VAL:HA	1.88	0.54
1:F:289:PHE:CE1	1:F:301:CYS:HB2	2.42	0.54
1:D:244:ILE:HD12	1:D:244:ILE:O	2.07	0.54
1:E:123:ASN:ND2	1:E:285:ALA:O	2.42	0.53
1:E:152:TRP:CD1	1:E:202:CYS:HB2	2.44	0.53
1:F:247:SER:O	1:F:251:LYS:HB2	2.07	0.53
1:C:53:GLY:HA2	1:C:113:ARG:HE	1.72	0.53
2:H:3:ILE:HB	2:H:6:LEU:HD13	1.89	0.53
1:E:10:VAL:HG11	1:E:19:VAL:HG13	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:305:CYS:O	1:F:309:ILE:HG12	2.08	0.53
1:B:123:ASN:ND2	1:B:285:ALA:O	2.32	0.53
1:E:58:VAL:HG12	1:E:58:VAL:O	2.08	0.53
1:F:137:LEU:HD12	1:F:152:TRP:CH2	2.44	0.53
1:F:171:TYR:CE1	1:F:181:ARG:HB3	2.44	0.53
1:C:123:ASN:ND2	1:C:285:ALA:O	2.42	0.53
1:E:210:ASP:OD2	1:E:226:ARG:NH1	2.41	0.53
1:C:105:THR:HG21	1:D:175:ALA:HB2	1.91	0.53
1:D:41:PHE:CZ	1:D:106:LEU:HD23	2.44	0.52
1:B:233:ASP:HB3	1:B:236:GLN:HB2	1.92	0.52
1:E:42:PRO:HG3	1:E:103:ARG:HH12	1.74	0.52
1:D:162:PHE:O	1:D:166:VAL:HG22	2.10	0.52
1:E:210:ASP:OD1	1:E:210:ASP:N	2.41	0.52
1:F:42:PRO:HG3	1:F:103:ARG:HD3	1.92	0.52
1:C:227:ILE:HG12	1:C:241:ILE:HD13	1.91	0.51
1:C:201:VAL:HG11	2:I:2:PHE:HD2	1.76	0.50
1:A:16:ASP:HB3	1:A:19:VAL:HG22	1.93	0.50
1:F:261:VAL:HG13	1:F:263:LEU:HG	1.93	0.50
1:B:212:VAL:HB	1:B:270:ILE:HG13	1.94	0.49
1:C:272:ALA:HA	1:C:278:TYR:HA	1.94	0.49
1:E:9:VAL:HB	1:E:69:VAL:HG22	1.94	0.49
1:C:217:ILE:HD12	1:C:222:ILE:HG13	1.95	0.49
1:A:233:ASP:HB3	1:A:236:GLN:HB2	1.94	0.49
1:E:134:PRO:HG2	1:F:109:ALA:HB2	1.94	0.49
1:A:38:THR:HG23	1:A:75:TYR:HD2	1.78	0.49
1:F:136:GLN:OE1	1:F:283:LEU:N	2.44	0.49
1:F:137:LEU:HD12	1:F:152:TRP:CZ2	2.47	0.49
1:C:113:ARG:HH21	1:D:138:ALA:HB2	1.78	0.49
1:C:105:THR:HG23	1:D:132:THR:HG23	1.93	0.49
1:A:271:LYS:HG2	1:A:272:ALA:O	2.13	0.48
1:E:233:ASP:OD1	1:E:234:PHE:N	2.42	0.48
1:B:29:ARG:NH1	1:B:306:ASP:OD1	2.47	0.48
1:E:72:ARG:NH1	1:E:286:SER:OG	2.47	0.48
1:E:24:GLU:HA	1:E:27:ARG:HD2	1.96	0.48
1:F:9:VAL:HB	1:F:69:VAL:HG22	1.96	0.47
1:A:201:VAL:HG21	2:G:2:PHE:HD2	1.79	0.47
1:C:289:PHE:HE2	1:C:301:CYS:HB2	1.80	0.47
1:D:8:ILE:HG23	1:D:33:PRO:HB3	1.95	0.47
1:A:212:VAL:HB	1:A:270:ILE:HG13	1.96	0.47
1:F:241:ILE:HD12	1:F:295:ARG:HD2	1.97	0.47
1:D:227:ILE:HD11	1:D:292:PHE:HE2	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:226:ARG:NH1	1:A:228:VAL:HG11	2.30	0.46
1:B:227:ILE:HG12	1:B:292:PHE:HE2	1.80	0.46
1:D:289:PHE:C	1:D:289:PHE:CD1	2.89	0.46
1:F:171:TYR:HE1	1:F:182:LYS:O	1.98	0.46
1:C:159:VAL:HG21	1:C:196:LEU:HD11	1.97	0.46
1:F:226:ARG:O	1:F:241:ILE:HA	2.16	0.46
1:A:58:VAL:HG12	1:A:59:ASP:OD1	2.15	0.46
1:F:148:PRO:HD3	1:F:280:VAL:O	2.15	0.46
1:D:227:ILE:HG12	1:D:241:ILE:HG23	1.98	0.45
1:B:251:LYS:HB2	1:B:251:LYS:HE3	1.83	0.45
1:D:65:ARG:HG2	1:D:65:ARG:O	2.16	0.45
1:E:102:GLU:OE2	1:F:174:VAL:N	2.49	0.45
1:B:4:LEU:HA	1:B:61:GLN:HE22	1.81	0.45
1:B:215:TYR:OH	1:B:288:MET:O	2.33	0.45
1:A:278:TYR:H	1:A:278:TYR:HD1	1.65	0.45
1:F:172:LYS:HG2	1:F:173:PRO:HD2	1.97	0.45
1:B:9:VAL:O	1:B:69:VAL:HA	2.17	0.45
1:B:51:GLU:HG2	1:B:52:GLN:N	2.31	0.45
1:C:14:PRO:HD2	1:C:37:ASP:OD2	2.17	0.45
1:B:137:LEU:HD23	1:B:137:LEU:HA	1.74	0.45
1:C:250:VAL:HA	1:C:253:GLN:HB2	1.98	0.45
1:C:128:SER:HA	1:C:131:ILE:HG12	1.98	0.45
1:F:49:LEU:HD22	1:F:56:ILE:HG12	1.99	0.45
1:C:51:GLU:HG2	1:C:52:GLN:N	2.32	0.44
1:E:156:PRO:HB3	1:E:193:ILE:HG13	1.99	0.44
1:F:49:LEU:HA	1:F:55:SER:O	2.18	0.44
1:A:130:ASN:HD21	1:B:126:ARG:HH12	1.64	0.44
1:A:166:VAL:CG1	1:A:205:GLU:HB3	2.48	0.44
1:C:185:ALA:HA	1:C:188:LEU:HD12	2.00	0.44
1:A:217:ILE:HD13	1:A:222:ILE:HG13	2.00	0.44
1:D:8:ILE:HD11	1:D:308:LEU:HB3	2.00	0.44
1:F:312:THR:O	1:F:312:THR:CG2	2.65	0.44
1:E:251:LYS:HB3	1:E:251:LYS:HE3	1.71	0.43
1:A:241:ILE:HD13	1:A:292:PHE:CD2	2.52	0.43
1:B:131:ILE:O	1:B:132:THR:C	2.56	0.43
1:F:8:ILE:HD13	1:F:308:LEU:HB3	2.00	0.43
1:F:222:ILE:HD13	1:F:222:ILE:HA	1.82	0.43
1:F:268:MET:HB3	1:F:283:LEU:HG	2.00	0.43
1:D:152:TRP:NE1	1:D:202:CYS:HB2	2.34	0.43
1:F:275:ASP:OD1	1:F:275:ASP:N	2.51	0.43
1:A:18:HIS:HB2	1:A:72:ARG:HE	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:69:VAL:HB	1:E:121:VAL:HA	2.00	0.43
1:F:37:ASP:O	1:F:40:ARG:HG2	2.18	0.43
1:D:152:TRP:CD1	1:D:202:CYS:HB2	2.53	0.43
1:F:215:TYR:OH	1:F:288:MET:O	2.30	0.43
1:B:209:GLY:O	1:B:271:LYS:NZ	2.45	0.43
1:C:156:PRO:HB3	1:C:193:ILE:HG23	2.00	0.43
1:E:137:LEU:HD12	1:E:152:TRP:CZ2	2.54	0.43
1:A:106:LEU:HD12	1:A:106:LEU:HA	1.83	0.43
1:F:74:LEU:HD11	1:F:111:LEU:HD12	2.01	0.43
1:F:261:VAL:HG11	1:F:283:LEU:HD22	2.01	0.43
1:A:49:LEU:O	1:B:151:LEU:HA	2.19	0.42
1:D:48:SER:C	1:D:49:LEU:HD12	2.39	0.42
1:B:217:ILE:HD12	1:B:222:ILE:HG13	2.00	0.42
1:E:233:ASP:HB3	1:E:236:GLN:HB2	2.00	0.42
1:B:122:TYR:OH	1:B:218:ASP:OD2	2.32	0.42
1:C:232:ILE:H	1:C:237:ALA:HA	1.84	0.42
1:D:212:VAL:HB	1:D:270:ILE:HG13	2.00	0.42
1:F:108:SER:O	1:F:112:LEU:HG	2.19	0.42
1:A:171:TYR:HA	1:A:202:CYS:O	2.20	0.42
1:D:208:THR:HB	1:D:274:ALA:HA	2.00	0.42
1:F:131:ILE:HD11	1:F:263:LEU:HD11	2.01	0.42
1:C:222:ILE:HD13	1:C:222:ILE:HA	1.90	0.42
1:E:275:ASP:OD2	1:E:277:ASN:ND2	2.52	0.42
1:F:72:ARG:HA	1:F:72:ARG:HD2	1.92	0.42
1:D:57:PHE:CE1	1:D:62:GLN:HB2	2.55	0.42
1:D:211:ASP:OD1	1:D:271:LYS:HD3	2.20	0.42
1:A:225:LEU:HD13	1:A:292:PHE:HB3	2.01	0.42
1:B:152:TRP:CD1	1:B:202:CYS:HB2	2.55	0.42
1:E:106:LEU:HA	1:E:106:LEU:HD12	1.66	0.42
1:E:128:SER:O	1:E:131:ILE:HG12	2.19	0.42
1:A:152:TRP:HB3	1:B:106:LEU:HD11	2.02	0.42
1:C:137:LEU:HD11	1:C:281:LEU:O	2.20	0.42
1:C:152:TRP:CD1	1:C:174:VAL:HG13	2.55	0.42
1:C:212:VAL:O	1:C:270:ILE:HG12	2.19	0.42
1:F:122:TYR:CD2	1:F:264:ARG:HB3	2.54	0.42
1:D:10:VAL:HG22	1:D:70:TYR:HB3	2.02	0.42
1:D:156:PRO:O	1:D:160:ARG:HG3	2.20	0.42
1:F:23:THR:O	1:F:27:ARG:HB2	2.19	0.42
1:F:99:ALA:O	1:F:103:ARG:HG3	2.19	0.42
1:C:289:PHE:CE2	1:C:301:CYS:HB2	2.55	0.41
1:F:170:ILE:O	1:F:203:PHE:HA	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:248:ASP:HA	1:B:251:LYS:HE3	2.03	0.41
1:C:155:ASP:O	1:C:159:VAL:HG23	2.20	0.41
1:D:23:THR:HG22	1:D:33:PRO:HG2	2.01	0.41
1:E:176:GLY:O	1:F:101:ARG:NH2	2.54	0.41
1:F:215:TYR:CD2	1:F:300:ILE:HD13	2.56	0.41
1:B:226:ARG:O	1:B:241:ILE:HA	2.21	0.41
1:F:137:LEU:HD23	1:F:137:LEU:HA	1.83	0.41
1:B:14:PRO:HG3	1:B:35:VAL:HG11	2.03	0.41
1:C:260:LEU:HD23	1:C:260:LEU:HA	1.93	0.41
1:E:222:ILE:HD13	1:E:222:ILE:HA	1.90	0.41
1:B:178:ALA:HB2	2:H:6:LEU:HD12	2.02	0.41
1:B:224:ALA:O	1:B:244:ILE:HG12	2.20	0.41
1:D:27:ARG:HA	1:D:31:HIS:O	2.20	0.41
1:B:193:ILE:HD12	1:B:193:ILE:HA	1.96	0.41
1:A:239:GLU:OE1	1:E:235:ARG:NH2	2.50	0.41
1:B:201:VAL:HG21	2:H:2:PHE:CD2	2.55	0.41
1:F:41:PHE:O	1:F:45:MET:O	2.38	0.41
1:A:136:GLN:OE1	1:A:283:LEU:N	2.45	0.41
1:B:122:TYR:OH	1:B:307:ALA:HB1	2.21	0.41
1:F:212:VAL:HG22	1:F:226:ARG:HA	2.03	0.41
1:A:36:PHE:HE1	1:A:45:MET:SD	2.44	0.40
1:A:166:VAL:HG13	1:A:205:GLU:HB3	2.04	0.40
1:E:36:PHE:CE1	1:E:38:THR:HG22	2.56	0.40
1:E:121:VAL:O	1:E:121:VAL:HG13	2.20	0.40
1:F:17:LEU:O	1:F:21:SER:OG	2.30	0.40
1:A:131:ILE:HA	1:A:131:ILE:HD13	1.80	0.40
1:F:156:PRO:O	1:F:159:VAL:HG22	2.22	0.40
1:B:71:LEU:HD13	1:B:111:LEU:HD21	2.03	0.40
1:C:8:ILE:HA	1:C:68:ALA:O	2.21	0.40
1:C:16:ASP:HB3	1:C:19:VAL:HG13	2.03	0.40
1:C:228:VAL:HG23	1:C:240:ARG:HB3	2.03	0.40
1:B:169:CYS:HB2	1:B:204:GLN:O	2.21	0.40
1:B:225:LEU:HD22	1:B:243:ALA:HA	2.03	0.40
1:A:99:ALA:O	1:A:103:ARG:HG3	2.21	0.40
1:C:5:ASP:OD1	1:C:6:THR:N	2.54	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	295/334 (88%)	274 (93%)	21 (7%)	0	100	100
1	B	294/334 (88%)	277 (94%)	17 (6%)	0	100	100
1	C	299/334 (90%)	272 (91%)	27 (9%)	0	100	100
1	D	281/334 (84%)	258 (92%)	23 (8%)	0	100	100
1	E	290/334 (87%)	265 (91%)	25 (9%)	0	100	100
1	F	277/334 (83%)	258 (93%)	19 (7%)	0	100	100
2	G	4/25 (16%)	3 (75%)	1 (25%)	0	100	100
2	H	3/25 (12%)	3 (100%)	0	0	100	100
2	I	4/25 (16%)	4 (100%)	0	0	100	100
2	J	4/25 (16%)	4 (100%)	0	0	100	100
All	All	1751/2104 (83%)	1618 (92%)	133 (8%)	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	228/274 (83%)	227 (100%)	1 (0%)	91	94
1	B	218/274 (80%)	217 (100%)	1 (0%)	88	93
1	C	219/274 (80%)	219 (100%)	0	100	100
1	D	198/274 (72%)	197 (100%)	1 (0%)	88	93

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	E	213/274 (78%)	209 (98%)	4 (2%)	57 76
1	F	194/274 (71%)	191 (98%)	3 (2%)	65 80
2	G	4/18 (22%)	4 (100%)	0	100 100
2	H	3/18 (17%)	3 (100%)	0	100 100
2	I	5/18 (28%)	5 (100%)	0	100 100
2	J	5/18 (28%)	5 (100%)	0	100 100
All	All	1287/1716 (75%)	1277 (99%)	10 (1%)	81 89

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	149	ARG
1	B	248	ASP
1	D	289	PHE
1	E	36	PHE
1	E	65	ARG
1	E	218	ASP
1	E	265	TYR
1	F	248	ASP
1	F	279	ARG
1	F	290	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	61	GLN

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	299/334 (89%)	0.04	2 (0%) 87 88	31, 49, 85, 97	0
1	B	300/334 (89%)	0.15	4 (1%) 77 75	35, 72, 95, 108	0
1	C	303/334 (90%)	0.35	5 (1%) 70 67	73, 90, 110, 115	0
1	D	289/334 (86%)	0.31	12 (4%) 36 33	75, 94, 114, 128	0
1	E	296/334 (88%)	0.25	5 (1%) 70 67	36, 74, 116, 129	0
1	F	285/334 (85%)	0.47	15 (5%) 26 24	48, 96, 124, 130	0
2	G	6/25 (24%)	0.26	1 (16%) 1 1	50, 62, 66, 68	0
2	H	5/25 (20%)	0.13	0 100 100	79, 80, 83, 83	0
2	I	6/25 (24%)	1.05	2 (33%) 0 0	96, 99, 102, 102	0
2	J	6/25 (24%)	0.07	0 100 100	48, 52, 57, 60	0
All	All	1795/2104 (85%)	0.26	46 (2%) 56 52	31, 84, 114, 130	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	171	TYR	3.9
2	I	1	LEU	3.6
1	B	160	ARG	3.6
1	F	168	ASP	3.5
1	E	88	ALA	3.3
1	E	43	GLU	3.3
1	F	170	ILE	3.2
1	F	230	ASP	2.9
1	F	198	ALA	2.9
1	F	169	CYS	2.8
1	C	96	THR	2.8
1	E	86	ASP	2.8
1	D	273	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
1	D	210	ASP	2.7
1	C	92	ASN	2.7
1	A	43	GLU	2.7
1	B	298	VAL	2.7
2	I	2	PHE	2.6
1	F	152	TRP	2.5
1	D	169	CYS	2.5
1	D	272	ALA	2.4
1	F	197	SER	2.4
1	F	200	PRO	2.4
1	F	88	ALA	2.4
1	D	43	GLU	2.3
1	F	199	ALA	2.3
1	F	24	GLU	2.3
1	B	197	SER	2.2
1	D	96	THR	2.2
1	E	42	PRO	2.2
1	F	204	GLN	2.2
1	E	106	LEU	2.2
1	F	172	LYS	2.2
1	B	169	CYS	2.2
1	D	90	GLN	2.1
1	A	89	MET	2.1
1	C	24	GLU	2.1
1	D	200	PRO	2.1
1	D	182	LYS	2.1
1	D	91	ASP	2.1
1	C	199	ALA	2.0
1	C	296	ALA	2.0
1	F	144	GLY	2.0
1	D	63	ILE	2.0
2	G	1	LEU	2.0
1	D	33	PRO	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

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.