



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 10:18 PM GMT

PDB ID : 5CQR
Title : Dimerization of Elp1 is essential for Elongator complex assembly
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Deposited on : 2015-07-22
Resolution : 3.02 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20026982

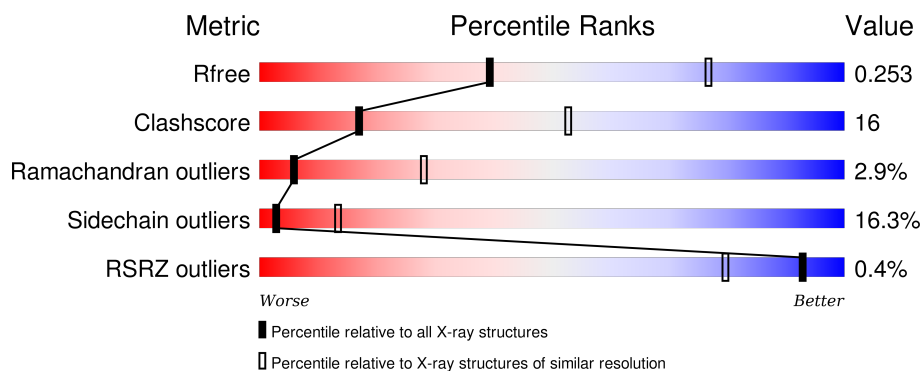
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


The reported resolution of this entry is 3.02 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}	91344	1773 (3.04-3.00)
Clashscore	102246	2117 (3.04-3.00)
Ramachandran outliers	100387	2050 (3.04-3.00)
Sidechain outliers	100360	2053 (3.04-3.00)
RSRZ outliers	91569	1788 (3.04-3.00)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	622	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3600 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 Elongator complex protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	455	3595	2310	598	665	22	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	711	GLY	-	expression tag	UNP O95163
A	712	PRO	-	expression tag	UNP O95163
A	713	GLY	-	expression tag	UNP O95163
A	714	SER	-	expression tag	UNP O95163

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	5	Total	O	0	0
			5	5		

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ($\text{RSRZ} > 2$). 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.

Chain A:

Sequence logo for Chain A. The y-axis represents information content in bits (0.00 to 0.15). The x-axis shows positions 1 to 100. The color scale at the top indicates conservation levels: 45% (yellow), 23% (orange), 5% (red), and 27% (purple).

Position	Most Conserved Residue	Information Content (bits)
1	ALA	0.02
2	SER	0.02
3	TYR	0.02
4	GLN	0.02
5	GLN	0.02
6	GLN	0.02
7	GLN	0.02
8	LYS	0.02
9	LYS	0.02
10	THR	0.02
11	SER	0.02
12	VAL	0.02
13	PRO	0.02
14	VAL	0.02
15	LEU	0.02
16	ASP	0.02
17	ASP	0.02
18	ALA	0.02
19	GLU	0.02
20	LEU	0.02
21	PHE	0.02
22	ILE	0.02
23	PRO	0.02
24	PRO	0.02
25	PRO	0.02
26	LYS	0.02
27	ILE	0.02
28	ASP	0.02
29	ASP	0.02
30	ASP	0.02
31	ASP	0.02
32	ASP	0.02
33	ASP	0.02
34	ASP	0.02
35	ASP	0.02
36	ASP	0.02
37	ASP	0.02
38	ASP	0.02
39	ASP	0.02
40	ASP	0.02
41	ASP	0.02
42	ASP	0.02
43	ASP	0.02
44	ASP	0.02
45	ASP	0.02
46	ASP	0.02
47	ASP	0.02
48	ASP	0.02
49	ASP	0.02
50	ASP	0.02
51	ASP	0.02
52	ASP	0.02
53	ASP	0.02
54	ASP	0.02
55	ASP	0.02
56	ASP	0.02
57	ASP	0.02
58	ASP	0.02
59	ASP	0.02
60	ASP	0.02
61	ASP	0.02
62	ASP	0.02
63	ASP	0.02
64	ASP	0.02
65	ASP	0.02
66	ASP	0.02
67	ASP	0.02
68	ASP	0.02
69	ASP	0.02
70	ASP	0.02
71	ASP	0.02
72	ASP	0.02
73	ASP	0.02
74	ASP	0.02
75	ASP	0.02
76	ASP	0.02
77	ASP	0.02
78	ASP	0.02
79	ASP	0.02
80	ASP	0.02
81	ASP	0.02
82	ASP	0.02
83	ASP	0.02
84	ASP	0.02
85	ASP	0.02
86	ASP	0.02
87	ASP	0.02
88	ASP	0.02
89	ASP	0.02
90	ASP	0.02
91	ASP	0.02
92	ASP	0.02
93	ASP	0.02
94	ASP	0.02
95	ASP	0.02
96	ASP	0.02
97	ASP	0.02
98	ASP	0.02
99	ASP	0.02
100	ASP	0.02

4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	73.02Å 73.02Å 479.51Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.47 – 3.02 46.47 – 3.02	Depositor EDS
% Data completeness (in resolution range)	86.8 (46.47-3.02) 86.8 (46.47-3.02)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.32 (at 3.01Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.221 , 0.270 0.202 , 0.253	Depositor DCC
R_{free} test set	1398 reflections (9.97%)	DCC
Wilson B-factor (Å ²)	50.3	Xtriage
Anisotropy	0.323	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 44.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 14027 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	3600	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.39% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.43	0/3664	0.62	0/4957

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 [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	3595	0	3506	116	0
2	A	5	0	0	1	0
All	All	3600	0	3506	116	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 16.

All (116) 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:A:1090:GLU:HG3	1:A:1238:HIS:HE1	1.37	0.87
1:A:776:SER:O	1:A:780:ILE:HG22	1.74	0.87
1:A:855:LEU:HD13	1:A:893:HIS:HB3	1.58	0.86
1:A:722:ARG:HH11	1:A:722:ARG:CG	1.89	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:791:ASP:OD1	1:A:793:THR:HB	1.81	0.81
1:A:1090:GLU:HG3	1:A:1238:HIS:CE1	2.17	0.79
1:A:996:LEU:HB3	1:A:1005:ALA:HB2	1.63	0.78
1:A:918:LEU:N	1:A:919:PRO:HD2	1.97	0.78
1:A:722:ARG:HG2	1:A:722:ARG:HH11	1.47	0.77
1:A:830:ILE:O	1:A:831:ASN:HB2	1.87	0.73
1:A:1227:GLN:HG3	1:A:1229:THR:HG23	1.80	0.64
1:A:1235:GLU:O	1:A:1239:ILE:HG22	1.98	0.63
1:A:824:ARG:HG3	1:A:839:ILE:HG23	1.80	0.62
1:A:958:PHE:N	1:A:959:PRO:HD2	2.15	0.61
1:A:975:LEU:HD21	1:A:988:ILE:HG22	1.82	0.61
1:A:950:LEU:HD13	1:A:961:CYS:HB2	1.83	0.61
1:A:1023:LEU:CD2	1:A:1052:LEU:HD23	2.30	0.60
1:A:780:ILE:HD11	1:A:827:MET:SD	2.41	0.60
1:A:928:GLU:OE1	1:A:930:ASN:HB2	2.01	0.60
1:A:1103:ASP:O	1:A:1107:THR:HG23	2.02	0.59
1:A:919:PRO:O	1:A:923:THR:HG23	2.01	0.59
1:A:1121:MET:HE1	1:A:1258:ALA:HB3	1.84	0.59
1:A:1046:VAL:HG22	1:A:1073:ALA:HA	1.85	0.59
1:A:904:LEU:O	1:A:908:GLU:HG2	2.03	0.58
1:A:749:ARG:HB2	1:A:749:ARG:CZ	2.32	0.58
1:A:928:GLU:HG2	1:A:929:THR:N	2.17	0.58
1:A:794:LYS:HA	1:A:794:LYS:HE3	1.86	0.58
1:A:1264:GLN:C	1:A:1266:MET:H	2.08	0.57
1:A:835:TYR:O	1:A:839:ILE:HG13	2.05	0.57
1:A:769:THR:O	1:A:773:GLN:HG3	2.06	0.56
1:A:917:TYR:CE1	1:A:918:LEU:HD22	2.41	0.56
1:A:918:LEU:N	1:A:919:PRO:CD	2.68	0.56
1:A:1023:LEU:HD23	1:A:1052:LEU:HD23	1.87	0.56
1:A:722:ARG:HG2	1:A:722:ARG:NH1	2.14	0.55
1:A:1330:LEU:O	1:A:1331:LEU:HD23	2.07	0.55
1:A:761:LYS:HE3	1:A:811:PRO:N	2.22	0.55
1:A:1002:TYR:CE1	1:A:1024:THR:HG21	2.42	0.55
1:A:924:LEU:O	1:A:927:MET:HG3	2.07	0.54
1:A:743:GLU:HA	1:A:743:GLU:OE1	2.07	0.54
1:A:745:MET:SD	1:A:755:ILE:HG22	2.48	0.54
1:A:1063:ILE:HD12	1:A:1088:ALA:HB2	1.89	0.54
1:A:1003:GLU:HB3	1:A:1004:PRO:HD3	1.90	0.54
1:A:814:ASN:O	1:A:818:LEU:HG	2.08	0.53
1:A:1121:MET:HE1	1:A:1258:ALA:CB	2.38	0.53
1:A:824:ARG:O	1:A:828:GLU:HG2	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:927:MET:HB2	1:A:932:GLN:HB2	1.90	0.53
1:A:978:TYR:CD1	1:A:978:TYR:N	2.76	0.53
1:A:1015:HIS:HB2	1:A:1038:LEU:HD21	1.91	0.52
1:A:978:TYR:N	1:A:978:TYR:HD1	2.08	0.52
1:A:1261:ASP:C	1:A:1263:LEU:H	2.13	0.51
1:A:771:ILE:CD1	1:A:780:ILE:HD12	2.40	0.51
1:A:855:LEU:HD13	1:A:893:HIS:CB	2.34	0.51
1:A:722:ARG:HH11	1:A:722:ARG:HG3	1.75	0.51
1:A:950:LEU:HD22	1:A:957:TYR:HB3	1.94	0.50
1:A:1028:TRP:CE3	1:A:1068:VAL:HG22	2.47	0.50
1:A:1256:GLN:HE22	1:A:1328:LEU:H	1.60	0.49
1:A:780:ILE:O	1:A:780:ILE:HG12	2.11	0.49
1:A:903:VAL:O	1:A:906:VAL:HG22	2.13	0.49
1:A:943:TYR:O	1:A:947:ILE:HG12	2.12	0.49
1:A:1050:ARG:HH12	1:A:1075:ASP:CG	2.16	0.48
1:A:742:PHE:C	1:A:742:PHE:CD2	2.85	0.48
1:A:868:ASP:C	1:A:870:ASP:H	2.16	0.48
1:A:776:SER:O	1:A:780:ILE:CG2	2.56	0.48
1:A:1264:GLN:C	1:A:1266:MET:N	2.67	0.48
1:A:1328:LEU:C	1:A:1330:LEU:N	2.66	0.48
1:A:774:ILE:O	1:A:775:ASP:C	2.50	0.47
1:A:944:GLU:HG3	1:A:973:GLU:HG3	1.95	0.47
1:A:1232:LEU:O	1:A:1232:LEU:HG	2.15	0.47
1:A:1050:ARG:NH1	1:A:1075:ASP:OD2	2.47	0.47
1:A:1129:ALA:C	1:A:1131:PHE:H	2.17	0.47
1:A:756:TYR:C	1:A:756:TYR:CD2	2.87	0.47
1:A:812:ASP:OD1	1:A:812:ASP:C	2.52	0.47
1:A:843:HIS:HB3	1:A:854:VAL:HG23	1.95	0.47
1:A:958:PHE:N	1:A:959:PRO:CD	2.79	0.46
1:A:1259:PHE:O	1:A:1263:LEU:HB2	2.15	0.46
1:A:1328:LEU:HA	1:A:1328:LEU:HD22	1.75	0.46
1:A:953:CYS:O	1:A:957:TYR:HD2	1.98	0.46
1:A:1234:ASP:O	1:A:1237:TYR:HB3	2.15	0.46
1:A:1117:GLN:HG3	1:A:1118:LYS:N	2.31	0.45
1:A:1053:ALA:HB2	1:A:1069:LEU:HD13	1.98	0.45
1:A:728:GLN:CA	1:A:728:GLN:NE2	2.80	0.45
1:A:763:PHE:CD2	1:A:763:PHE:C	2.90	0.45
1:A:768:GLU:HA	1:A:826:VAL:HG11	1.99	0.45
1:A:1232:LEU:O	1:A:1236:VAL:HG23	2.17	0.44
1:A:1098:LYS:O	1:A:1098:LYS:HG2	2.16	0.44
1:A:1028:TRP:HA	1:A:1031:ALA:HB3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:980:PRO:O	1:A:981:SER:CB	2.66	0.44
1:A:975:LEU:CD2	1:A:988:ILE:HG22	2.47	0.44
1:A:1121:MET:HA	1:A:1121:MET:HE3	2.00	0.44
1:A:780:ILE:CG1	1:A:780:ILE:O	2.66	0.43
1:A:749:ARG:HB2	1:A:749:ARG:NH1	2.33	0.43
1:A:1261:ASP:O	1:A:1265:LEU:HB2	2.18	0.43
1:A:858:VAL:CG1	1:A:858:VAL:O	2.66	0.43
1:A:1256:GLN:HE22	1:A:1327:LYS:HA	1.83	0.43
1:A:1067:MET:O	1:A:1071:GLU:HG2	2.18	0.43
1:A:776:SER:HB3	1:A:779:HIS:HB2	2.00	0.43
1:A:861:LEU:HA	1:A:861:LEU:HD23	1.81	0.43
1:A:1028:TRP:CB	1:A:1052:LEU:HD13	2.49	0.42
1:A:788:LYS:NZ	1:A:788:LYS:HB2	2.34	0.42
1:A:780:ILE:HD13	1:A:780:ILE:HG21	1.76	0.42
1:A:852:GLU:HB2	2:A:1402:HOH:O	2.20	0.42
1:A:1055:LYS:NZ	1:A:1055:LYS:HB3	2.35	0.42
1:A:1328:LEU:C	1:A:1330:LEU:H	2.23	0.42
1:A:996:LEU:HD12	1:A:996:LEU:HA	1.68	0.41
1:A:1264:GLN:O	1:A:1266:MET:N	2.53	0.41
1:A:1028:TRP:HB2	1:A:1052:LEU:HD13	2.02	0.41
1:A:1262:THR:HG22	1:A:1262:THR:O	2.20	0.41
1:A:1235:GLU:H	1:A:1235:GLU:HG3	1.68	0.41
1:A:993:GLY:HA3	1:A:1009:PHE:CZ	2.55	0.41
1:A:1244:PHE:CD2	1:A:1244:PHE:C	2.94	0.41
1:A:1121:MET:HA	1:A:1121:MET:CE	2.50	0.41
1:A:852:GLU:O	1:A:856:GLN:HG2	2.20	0.41
1:A:1261:ASP:C	1:A:1263:LEU:N	2.73	0.41
1:A:721:HIS:CD2	1:A:721:HIS:H	2.38	0.41
1:A:1083:LEU:HD12	1:A:1092:ALA:HA	2.03	0.40
1:A:755:ILE:HG21	1:A:755:ILE:HD13	1.66	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	445/622 (72%)	389 (87%)	43 (10%)	13 (3%)	6	28

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1122	ALA
1	A	1126	SER
1	A	776	SER
1	A	831	ASN
1	A	895	LEU
1	A	1265	LEU
1	A	1130	THR
1	A	910	SER
1	A	1076	TYR
1	A	950	LEU
1	A	1262	THR
1	A	869	PRO
1	A	868	ASP

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	374/555 (67%)	313 (84%)	61 (16%)	3	13

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	722	ARG
1	A	724	LEU
1	A	728	GLN
1	A	744	CYS
1	A	754	LEU
1	A	755	ILE

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Mol	Chain	Res	Type
1	A	761	LYS
1	A	768	GLU
1	A	769	THR
1	A	774	ILE
1	A	775	ASP
1	A	779	HIS
1	A	780	ILE
1	A	782	LEU
1	A	794	LYS
1	A	812	ASP
1	A	838	SER
1	A	844	VAL
1	A	852	GLU
1	A	855	LEU
1	A	870	ASP
1	A	875	GLU
1	A	878	LEU
1	A	882	LEU
1	A	890	LEU
1	A	918	LEU
1	A	923	THR
1	A	928	GLU
1	A	941	LYS
1	A	964	LEU
1	A	968	LYS
1	A	978	TYR
1	A	989	SER
1	A	992	TYR
1	A	994	GLU
1	A	996	LEU
1	A	997	MET
1	A	1001	MET
1	A	1017	LYS
1	A	1048	LEU
1	A	1069	LEU
1	A	1075	ASP
1	A	1078	GLU
1	A	1085	GLU
1	A	1093	LEU
1	A	1105	ILE
1	A	1117	GLN
1	A	1125	ASP

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Mol	Chain	Res	Type
1	A	1227	GLN
1	A	1231	ASN
1	A	1232	LEU
1	A	1234	ASP
1	A	1247	GLU
1	A	1249	ASP
1	A	1251	GLN
1	A	1255	LEU
1	A	1264	GLN
1	A	1265	LEU
1	A	1324	THR
1	A	1325	GLN
1	A	1328	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	721	HIS
1	A	728	GLN
1	A	893	HIS
1	A	922	ASN
1	A	972	ASN
1	A	986	GLN
1	A	1117	GLN
1	A	1227	GLN
1	A	1238	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 carbohydrates 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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	455/622 (73%)	-0.32	2 (0%)	93 79	23, 53, 109, 158	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	812	ASP	3.0
1	A	1266	MET	2.2

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 carbohydrates 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.