



Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 08:02 am BST

PDB ID : 1SVX
Title : Crystal structure of a designed selected Ankyrin Repeat protein in complex with the Maltose Binding Protein
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Deposited on : 2004-03-30
Resolution : 2.24 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 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	:	2.11
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)	:	2.11

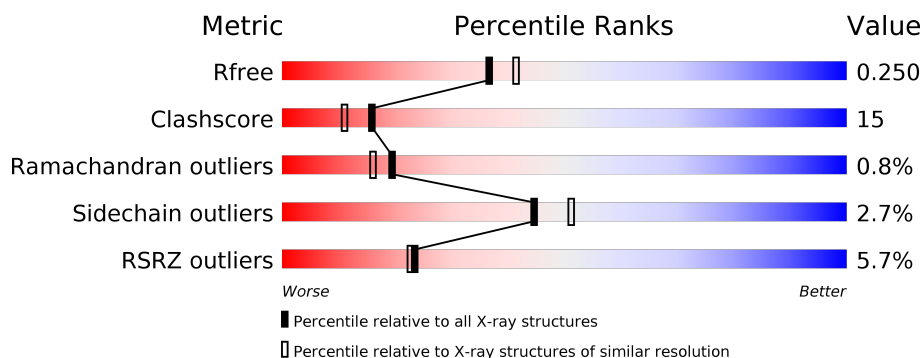
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.24 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	2391 (2.26-2.22)
Clashscore	141614	2539 (2.26-2.22)
Ramachandran outliers	138981	2489 (2.26-2.22)
Sidechain outliers	138945	2490 (2.26-2.22)
RSRZ outliers	127900	2353 (2.26-2.22)

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 on 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	169	<div> <div>3%</div> <div> <div></div> <div>72%</div> <div>20%</div> <div>• 7%</div> </div> </div>
2	B	395	<div> <div>6%</div> <div> <div></div> <div>67%</div> <div>24%</div> <div>• 7%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4245 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 Ankyrin Repeat Protein off7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	157	Total	C	N	O	S	0	0	0
			1187	748	201	235	3			

- Molecule 2 is a protein called Maltose-binding periplasmic protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	369	Total	C	N	O	S	0	0	0
			2843	1829	463	545	6			

There are 31 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-14	MET	-	EXPRESSION TAG	UNP P02928
B	-13	ARG	-	EXPRESSION TAG	UNP P02928
B	-12	GLY	-	EXPRESSION TAG	UNP P02928
B	-11	SER	-	EXPRESSION TAG	UNP P02928
B	-10	HIS	-	EXPRESSION TAG	UNP P02928
B	-9	HIS	-	EXPRESSION TAG	UNP P02928
B	-8	HIS	-	EXPRESSION TAG	UNP P02928
B	-7	HIS	-	EXPRESSION TAG	UNP P02928
B	-6	HIS	-	EXPRESSION TAG	UNP P02928
B	-5	HIS	-	EXPRESSION TAG	UNP P02928
B	-4	GLY	-	EXPRESSION TAG	UNP P02928
B	-3	SER	-	EXPRESSION TAG	UNP P02928
B	-2	GLY	-	EXPRESSION TAG	UNP P02928
B	-1	SER	-	EXPRESSION TAG	UNP P02928
B	0	MET	-	EXPRESSION TAG	UNP P02928
B	1	LYS	-	EXPRESSION TAG	UNP P02928
B	2	THR	-	EXPRESSION TAG	UNP P02928
B	367	GLY	-	CLONING ARTIFACT	UNP P02928
B	368	SER	-	CLONING ARTIFACT	UNP P02928
B	369	GLY	-	CLONING ARTIFACT	UNP P02928

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Chain	Residue	Modelled	Actual	Comment	Reference
B	370	GLY	-	CLONING ARTIFACT	UNP P02928
B	371	THR	-	CLONING ARTIFACT	UNP P02928
B	372	PRO	-	CLONING ARTIFACT	UNP P02928
B	373	GLY	-	CLONING ARTIFACT	UNP P02928
B	374	ARG	-	CLONING ARTIFACT	UNP P02928
B	375	PRO	-	CLONING ARTIFACT	UNP P02928
B	376	ALA	-	CLONING ARTIFACT	UNP P02928
B	377	ALA	-	CLONING ARTIFACT	UNP P02928
B	378	LYS	-	CLONING ARTIFACT	UNP P02928
B	379	LEU	-	CLONING ARTIFACT	UNP P02928
B	380	ASN	-	CLONING ARTIFACT	UNP P02928

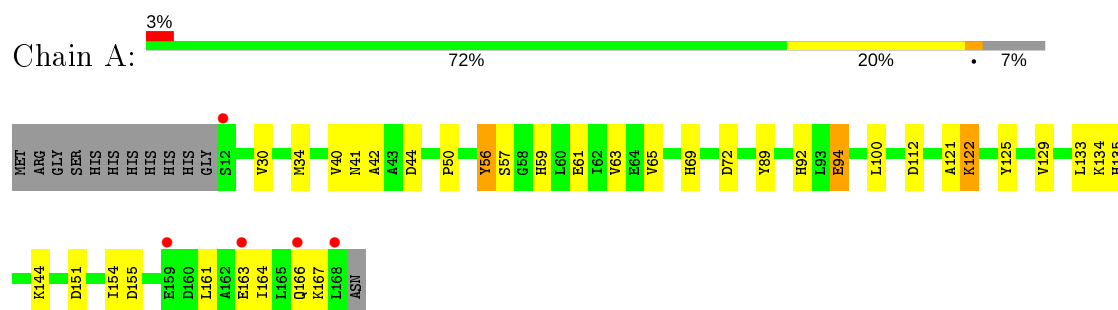
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	51	Total O 51 51	0	0
3	B	164	Total O 164 164	0	0

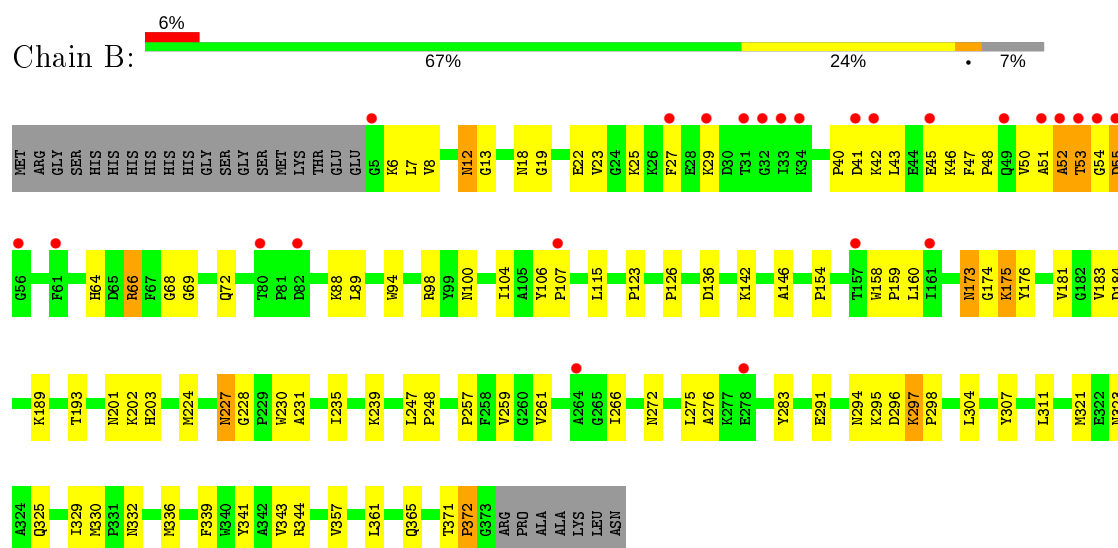
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Ankyrin Repeat Protein off7



• Molecule 2: Maltose-binding periplasmic protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	74.68Å 45.15Å 79.57Å 90.00° 107.24° 90.00°	Depositor
Resolution (Å)	25.00 – 2.24 24.48 – 2.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (25.00-2.24) 97.5 (24.48-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.21 (at 2.19Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.195 , 0.249 0.198 , 0.250	Depositor DCC
R_{free} test set	1228 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å ²)	31.6	Xtriage
Anisotropy	0.230	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 47.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4245	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.63% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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	0.30	0/1207	0.51	0/1640
2	B	0.35	0/2913	0.55	0/3956
All	All	0.34	0/4120	0.54	0/5596

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	1187	0	1159	29	0
2	B	2843	0	2807	89	0
3	A	51	0	0	3	0
3	B	164	0	0	3	0
All	All	4245	0	3966	117	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 15.

All (117) 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:41:ASN:HD21	1:A:72:ASP:H	1.07	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:227:ASN:HD22	2:B:228:GLY:H	1.21	0.84
2:B:115:LEU:HD21	2:B:224:MET:CE	2.12	0.79
2:B:98:ARG:HD2	2:B:174:GLY:HA2	1.66	0.78
2:B:247:LEU:H	2:B:323:ASN:HD21	1.31	0.76
2:B:115:LEU:HD21	2:B:224:MET:HE1	1.66	0.75
2:B:64:HIS:HD2	2:B:261:VAL:H	1.33	0.74
1:A:34:MET:HE1	1:A:40:VAL:HG13	1.70	0.73
2:B:68:GLY:HA3	2:B:332:ASN:O	1.89	0.72
2:B:126:PRO:HD2	2:B:224:MET:CE	2.19	0.71
2:B:54:GLY:HA3	3:B:544:HOH:O	1.90	0.71
2:B:175:LYS:HE2	2:B:175:LYS:HA	1.74	0.70
2:B:266:ILE:HD12	2:B:276:ALA:HB1	1.74	0.69
1:A:34:MET:HE3	1:A:40:VAL:HG22	1.76	0.68
2:B:272:ASN:HB2	2:B:275:LEU:HD12	1.76	0.68
1:A:94:GLU:HB2	3:A:186:HOH:O	1.94	0.67
2:B:175:LYS:HE2	2:B:176:TYR:H	1.60	0.66
2:B:239:LYS:HB2	2:B:239:LYS:NZ	2.12	0.65
2:B:189:LYS:O	2:B:193:THR:HG23	1.97	0.64
1:A:163:GLU:O	1:A:166:GLN:HB2	1.97	0.63
2:B:64:HIS:HE1	2:B:330:MET:O	1.80	0.63
2:B:64:HIS:CD2	2:B:261:VAL:H	2.17	0.62
2:B:42:LYS:HG2	2:B:42:LYS:O	2.01	0.61
2:B:51:ALA:O	2:B:53:THR:N	2.34	0.61
2:B:89:LEU:HD22	2:B:94:TRP:CZ2	2.36	0.61
1:A:134:LYS:HB2	1:A:134:LYS:NZ	2.17	0.60
2:B:371:THR:CG2	2:B:372:PRO:HD2	2.31	0.59
2:B:371:THR:HG22	2:B:372:PRO:HD2	1.84	0.59
2:B:126:PRO:HD2	2:B:224:MET:HE3	1.84	0.59
2:B:100:ASN:HA	2:B:175:LYS:HD2	1.85	0.58
1:A:125:TYR:O	1:A:129:VAL:HG23	2.03	0.58
2:B:142:LYS:HG3	2:B:142:LYS:O	2.03	0.58
1:A:151:ASP:O	1:A:154:ILE:HG12	2.04	0.58
2:B:126:PRO:HD2	2:B:224:MET:HE1	1.86	0.58
2:B:227:ASN:HD22	2:B:228:GLY:N	1.96	0.57
1:A:89:TYR:OH	2:B:203:HIS:HE1	1.86	0.57
1:A:41:ASN:ND2	1:A:72:ASP:H	1.91	0.57
2:B:115:LEU:HD21	2:B:224:MET:HE2	1.86	0.57
2:B:227:ASN:HD21	2:B:230:TRP:HE1	1.51	0.56
2:B:184:ASP:HB2	2:B:365:GLN:HB2	1.86	0.56
2:B:22:GLU:O	2:B:25:LYS:HB3	2.06	0.56
2:B:193:THR:HG22	2:B:357:VAL:HG21	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:66:ARG:HH11	2:B:66:ARG:HG2	1.72	0.54
2:B:175:LYS:HE2	2:B:175:LYS:CA	2.37	0.54
2:B:52:ALA:O	2:B:53:THR:HG22	2.08	0.54
2:B:53:THR:HG23	2:B:54:GLY:N	2.23	0.53
1:A:122:LYS:HD2	3:A:200:HOH:O	2.07	0.53
2:B:341:TYR:HD2	2:B:344:ARG:HH21	1.57	0.52
1:A:30:VAL:O	1:A:34:MET:HG2	2.10	0.52
2:B:239:LYS:HB2	2:B:239:LYS:HZ2	1.73	0.51
2:B:136:ASP:HA	2:B:146:ALA:HB2	1.92	0.51
2:B:291:GLU:O	2:B:295:LYS:HG2	2.10	0.51
1:A:121:ALA:HA	1:A:161:LEU:CD2	2.41	0.51
2:B:19:GLY:O	2:B:23:VAL:HG23	2.11	0.50
2:B:7:LEU:HD23	2:B:272:ASN:ND2	2.27	0.50
2:B:50:VAL:HG22	2:B:55:ASP:O	2.12	0.49
1:A:34:MET:CE	1:A:40:VAL:HG22	2.41	0.49
2:B:154:PRO:HB3	2:B:343:VAL:HG12	1.94	0.49
2:B:294:ASN:OD1	2:B:298:PRO:HA	2.13	0.49
2:B:41:ASP:O	2:B:42:LYS:HB3	2.13	0.49
2:B:98:ARG:HD2	2:B:174:GLY:CA	2.38	0.48
1:A:56:TYR:O	1:A:92:HIS:HE1	1.97	0.48
2:B:27:PHE:HA	2:B:283:TYR:CE2	2.48	0.48
1:A:72:ASP:HB3	3:A:174:HOH:O	2.14	0.47
2:B:181:VAL:HG12	2:B:183:VAL:HG13	1.94	0.47
2:B:142:LYS:O	2:B:142:LYS:CG	2.63	0.47
2:B:115:LEU:HD22	2:B:248:PRO:HD3	1.97	0.47
2:B:12:ASN:ND2	2:B:13:GLY:H	2.12	0.47
2:B:43:LEU:C	2:B:43:LEU:HD12	2.34	0.47
1:A:154:ILE:HG13	1:A:155:ASP:N	2.30	0.46
2:B:136:ASP:OD2	2:B:203:HIS:HD2	1.98	0.46
1:A:57:SER:HB2	1:A:59:HIS:CD2	2.51	0.46
2:B:158:TRP:N	2:B:159:PRO:CD	2.79	0.46
1:A:100:LEU:HD13	1:A:135:HIS:CD2	2.51	0.46
2:B:40:PRO:O	2:B:43:LEU:HB3	2.16	0.46
2:B:6:LYS:HE2	2:B:8:VAL:HG22	1.98	0.46
1:A:164:ILE:C	1:A:166:GLN:H	2.19	0.45
2:B:29:LYS:O	2:B:29:LYS:HG2	2.16	0.45
1:A:42:ALA:O	1:A:50:PRO:HD3	2.16	0.45
2:B:307:TYR:CE2	2:B:311:LEU:HD11	2.50	0.45
2:B:100:ASN:OD1	2:B:175:LYS:HD2	2.17	0.45
1:A:59:HIS:O	1:A:63:VAL:HG23	2.17	0.45
2:B:175:LYS:HA	2:B:175:LYS:CE	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:272:ASN:CB	2:B:275:LEU:HD12	2.44	0.44
2:B:266:ILE:HD12	2:B:276:ALA:CB	2.44	0.44
2:B:104:ILE:C	2:B:104:ILE:HD12	2.37	0.44
2:B:64:HIS:CE1	2:B:330:MET:O	2.68	0.44
2:B:100:ASN:HA	2:B:175:LYS:CD	2.47	0.43
1:A:61:GLU:O	1:A:65:VAL:HG23	2.19	0.43
1:A:167:LYS:O	1:A:167:LYS:HG3	2.18	0.43
2:B:18:ASN:HB2	2:B:296:ASP:CG	2.39	0.43
2:B:159:PRO:HG3	2:B:257:PRO:HA	2.01	0.43
2:B:42:LYS:HG2	2:B:45:GLU:HB2	2.00	0.43
2:B:47:PHE:N	2:B:48:PRO:HD2	2.34	0.43
1:A:129:VAL:O	1:A:133:LEU:HG	2.19	0.42
2:B:88:LYS:O	2:B:304:LEU:HD12	2.19	0.42
2:B:69:GLY:O	2:B:72:GLN:HB3	2.18	0.42
2:B:336:MET:O	2:B:339:PHE:HB3	2.18	0.42
2:B:175:LYS:HE2	2:B:176:TYR:N	2.29	0.42
2:B:321:MET:O	2:B:325:GLN:HG3	2.19	0.42
2:B:231:ALA:O	2:B:235:ILE:HG13	2.20	0.42
2:B:46:LYS:O	2:B:50:VAL:HG12	2.19	0.42
1:A:121:ALA:HA	1:A:161:LEU:HD21	2.01	0.42
2:B:12:ASN:HD22	2:B:13:GLY:H	1.66	0.42
2:B:201:ASN:O	2:B:202:LYS:HB2	2.20	0.42
2:B:193:THR:HG23	2:B:357:VAL:HG11	2.00	0.42
1:A:44:ASP:C	1:A:44:ASP:OD1	2.58	0.42
2:B:297:LYS:HD2	3:B:466:HOH:O	2.19	0.42
2:B:100:ASN:H	2:B:175:LYS:HE3	1.84	0.41
2:B:54:GLY:O	2:B:55:ASP:CG	2.59	0.41
2:B:259:VAL:HB	2:B:329:ILE:HD13	2.03	0.41
2:B:361:LEU:HD23	2:B:361:LEU:HA	1.89	0.41
2:B:106:TYR:HA	2:B:107:PRO:HD3	1.92	0.41
2:B:181:VAL:CG1	2:B:183:VAL:HG13	2.51	0.41
1:A:112:ASP:HA	1:A:144:LYS:HE2	2.03	0.41
1:A:40:VAL:HG21	1:A:69:HIS:HB3	2.02	0.40
2:B:123:PRO:HG2	3:B:383:HOH:O	2.22	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	155/169 (92%)	148 (96%)	7 (4%)	0	100	100
2	B	367/395 (93%)	348 (95%)	15 (4%)	4 (1%)	14	9
All	All	522/564 (93%)	496 (95%)	22 (4%)	4 (1%)	19	16

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	173	ASN
2	B	52	ALA
2	B	55	ASP
2	B	372	PRO

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	122/132 (92%)	119 (98%)	3 (2%)	47	54
2	B	292/313 (93%)	284 (97%)	8 (3%)	44	51
All	All	414/445 (93%)	403 (97%)	11 (3%)	44	51

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	56	TYR
1	A	94	GLU

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Mol	Chain	Res	Type
1	A	122	LYS
2	B	12	ASN
2	B	53	THR
2	B	66	ARG
2	B	160	LEU
2	B	173	ASN
2	B	175	LYS
2	B	227	ASN
2	B	297	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	ASN
1	A	92	HIS
1	A	135	HIS
1	A	140	ASN
2	B	12	ASN
2	B	49	GLN
2	B	64	HIS
2	B	201	ASN
2	B	203	HIS
2	B	218	ASN
2	B	227	ASN
2	B	323	ASN
2	B	349	ASN
2	B	355	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	157/169 (92%)	-0.06	5 (3%) 47 47	20, 34, 62, 83	0
2	B	369/395 (93%)	0.10	25 (6%) 17 17	14, 31, 66, 83	0
All	All	526/564 (93%)	0.05	30 (5%) 23 23	14, 33, 66, 83	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	53	THR	5.6
1	A	12	SER	5.5
2	B	52	ALA	4.7
2	B	32	GLY	4.0
2	B	80	THR	3.8
2	B	55	ASP	3.6
2	B	54	GLY	3.5
2	B	41	ASP	3.3
2	B	31	THR	3.2
2	B	42	LYS	2.8
2	B	5	GLY	2.7
2	B	29	LYS	2.6
2	B	264	ALA	2.6
2	B	56	GLY	2.4
2	B	82	ASP	2.4
1	A	159	GLU	2.3
2	B	49	GLN	2.3
1	A	163	GLU	2.3
2	B	34	LYS	2.2
2	B	45	GLU	2.2
2	B	51	ALA	2.2
1	A	168	LEU	2.2
2	B	33	ILE	2.2
2	B	278	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
2	B	161	ILE	2.1
2	B	27	PHE	2.1
2	B	61	PHE	2.1
2	B	157	THR	2.1
2	B	107	PRO	2.1
1	A	166	GLN	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 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.