



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 13, 2026 – 07:29 PM UTC

PDB ID : 5VAY / pdb_00005vay
Title : Bcl-2 complex with Beclin 1 T108D BH3 domain
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Deposited on : 2017-03-28
Resolution : 1.80 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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

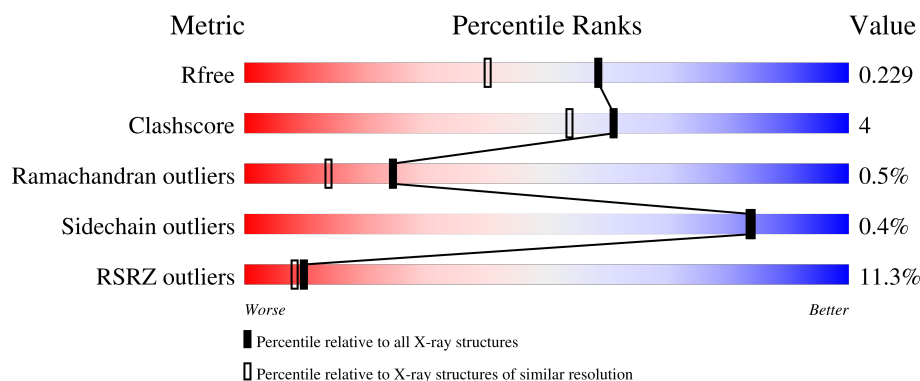
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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.



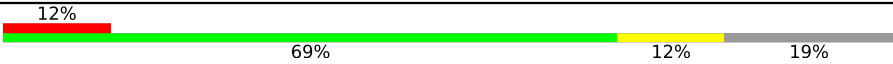
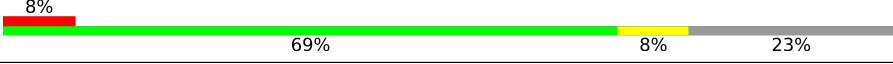
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	168	8% 82% 8% 10%
1	B	168	10% 75% 11% 14%
1	C	168	8% 71% 11% 17%
1	D	168	12% 71% 10% 19%
2	E	26	15% 65% 15% 19%

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Mol	Chain	Length	Quality of chain
2	F	26	
2	G	26	
2	H	26	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5762 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 Apoptosis regulator Bcl-2 – Bcl-2-like protein 1 Chimera.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	151	Total	C	N	O	S	0	9	0
			1306	829	230	239	8			
1	B	145	Total	C	N	O	S	0	5	0
			1224	774	220	224	6			
1	C	139	Total	C	N	O	S	0	4	0
			1175	750	206	213	6			
1	D	136	Total	C	N	O	S	0	3	0
			1135	727	194	207	7			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P10415
A	0	SER	-	expression tag	UNP P10415
B	-1	GLY	-	expression tag	UNP P10415
B	0	SER	-	expression tag	UNP P10415
C	-1	GLY	-	expression tag	UNP P10415
C	0	SER	-	expression tag	UNP P10415
D	-1	GLY	-	expression tag	UNP P10415
D	0	SER	-	expression tag	UNP P10415

- Molecule 2 is a protein called Beclin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	21	Total	C	N	O	S	0	4	0
			177	109	30	36	2			
2	G	21	Total	C	N	O	S	0	1	0
			164	101	27	34	2			
2	F	21	Total	C	N	O	S	0	0	0
			161	99	29	31	2			
2	H	20	Total	C	N	O	S	0	1	0
			164	102	29	31	2			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	108	ASP	THR	engineered mutation	UNP Q14457
G	108	ASP	THR	engineered mutation	UNP Q14457
F	108	ASP	THR	engineered mutation	UNP Q14457
H	108	ASP	THR	engineered mutation	UNP Q14457

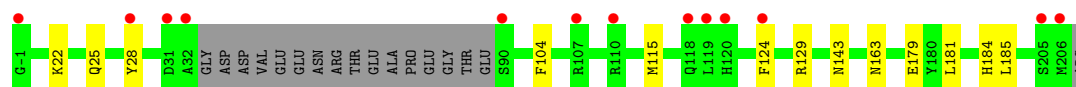
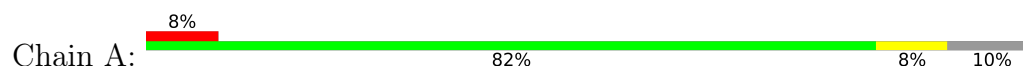
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	98	Total O 98 98	0	0
3	B	68	Total O 68 68	0	0
3	C	37	Total O 37 37	0	0
3	D	36	Total O 36 36	0	0
3	E	3	Total O 3 3	0	0
3	G	4	Total O 4 4	0	0
3	F	6	Total O 6 6	0	0
3	H	4	Total O 4 4	0	0

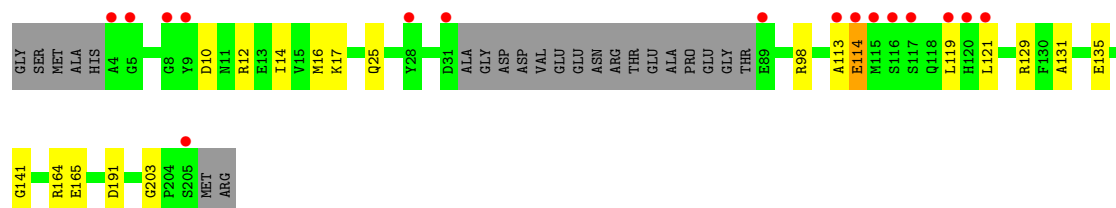
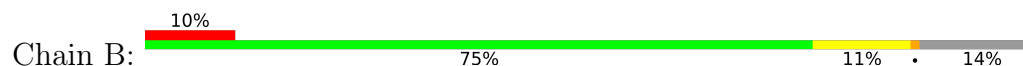
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

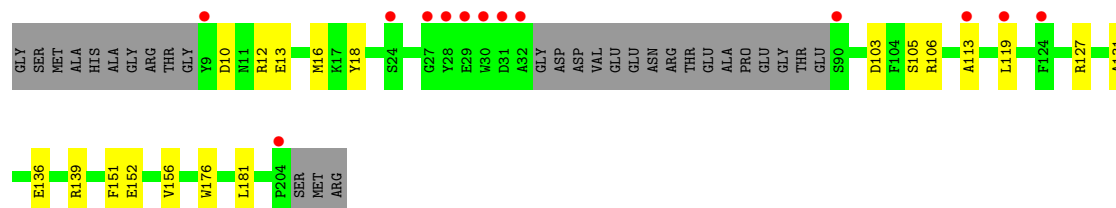
- Molecule 1: Apoptosis regulator Bcl-2 – Bcl-2-like protein 1 Chimera



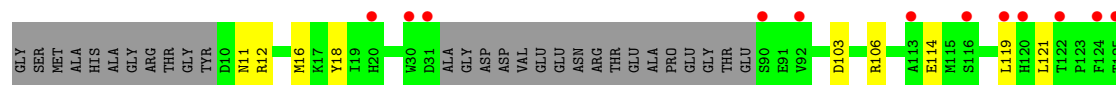
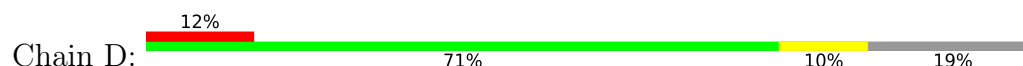
- Molecule 1: Apoptosis regulator Bcl-2 – Bcl-2-like protein 1 Chimera

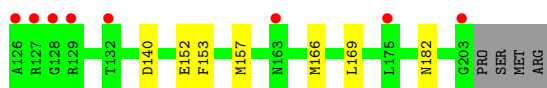


- Molecule 1: Apoptosis regulator Bcl-2 – Bcl-2-like protein 1 Chimera



- Molecule 1: Apoptosis regulator Bcl-2 – Bcl-2-like protein 1 Chimera





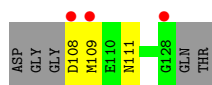
● Molecule 2: Beclin-1



● Molecule 2: Beclin-1



● Molecule 2: Beclin-1



● Molecule 2: Beclin-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	85.20Å 53.19Å 91.41Å 90.00° 108.39° 90.00°	Depositor
Resolution (Å)	50.00 – 1.80 50.00 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.0 (50.00-1.80) 99.0 (50.00-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 1.81Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.184 , 0.228 0.186 , 0.229	Depositor DCC
R_{free} test set	3560 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	24.1	Xtriage
Anisotropy	0.217	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 45.4	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	0.96	EDS
Total number of atoms	5762	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.90% 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	0.50	0/1340	0.71	0/1811
1	B	0.48	0/1255	0.75	3/1696 (0.2%)
1	C	0.42	0/1207	0.68	0/1634
1	D	0.39	0/1164	0.68	0/1573
2	E	0.43	0/177	0.68	0/236
2	F	0.44	0/161	0.78	0/213
2	G	0.46	0/164	0.63	0/218
2	H	0.37	0/164	0.64	0/218
All	All	0.45	0/5632	0.70	3/7599 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	203	GLY	CA-C-N	5.18	125.26	119.87
1	B	203	GLY	C-N-CA	5.18	125.26	119.87
1	B	141	GLY	N-CA-C	5.10	117.25	111.85

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	114	GLU	Peptide

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	1306	0	1210	12	1
1	B	1224	0	1136	12	1
1	C	1175	0	1092	11	0
1	D	1135	0	1048	11	0
2	E	177	0	165	4	0
2	F	161	0	161	2	0
2	G	164	0	155	2	0
2	H	164	0	166	1	0
3	A	98	0	0	0	1
3	B	68	0	0	2	1
3	C	37	0	0	0	0
3	D	36	0	0	0	1
3	E	3	0	0	0	0
3	F	6	0	0	0	0
3	G	4	0	0	0	0
3	H	4	0	0	0	0
All	All	5762	0	5133	45	3

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 4.

All (45) 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:131:ALA:O	1:B:135:GLU:HG3	1.83	0.78
2:G:107:GLY:O	2:G:111:ASN:ND2	2.27	0.68
1:C:103[A]:ASP:OD1	1:C:106:ARG:NH2	2.26	0.68
1:C:105[A]:SER:OG	1:C:152:GLU:OE1	2.11	0.67
1:D:103:ASP:OD1	1:D:106:ARG:NH1	2.31	0.64
1:B:12:ARG:O	1:B:16:MET:HG2	2.05	0.56
1:D:119:LEU:HD21	1:D:157[B]:MET:HE1	1.89	0.54
1:A:28[B]:TYR:OH	1:A:163:ASN:OD1	2.18	0.52
1:B:129:ARG:HB3	2:F:108:ASP:HB2	1.92	0.52
1:D:153:PHE:CD1	1:D:157[B]:MET:HE3	2.45	0.51
2:F:109:MET:HB3	2:F:111:ASN:HB2	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:124:PHE:HD2	1:B:25:GLN:HG2	1.75	0.51
1:C:12[A]:ARG:O	1:C:16:MET:HG2	2.12	0.49
1:B:17:LYS:NZ	3:B:306:HOH:O	2.45	0.48
1:C:18:TYR:OH	1:C:152:GLU:OE2	2.24	0.47
1:C:127:ARG:HD3	1:C:176:TRP:CE2	2.49	0.47
1:C:136:GLU:OE2	1:C:139:ARG:NH1	2.48	0.47
1:A:181:LEU:HD12	1:A:185:LEU:HB2	1.95	0.47
1:C:10:ASP:OD2	1:C:13:GLU:HG2	2.14	0.47
1:D:11:ASN:ND2	1:D:182:ASN:OD1	2.41	0.47
1:A:124:PHE:CD2	1:B:25:GLN:HG2	2.51	0.46
2:H:110:GLU:O	2:H:114:ARG:HG3	2.16	0.46
1:C:119:LEU:HD11	1:C:156:VAL:HG12	1.98	0.45
1:D:12:ARG:O	1:D:16:MET:HG2	2.17	0.45
1:A:179[A]:GLU:OE2	1:B:119:LEU:HD22	2.15	0.45
1:B:119:LEU:O	1:B:164:ARG:HD3	2.17	0.45
1:B:98[A]:ARG:HD2	3:B:334:HOH:O	2.17	0.44
1:D:140:ASP:OD1	1:D:140:ASP:N	2.44	0.44
1:C:127:ARG:NH1	1:C:131:ALA:HB2	2.32	0.44
1:D:169:LEU:HD12	1:D:169:LEU:HA	1.83	0.44
1:A:129:ARG:NH1	2:E:109:MET:HE3	2.32	0.44
1:A:184:HIS:NE2	1:B:165:GLU:OE1	2.40	0.44
1:D:121:LEU:HG	1:D:166:MET:HE1	2.00	0.43
1:C:151:PHE:CZ	1:C:181:LEU:HD11	2.53	0.43
1:B:10[B]:ASP:O	1:B:14:ILE:HG13	2.20	0.42
1:C:12[B]:ARG:O	1:C:16:MET:HG2	2.18	0.42
1:A:115:MET:HE3	1:A:115:MET:HB2	1.97	0.42
1:A:143:ASN:HB2	2:E:124[A]:ASP:OD2	2.19	0.42
1:D:18:TYR:OH	1:D:152:GLU:OE2	2.32	0.42
1:A:104:PHE:HA	2:E:123:PHE:CZ	2.55	0.41
1:A:179[A]:GLU:CD	1:B:119:LEU:HD22	2.46	0.41
1:D:157[B]:MET:N	1:D:157[B]:MET:HE2	2.37	0.40
2:E:122:LEU:HA	2:G:118:VAL:HG21	2.01	0.40
1:D:114:GLU:OE1	1:D:114:GLU:HA	2.21	0.40
1:A:22:LYS:HA	1:A:22:LYS:HD2	1.88	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:25:GLN:OE1	3:A:395:HOH:O[2_746]	1.85	0.35

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:191:ASP:OD1	3:B:346:HOH:O[2_856]	2.15	0.05
3:D:323:HOH:O	3:D:332:HOH:O[2_645]	2.17	0.03

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	156/168 (93%)	156 (100%)	0	0	100	100
1	B	146/168 (87%)	142 (97%)	2 (1%)	2 (1%)	9	2
1	C	139/168 (83%)	136 (98%)	2 (1%)	1 (1%)	18	8
1	D	135/168 (80%)	132 (98%)	3 (2%)	0	100	100
2	E	23/26 (88%)	23 (100%)	0	0	100	100
2	F	19/26 (73%)	19 (100%)	0	0	100	100
2	G	20/26 (77%)	20 (100%)	0	0	100	100
2	H	19/26 (73%)	18 (95%)	1 (5%)	0	100	100
All	All	657/776 (85%)	646 (98%)	8 (1%)	3 (0%)	24	14

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	114	GLU
1	B	113	ALA
1	C	113	ALA

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	133/142 (94%)	133 (100%)	0	100	100
1	B	125/142 (88%)	124 (99%)	1 (1%)	73	70
1	C	121/142 (85%)	121 (100%)	0	100	100
1	D	116/142 (82%)	116 (100%)	0	100	100
2	E	19/22 (86%)	19 (100%)	0	100	100
2	F	18/22 (82%)	18 (100%)	0	100	100
2	G	18/22 (82%)	17 (94%)	1 (6%)	19	8
2	H	19/22 (86%)	19 (100%)	0	100	100
All	All	569/656 (87%)	567 (100%)	2 (0%)	84	83

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	121	LEU
2	G	115	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	99	GLN
1	A	120	HIS
1	A	172	ASN
1	B	20	HIS
1	B	186	HIS
1	D	20	HIS
1	D	172	ASN

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 [i](#)

There are no oligosaccharides 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, 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	151/168 (89%)	0.04	13 (8%) 16 14	8, 20, 54, 65	9 (5%)
1	B	145/168 (86%)	0.40	16 (11%) 10 9	10, 27, 68, 83	5 (3%)
1	C	139/168 (82%)	0.37	13 (9%) 14 12	13, 30, 56, 81	4 (2%)
1	D	136/168 (80%)	0.82	20 (14%) 6 4	15, 36, 65, 74	3 (2%)
2	E	21/26 (80%)	0.89	4 (19%) 3 2	10, 28, 53, 66	4 (19%)
2	F	21/26 (80%)	0.81	3 (14%) 6 5	22, 30, 57, 61	0
2	G	21/26 (80%)	0.77	3 (14%) 6 5	14, 31, 53, 62	1 (4%)
2	H	20/26 (76%)	0.75	2 (10%) 12 11	14, 34, 62, 71	1 (5%)
All	All	654/776 (84%)	0.45	74 (11%) 10 8	8, 29, 62, 83	27 (4%)

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	128	GLY	5.9
1	B	9	TYR	5.7
1	C	32	ALA	5.0
1	A	-1	GLY	4.3
2	E	108	ASP	4.3
1	B	120	HIS	4.1
2	F	108	ASP	4.0
1	A	90	SER	4.0
1	A	206	MET	4.0
1	B	31	ASP	4.0
2	E	111	ASN	3.9
2	E	123	PHE	3.9
1	D	31	ASP	3.9
1	C	204	PRO	3.9
1	A	32	ALA	3.8
1	C	28	TYR	3.7

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Mol	Chain	Res	Type	RSRZ
1	D	125[A]	THR	3.6
1	B	114	GLU	3.6
1	D	126	ALA	3.5
1	B	4	ALA	3.5
1	D	203	GLY	3.5
2	F	109	MET	3.4
1	D	120	HIS	3.1
2	F	128	GLY	3.1
1	B	205	SER	3.1
2	G	125	ILE	3.0
1	B	119	LEU	3.0
1	D	124	PHE	3.0
1	C	119	LEU	3.0
1	C	9	TYR	3.0
1	C	124	PHE	3.0
2	E	128	GLY	3.0
1	C	113	ALA	3.0
1	D	122	THR	2.9
1	B	113	ALA	2.9
1	D	119	LEU	2.9
2	G	107	GLY	2.9
1	D	20	HIS	2.9
1	A	107	ARG	2.9
2	G	127	SER	2.8
1	A	110	ARG	2.8
2	H	109	MET	2.7
1	D	132	THR	2.6
1	A	124	PHE	2.6
1	D	129	ARG	2.6
2	H	108	ASP	2.6
1	C	30	TRP	2.5
1	D	127	ARG	2.5
1	B	89	GLU	2.5
1	D	92	VAL	2.5
1	B	28	TYR	2.5
1	B	5	GLY	2.5
1	C	31	ASP	2.4
1	D	30	TRP	2.4
1	B	121	LEU	2.4
1	C	27	GLY	2.4
1	A	31	ASP	2.3
1	B	116	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	118	GLN	2.3
1	B	8	GLY	2.3
1	D	90	SER	2.3
1	C	29	GLU	2.2
1	C	90	SER	2.2
1	B	117	SER	2.2
1	C	24	SER	2.2
1	B	115	MET	2.2
1	D	175	LEU	2.2
1	D	116	SER	2.2
1	D	113	ALA	2.2
1	D	163	ASN	2.1
1	A	205	SER	2.1
1	A	120	HIS	2.1
1	A	119	LEU	2.1
1	A	28[A]	TYR	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 oligosaccharides 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.