



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:19 AM UTC

PDB ID : 3BZD / pdb_00003bzd
Title : Manipulating the coupled folding and binding process drives affinity maturation in a protein-protein complex
Authors : Cho, S.
Deposited on : 2008-01-17
Resolution : 2.30 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
Mogul : 2022.3.0, CSD as543be (2022)
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

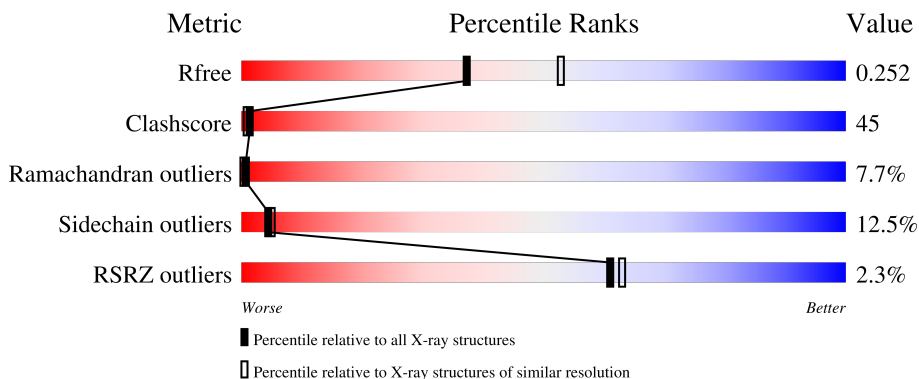
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

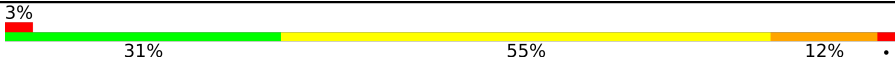
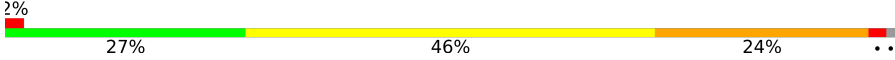
The reported resolution of this entry is 2.30 Å.

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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	109	 3% 31% 55% 12% .
2	B	237	 2% 27% 46% 24% ..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2849 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 T cell receptor beta chain 8.2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	109	Total	C	N	O	S	0	0	0
			828	513	147	165	3			

- Molecule 2 is a protein called Enterotoxin type C-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	234	Total	C	N	O	S	0	0	0
			1926	1225	316	375	10			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	GLY	SEE REMARK 999	UNP P0A0L5
B	?	-	LYS	SEE REMARK 999	UNP P0A0L5
B	102	TRP	VAL	SEE REMARK 999	UNP P0A0L5
B	103	TRP	THR	SEE REMARK 999	UNP P0A0L5
B	104	HIS	GLY	SEE REMARK 999	UNP P0A0L5

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

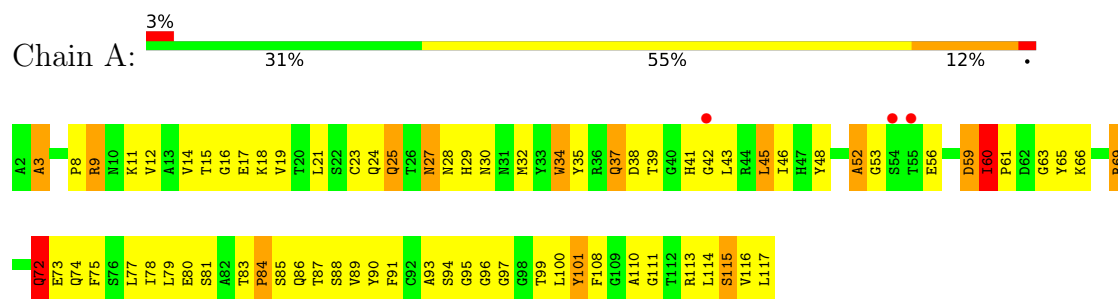
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	25	Total	O	0	0
			25	25		
4	B	60	Total	O	0	0
			60	60		

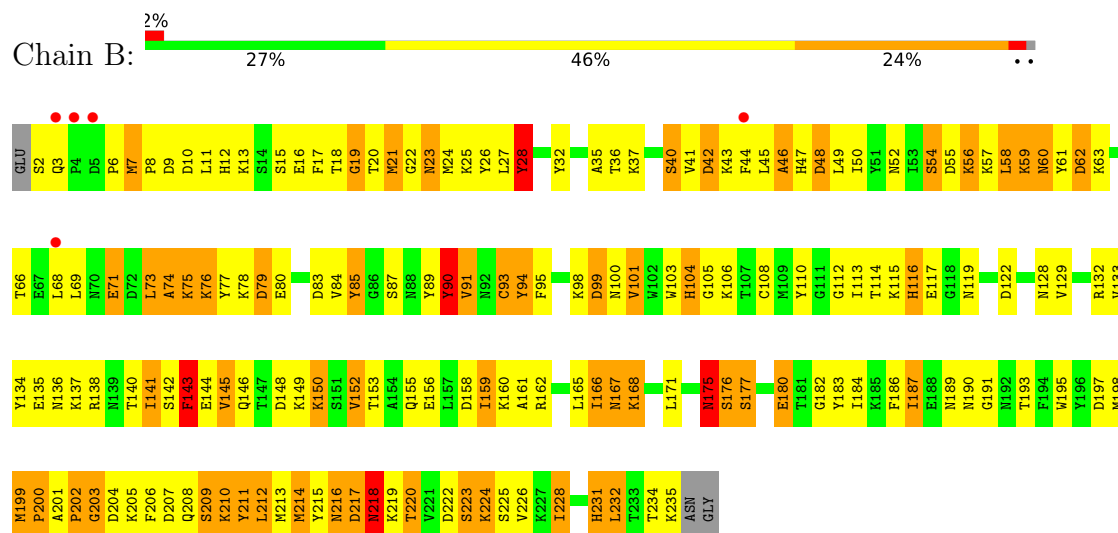
3 Residue-property plots

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: T cell receptor beta chain 8.2



- Molecule 2: Enterotoxin type C-3



4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	96.97Å 96.97Å 92.51Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	27.99 – 2.30 27.99 – 2.30	Depositor EDS
% Data completeness (in resolution range)	100.0 (27.99-2.30) 99.6 (27.99-2.30)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	17.14 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.210 , 0.258 0.209 , 0.252	Depositor DCC
R_{free} test set	1073 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	17.4	Xtriage
Anisotropy	0.446	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.11 , 97.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	0.119 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	2849	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.90% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	2.02	9/846 (1.1%)	1.55	9/1145 (0.8%)
2	B	1.83	30/1972 (1.5%)	1.54	25/2660 (0.9%)
All	All	1.89	39/2818 (1.4%)	1.55	34/3805 (0.9%)

All (39) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	101	TYR	C-N	29.07	1.74	1.33
1	A	63	GLY	C-N	18.85	1.60	1.33
2	B	150	LYS	N-CA	8.55	1.57	1.46
1	A	69	ARG	N-CA	8.53	1.55	1.46
1	A	75	PHE	N-CA	7.72	1.55	1.45
2	B	202	PRO	N-CA	-7.21	1.38	1.47
1	A	72	GLN	C-O	-6.85	1.15	1.24
2	B	214	MET	C-O	6.81	1.32	1.24
2	B	48	ASP	C-O	-6.43	1.16	1.23
2	B	211	TYR	C-O	6.42	1.31	1.24
2	B	60	ASN	C-O	-6.41	1.16	1.24
2	B	228	ILE	CA-CB	-6.36	1.46	1.54
2	B	110	TYR	C-O	-6.28	1.16	1.23
2	B	74	ALA	N-CA	6.22	1.53	1.46
2	B	187	ILE	CA-CB	-6.17	1.46	1.54
1	A	60	ILE	CA-C	6.06	1.59	1.52
2	B	46	ALA	CA-CB	-5.98	1.43	1.53
2	B	228	ILE	N-CA	5.96	1.52	1.46
2	B	220	THR	C-O	5.92	1.31	1.23
2	B	40	SER	C-O	-5.92	1.16	1.24
2	B	143	PHE	C-O	-5.87	1.18	1.24
1	A	34	TRP	CA-C	-5.85	1.45	1.52
2	B	85	TYR	C-O	5.67	1.29	1.23
2	B	212	LEU	CA-C	-5.58	1.44	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	52	ALA	CA-CB	5.56	1.62	1.53
1	A	91	PHE	N-CA	5.54	1.52	1.46
2	B	220	THR	CA-C	5.41	1.59	1.52
2	B	218	ASN	C-O	-5.41	1.17	1.24
2	B	219	LYS	CD-CE	5.36	1.68	1.52
2	B	90	TYR	CD1-CE1	5.35	1.54	1.38
2	B	222	ASP	C-O	5.23	1.30	1.23
2	B	150	LYS	C-O	5.16	1.30	1.24
2	B	93	CYS	CA-C	-5.12	1.46	1.53
2	B	79	ASP	N-CA	5.11	1.53	1.46
2	B	145	VAL	C-O	-5.08	1.18	1.23
2	B	35	ALA	C-O	-5.05	1.17	1.23
2	B	175	ASN	N-CA	5.05	1.52	1.45
2	B	219	LYS	N-CA	-5.02	1.39	1.46
2	B	11	LEU	N-CA	5.01	1.52	1.45

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	101	TYR	CA-C-N	-14.79	99.37	122.59
1	A	101	TYR	C-N-CA	-14.79	99.37	122.59
2	B	150	LYS	N-CA-C	-9.21	102.06	113.38
2	B	177	SER	CA-C-N	8.85	128.50	119.82
2	B	177	SER	C-N-CA	8.85	128.50	119.82
1	A	35	TYR	N-CA-C	7.27	120.93	109.81
2	B	217	ASP	N-CA-C	-7.24	104.33	113.02
2	B	79	ASP	N-CA-C	7.12	118.99	110.44
1	A	110	ALA	N-CA-C	-6.95	104.42	113.17
2	B	232	LEU	N-CA-C	6.76	120.54	109.85
2	B	73	LEU	N-CA-C	-6.57	103.95	112.23
2	B	54	SER	N-CA-C	6.40	119.67	109.24
2	B	211	TYR	N-CA-C	-6.14	104.51	111.14
2	B	25	LYS	N-CA-C	-6.00	104.07	111.33
1	A	45	LEU	N-CA-C	5.85	123.26	110.80
2	B	7	MET	CA-C-N	5.81	127.10	119.84
2	B	7	MET	C-N-CA	5.81	127.10	119.84
2	B	28	TYR	N-CA-C	5.80	123.06	113.89
2	B	50	ILE	CB-CA-C	-5.58	103.42	111.34
2	B	180	GLU	N-CA-C	-5.46	106.29	113.12
2	B	203	GLY	N-CA-C	5.45	119.91	111.08
2	B	62	ASP	N-CA-C	-5.44	106.55	114.12
1	A	59	ASP	O-C-N	5.42	127.88	122.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	199	MET	CA-C-N	5.37	126.55	119.84
2	B	199	MET	C-N-CA	5.37	126.55	119.84
2	B	204	ASP	N-CA-C	5.25	118.15	111.69
1	A	69	ARG	CA-C-N	5.24	127.23	120.89
1	A	69	ARG	C-N-CA	5.24	127.23	120.89
1	A	19	VAL	N-CA-C	5.23	115.49	108.17
2	B	71	GLU	N-CA-C	5.23	116.67	111.07
2	B	85	TYR	CA-CB-CG	-5.18	104.58	113.90
2	B	231	HIS	N-CA-C	5.17	116.82	108.34
2	B	9	ASP	N-CA-C	-5.17	107.00	113.15
2	B	152	VAL	CB-CA-C	-5.13	102.75	110.55

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	828	0	787	75	0
2	B	1926	0	1854	172	0
3	B	10	0	0	1	0
4	A	25	0	0	1	0
4	B	60	0	0	2	0
All	All	2849	0	2641	245	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 45.

All (245) 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:101:TYR:C	1:A:108:PHE:N	1.74	1.45
2:B:58:LEU:HD12	2:B:60:ASN:ND2	1.51	1.22
2:B:58:LEU:CD1	2:B:60:ASN:HD21	1.61	1.12
2:B:80:GLU:HB3	2:B:115:LYS:HE3	1.22	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:80:GLU:HB3	2:B:115:LYS:CE	1.96	0.95
2:B:85:TYR:CD2	2:B:156:GLU:HG3	2.07	0.90
2:B:94:TYR:H	2:B:94:TYR:HD1	1.17	0.90
1:A:84:PRO:HA	1:A:116:VAL:HB	1.53	0.89
2:B:61:TYR:HA	2:B:105:GLY:HA2	1.52	0.89
1:A:101:TYR:C	1:A:108:PHE:CA	2.46	0.87
1:A:117:LEU:OXT	1:A:117:LEU:HD12	1.73	0.86
2:B:223:SER:O	2:B:225:SER:N	2.10	0.85
2:B:152:VAL:HG22	2:B:153:THR:N	1.90	0.84
2:B:80:GLU:HG3	2:B:115:LYS:NZ	1.91	0.84
1:A:30:ASN:HA	1:A:72:GLN:HE22	1.41	0.84
1:A:30:ASN:HA	1:A:72:GLN:NE2	1.93	0.82
2:B:42:ASP:OD2	2:B:43:LYS:N	2.11	0.82
1:A:25:GLN:HE21	1:A:73:GLU:HA	1.44	0.81
2:B:37:LYS:HB2	2:B:116:HIS:HD2	1.46	0.80
2:B:3:GLN:NE2	2:B:195:TRP:H	1.79	0.79
2:B:116:HIS:HD1	2:B:116:HIS:C	1.90	0.78
1:A:61:PRO:HG2	4:A:139:HOH:O	1.83	0.78
1:A:38:ASP:HB2	1:A:41:HIS:HB2	1.64	0.78
2:B:148:ASP:OD2	2:B:149:LYS:HD3	1.85	0.77
1:A:37:GLN:HB2	1:A:42:GLY:C	2.09	0.77
2:B:42:ASP:CG	2:B:43:LYS:H	1.91	0.75
1:A:37:GLN:HB2	1:A:42:GLY:O	1.86	0.75
2:B:37:LYS:HB2	2:B:116:HIS:CD2	2.21	0.75
2:B:116:HIS:C	2:B:116:HIS:ND1	2.44	0.75
2:B:58:LEU:HD12	2:B:60:ASN:HD21	0.69	0.74
2:B:112:GLY:HA2	2:B:153:THR:HG21	1.70	0.74
2:B:152:VAL:CG2	2:B:153:THR:N	2.51	0.73
1:A:25:GLN:NE2	1:A:73:GLU:HA	2.03	0.72
1:A:45:LEU:O	1:A:59:ASP:N	2.23	0.72
2:B:140:THR:OG1	2:B:141:ILE:HG22	1.90	0.72
2:B:158:ASP:OD1	2:B:184:ILE:HG21	1.90	0.71
1:A:65:TYR:HE1	1:A:79:LEU:HD21	1.55	0.71
2:B:98:LYS:HG2	2:B:101:VAL:HG23	1.73	0.71
2:B:80:GLU:HG3	2:B:115:LYS:HZ2	1.55	0.70
2:B:62:ASP:OD2	2:B:63:LYS:HG3	1.91	0.70
1:A:83:THR:C	1:A:116:VAL:HG11	2.17	0.69
2:B:32:TYR:CD1	2:B:32:TYR:C	2.70	0.68
2:B:83:ASP:O	2:B:113:ILE:HA	1.94	0.68
1:A:25:GLN:NE2	1:A:28:ASN:HA	2.10	0.67
2:B:75:LYS:O	2:B:76:LYS:C	2.37	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:162:ARG:O	2:B:166:ILE:HD13	1.94	0.67
2:B:129:VAL:HB	2:B:145:VAL:CG2	2.24	0.67
1:A:88:SER:OG	1:A:89:VAL:N	2.24	0.67
2:B:197:ASP:OD1	2:B:199:MET:N	2.24	0.67
2:B:62:ASP:OD1	2:B:105:GLY:HA3	1.96	0.65
1:A:11:LYS:O	1:A:114:LEU:HD12	1.97	0.65
1:A:25:GLN:HE21	1:A:73:GLU:CA	2.09	0.65
2:B:132:ARG:HH11	2:B:132:ARG:HG2	1.62	0.65
1:A:101:TYR:O	1:A:108:PHE:HA	1.96	0.65
2:B:117:GLU:H	2:B:117:GLU:CD	2.06	0.64
2:B:75:LYS:O	2:B:77:TYR:N	2.31	0.64
2:B:7:MET:HB2	2:B:10:ASP:HB2	1.79	0.64
2:B:187:ILE:HG12	2:B:193:THR:HG22	1.80	0.64
1:A:15:THR:HG23	1:A:83:THR:HA	1.79	0.64
1:A:37:GLN:CB	1:A:43:LEU:HA	2.28	0.64
1:A:90:TYR:O	1:A:111:GLY:HA2	1.98	0.63
2:B:80:GLU:CG	2:B:115:LYS:NZ	2.62	0.62
2:B:28:TYR:N	2:B:28:TYR:CD1	2.65	0.62
1:A:53:GLY:HA3	2:B:26:TYR:CE2	2.35	0.62
2:B:61:TYR:HA	2:B:105:GLY:CA	2.27	0.62
1:A:24:GLN:HB3	1:A:74:GLN:NE2	2.15	0.62
2:B:133:VAL:HB	2:B:141:ILE:HG23	1.82	0.62
1:A:14:VAL:HA	1:A:117:LEU:OXT	2.00	0.62
2:B:186:PHE:O	2:B:193:THR:HA	2.00	0.61
1:A:24:GLN:HB3	1:A:74:GLN:HE22	1.65	0.61
2:B:13:LYS:HD2	2:B:16:GLU:OE1	2.01	0.61
2:B:68:LEU:HD23	2:B:73:LEU:HG	1.81	0.61
1:A:37:GLN:HB3	1:A:43:LEU:HA	1.82	0.61
1:A:94:SER:O	1:A:101:TYR:N	2.34	0.60
2:B:94:TYR:HD1	2:B:94:TYR:N	1.93	0.60
1:A:65:TYR:CE1	1:A:79:LEU:HD21	2.37	0.60
2:B:23:ASN:N	2:B:23:ASN:HD22	1.98	0.60
2:B:45:LEU:C	2:B:47:HIS:H	2.09	0.60
1:A:48:TYR:CE1	1:A:56:GLU:HB2	2.37	0.59
2:B:7:MET:HB2	2:B:10:ASP:CG	2.27	0.59
1:A:18:LYS:HA	1:A:80:GLU:O	2.03	0.58
2:B:6:PRO:HB3	2:B:195:TRP:CZ2	2.39	0.58
2:B:23:ASN:N	2:B:23:ASN:ND2	2.51	0.58
2:B:94:TYR:N	2:B:94:TYR:CD1	2.64	0.58
2:B:214:MET:HE2	2:B:215:TYR:CZ	2.39	0.58
1:A:101:TYR:C	1:A:108:PHE:HA	2.27	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:171:LEU:O	2:B:177:SER:OG	2.19	0.57
1:A:37:GLN:HB3	1:A:43:LEU:HD23	1.85	0.57
2:B:80:GLU:CG	2:B:115:LYS:HZ1	2.18	0.57
2:B:207:ASP:OD2	2:B:210:LYS:HB2	2.04	0.57
2:B:27:LEU:HB2	2:B:28:TYR:CE1	2.40	0.56
2:B:42:ASP:CG	2:B:43:LYS:N	2.60	0.56
2:B:209:SER:O	2:B:211:TYR:N	2.39	0.56
2:B:197:ASP:OD1	2:B:198:MET:N	2.39	0.55
2:B:234:THR:HG22	2:B:235:LYS:N	2.21	0.55
2:B:84:VAL:HG22	2:B:113:ILE:HG22	1.88	0.55
2:B:41:VAL:HG21	2:B:52:ASN:ND2	2.19	0.55
2:B:85:TYR:HD2	2:B:156:GLU:HA	1.70	0.55
2:B:3:GLN:HE22	2:B:195:TRP:H	1.52	0.55
2:B:112:GLY:O	2:B:113:ILE:HG23	2.06	0.55
1:A:84:PRO:CA	1:A:116:VAL:HB	2.33	0.54
2:B:45:LEU:O	2:B:47:HIS:N	2.36	0.54
2:B:80:GLU:CB	2:B:115:LYS:CE	2.79	0.54
2:B:128:ASN:OD1	2:B:146:GLN:HG2	2.08	0.54
2:B:141:ILE:HD12	2:B:142:SER:H	1.72	0.54
1:A:23:CYS:O	1:A:74:GLN:NE2	2.41	0.54
2:B:7:MET:HB2	2:B:10:ASP:CB	2.38	0.54
1:A:38:ASP:HB2	1:A:41:HIS:CB	2.34	0.53
2:B:12:HIS:CE1	2:B:201:ALA:HA	2.44	0.53
2:B:45:LEU:O	2:B:48:ASP:OD1	2.27	0.53
2:B:136:ASN:O	2:B:137:LYS:HB2	2.08	0.53
2:B:17:PHE:CE1	2:B:19:GLY:HA3	2.43	0.53
2:B:28:TYR:CE2	2:B:162:ARG:HD2	2.44	0.53
2:B:209:SER:O	2:B:212:LEU:N	2.42	0.53
1:A:53:GLY:HA3	2:B:26:TYR:CZ	2.44	0.53
2:B:155:GLN:NE2	2:B:215:TYR:HB3	2.22	0.53
1:A:93:ALA:HA	1:A:101:TYR:O	2.09	0.52
2:B:32:TYR:C	2:B:32:TYR:HD1	2.17	0.52
1:A:114:LEU:HD12	1:A:115:SER:H	1.75	0.52
2:B:134:TYR:N	2:B:134:TYR:CD1	2.77	0.52
1:A:83:THR:N	1:A:116:VAL:HG11	2.25	0.52
2:B:175:ASN:O	2:B:176:SER:HB2	2.09	0.52
2:B:182:GLY:HA2	2:B:231:HIS:O	2.10	0.52
2:B:129:VAL:HB	2:B:145:VAL:HG22	1.91	0.52
2:B:80:GLU:HG3	2:B:115:LYS:HZ1	1.71	0.52
2:B:152:VAL:CG2	2:B:153:THR:H	2.20	0.51
1:A:37:GLN:O	1:A:37:GLN:OE1	2.27	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:166:ILE:CD1	2:B:171:LEU:HD23	2.40	0.51
2:B:223:SER:OG	2:B:224:LYS:N	2.43	0.51
1:A:3:ALA:HB1	1:A:101:TYR:CD1	2.46	0.51
1:A:38:ASP:HB2	1:A:41:HIS:CG	2.46	0.51
2:B:129:VAL:HB	2:B:145:VAL:HG23	1.91	0.51
2:B:129:VAL:O	2:B:144:GLU:HA	2.11	0.51
1:A:85:SER:C	1:A:87:THR:H	2.18	0.50
1:A:32:MET:SD	1:A:69:ARG:NE	2.85	0.50
2:B:20:THR:O	2:B:22:GLY:N	2.43	0.50
1:A:69:ARG:NH1	1:A:72:GLN:O	2.41	0.50
2:B:90:TYR:O	2:B:91:VAL:C	2.53	0.50
2:B:32:TYR:CD1	2:B:32:TYR:O	2.64	0.50
1:A:25:GLN:HG3	1:A:73:GLU:HA	1.94	0.50
2:B:41:VAL:O	2:B:42:ASP:HB2	2.10	0.50
2:B:71:GLU:O	2:B:74:ALA:HB3	2.12	0.50
1:A:30:ASN:CA	1:A:72:GLN:HE22	2.19	0.49
2:B:134:TYR:HA	2:B:138:ARG:O	2.12	0.49
1:A:9:ARG:NH2	1:A:113:ARG:HG3	2.28	0.49
2:B:116:HIS:ND1	2:B:116:HIS:O	2.44	0.49
1:A:96:GLY:O	1:A:97:GLY:C	2.55	0.49
2:B:167:ASN:O	2:B:168:LYS:NZ	2.43	0.49
1:A:78:ILE:C	1:A:79:LEU:HD12	2.37	0.49
2:B:69:LEU:HD12	2:B:69:LEU:O	2.13	0.49
2:B:95:PHE:HB2	2:B:103:TRP:CH2	2.48	0.49
1:A:16:GLY:O	1:A:81:SER:HA	2.13	0.48
1:A:83:THR:CA	1:A:116:VAL:HG11	2.43	0.48
1:A:84:PRO:HA	1:A:116:VAL:O	2.12	0.48
1:A:95:GLY:HA2	1:A:99:THR:O	2.13	0.48
2:B:40:SER:HB3	2:B:78:LYS:O	2.14	0.48
2:B:12:HIS:ND1	2:B:200:PRO:O	2.46	0.48
2:B:85:TYR:CD2	2:B:156:GLU:HA	2.48	0.48
2:B:103:TRP:O	2:B:104:HIS:CB	2.61	0.48
2:B:160:LYS:NZ	4:B:502:HOH:O	2.39	0.48
2:B:75:LYS:HA	2:B:78:LYS:HB2	1.95	0.48
2:B:141:ILE:HD12	2:B:142:SER:N	2.29	0.47
2:B:208:GLN:O	2:B:209:SER:C	2.57	0.47
2:B:143:PHE:N	2:B:143:PHE:CD2	2.82	0.47
2:B:12:HIS:HA	4:B:523:HOH:O	2.15	0.47
2:B:27:LEU:C	2:B:28:TYR:CD1	2.93	0.47
2:B:75:LYS:C	2:B:77:TYR:N	2.72	0.47
2:B:63:LYS:N	2:B:105:GLY:O	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:213:MET:HE3	2:B:213:MET:HB2	1.69	0.47
1:A:66:LYS:HB3	1:A:78:ILE:HB	1.97	0.47
2:B:158:ASP:O	2:B:161:ALA:HB3	2.15	0.47
2:B:119:ASN:O	2:B:150:LYS:HB2	2.15	0.46
2:B:180:GLU:OE2	2:B:180:GLU:HA	2.15	0.46
2:B:89:TYR:CZ	2:B:108:CYS:HB2	2.51	0.46
2:B:13:LYS:HD2	2:B:16:GLU:CD	2.41	0.46
2:B:103:TRP:HB2	2:B:104:HIS:H	1.57	0.46
2:B:80:GLU:CD	2:B:115:LYS:HZ1	2.24	0.46
2:B:155:GLN:O	2:B:156:GLU:C	2.58	0.46
1:A:15:THR:HG23	1:A:84:PRO:HD3	1.98	0.46
2:B:7:MET:HB2	2:B:10:ASP:OD1	2.16	0.45
2:B:129:VAL:HG12	2:B:228:ILE:HD12	1.98	0.45
2:B:85:TYR:CE2	2:B:156:GLU:HG3	2.50	0.45
2:B:217:ASP:O	2:B:218:ASN:C	2.60	0.45
2:B:17:PHE:CZ	2:B:19:GLY:HA3	2.52	0.45
2:B:117:GLU:CD	2:B:117:GLU:N	2.72	0.45
1:A:84:PRO:HG3	1:A:116:VAL:O	2.16	0.45
2:B:45:LEU:N	2:B:48:ASP:OD1	2.49	0.45
1:A:93:ALA:HB1	1:A:100:LEU:HD12	1.98	0.44
2:B:103:TRP:CD1	2:B:103:TRP:N	2.84	0.44
2:B:56:LYS:HA	2:B:56:LYS:HD3	1.73	0.44
1:A:83:THR:C	1:A:116:VAL:CG1	2.89	0.44
2:B:212:LEU:C	2:B:214:MET:N	2.73	0.44
2:B:138:ARG:HB3	3:B:500:SO4:O4	2.17	0.44
2:B:167:ASN:C	2:B:168:LYS:HG2	2.41	0.44
2:B:2:SER:OG	2:B:193:THR:OG1	2.34	0.44
2:B:217:ASP:C	2:B:217:ASP:OD1	2.60	0.44
2:B:113:ILE:C	2:B:114:THR:HG23	2.43	0.44
2:B:6:PRO:HB3	2:B:195:TRP:CE2	2.53	0.43
2:B:24:MET:HE2	2:B:206:PHE:CZ	2.53	0.43
2:B:45:LEU:HD23	2:B:45:LEU:HA	1.87	0.43
2:B:158:ASP:OD2	2:B:215:TYR:OH	2.35	0.43
1:A:25:GLN:HE22	1:A:28:ASN:HA	1.83	0.43
1:A:101:TYR:HD2	1:A:101:TYR:HA	1.63	0.43
1:A:15:THR:CG2	1:A:84:PRO:HD3	2.48	0.43
1:A:25:GLN:HE21	1:A:73:GLU:CB	2.32	0.43
1:A:96:GLY:O	1:A:99:THR:HB	2.19	0.43
2:B:44:PHE:CD2	2:B:44:PHE:C	2.97	0.43
2:B:28:TYR:OH	2:B:162:ARG:NH1	2.52	0.42
2:B:183:TYR:CZ	2:B:231:HIS:HB2	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:211:TYR:O	2:B:214:MET:HG2	2.19	0.42
2:B:95:PHE:CE1	2:B:106:LYS:HD3	2.54	0.42
2:B:93:CYS:SG	2:B:108:CYS:N	2.93	0.42
1:A:15:THR:OG1	1:A:117:LEU:O	2.27	0.42
2:B:209:SER:C	2:B:211:TYR:N	2.75	0.42
2:B:66:THR:O	2:B:66:THR:HG23	2.20	0.42
2:B:135:GLU:OE2	2:B:140:THR:HG21	2.20	0.42
2:B:149:LYS:HB2	2:B:152:VAL:HB	2.02	0.42
1:A:30:ASN:O	1:A:69:ARG:NH1	2.53	0.42
2:B:28:TYR:CE2	2:B:159:ILE:HD12	2.54	0.42
1:A:29:HIS:HB2	1:A:94:SER:HB2	2.01	0.41
2:B:99:ASP:OD1	2:B:99:ASP:N	2.53	0.41
2:B:202:PRO:HG2	2:B:202:PRO:O	2.20	0.41
2:B:223:SER:C	2:B:225:SER:H	2.24	0.41
2:B:41:VAL:HG21	2:B:52:ASN:HD21	1.85	0.41
2:B:199:MET:HA	2:B:200:PRO:HD3	1.85	0.41
1:A:8:PRO:HD2	1:A:21:LEU:CD2	2.51	0.41
1:A:25:GLN:HG3	1:A:73:GLU:CA	2.50	0.41
1:A:52:ALA:HA	1:A:69:ARG:CG	2.51	0.41
2:B:20:THR:HG22	2:B:22:GLY:H	1.85	0.41
2:B:21:MET:HG3	2:B:21:MET:O	2.19	0.41
2:B:27:LEU:HB2	2:B:28:TYR:CD1	2.55	0.41
2:B:36:THR:O	2:B:37:LYS:HB3	2.21	0.41
2:B:85:TYR:CG	2:B:156:GLU:HG3	2.53	0.41
2:B:201:ALA:O	2:B:203:GLY:N	2.54	0.41
1:A:27:ASN:O	1:A:28:ASN:C	2.63	0.41
2:B:90:TYR:N	2:B:90:TYR:CD1	2.88	0.41
2:B:190:ASN:OD1	2:B:191:GLY:N	2.54	0.41
1:A:60:ILE:O	1:A:60:ILE:HG13	2.21	0.41
2:B:7:MET:CB	2:B:10:ASP:HB2	2.46	0.40
2:B:69:LEU:HB2	2:B:216:ASN:O	2.22	0.40
1:A:77:LEU:HA	1:A:77:LEU:HD12	1.88	0.40
2:B:54:SER:O	2:B:55:ASP:C	2.65	0.40
2:B:197:ASP:OD1	2:B:197:ASP:C	2.63	0.40
2:B:7:MET:O	2:B:10:ASP:N	2.52	0.40
2:B:58:LEU:HB2	2:B:59:LYS:H	1.57	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	107/109 (98%)	88 (82%)	14 (13%)	5 (5%)	2	1
2	B	232/237 (98%)	180 (78%)	31 (13%)	21 (9%)	0	0
All	All	339/346 (98%)	268 (79%)	45 (13%)	26 (8%)	1	0

All (26) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3	ALA
1	A	72	GLN
2	B	46	ALA
2	B	104	HIS
2	B	209	SER
2	B	210	LYS
2	B	223	SER
2	B	224	LYS
1	A	39	THR
2	B	21	MET
2	B	76	LYS
2	B	122	ASP
2	B	218	ASN
2	B	226	VAL
2	B	15	SER
2	B	189	ASN
2	B	200	PRO
2	B	42	ASP
2	B	59	LYS
2	B	167	ASN
2	B	176	SER
1	A	60	ILE
1	A	86	GLN
2	B	8	PRO
2	B	19	GLY

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Mol	Chain	Res	Type
2	B	91	VAL

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	88/88 (100%)	77 (88%)	11 (12%)	4	5
2	B	217/219 (99%)	190 (88%)	27 (12%)	4	5
All	All	305/307 (99%)	267 (88%)	38 (12%)	4	5

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	ARG
1	A	12	VAL
1	A	17	GLU
1	A	25	GLN
1	A	27	ASN
1	A	34	TRP
1	A	37	GLN
1	A	46	ILE
1	A	72	GLN
1	A	84	PRO
1	A	115	SER
2	B	18	THR
2	B	23	ASN
2	B	28	TYR
2	B	49	LEU
2	B	56	LYS
2	B	57	LYS
2	B	58	LEU
2	B	75	LYS
2	B	79	ASP
2	B	87	SER
2	B	90	TYR

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Mol	Chain	Res	Type
2	B	94	TYR
2	B	99	ASP
2	B	100	ASN
2	B	101	VAL
2	B	116	HIS
2	B	141	ILE
2	B	143	PHE
2	B	159	ILE
2	B	165	LEU
2	B	166	ILE
2	B	168	LYS
2	B	175	ASN
2	B	205	LYS
2	B	216	ASN
2	B	220	THR
2	B	232	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	ASN
1	A	25	GLN
1	A	28	ASN
1	A	31	ASN
1	A	72	GLN
1	A	74	GLN
2	B	3	GLN
2	B	23	ASN
2	B	60	ASN
2	B	100	ASN
2	B	139	ASN
2	B	146	GLN
2	B	155	GLN
2	B	170	ASN
2	B	189	ASN
2	B	208	GLN
2	B	216	ASN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	SO4	B	501	-	4,4,4	0.36	0	6,6,6	0.77	0
3	SO4	B	500	-	4,4,4	0.36	0	6,6,6	0.15	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	500	SO4	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	101:TYR	C	108:PHE	N	1.74

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	109/109 (100%)	0.28	3 (2%) 55 57	6, 24, 39, 43	0
2	B	234/237 (98%)	-0.10	5 (2%) 63 65	4, 13, 36, 50	0
All	All	343/346 (99%)	0.02	8 (2%) 61 63	4, 16, 39, 50	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	54	SER	3.7
2	B	4	PRO	3.1
1	A	42	GLY	3.0
2	B	5	ASP	2.4
2	B	68	LEU	2.2
1	A	55	THR	2.1
2	B	3	GLN	2.1
2	B	44	PHE	2.1

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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SO4	B	500	5/5	0.72	0.18	99,99,99,99	0
3	SO4	B	501	5/5	0.93	0.10	31,35,37,38	0

6.5 Other polymers [i](#)

There are no such residues in this entry.