



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:30 AM UTC

PDB ID : 6XRJ / pdb_00006xrj
Title : Crystal structure of the disulfide linked DH717.1 Fab dimer, derived from a macaque HIV-1 vaccine-induced Env glycan-reactive neutralizing antibody B cell lineage
Authors : Manne, K.; Nicely, N.I.; Acharya, P.
Deposited on : 2020-07-13
Resolution : 3.15 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

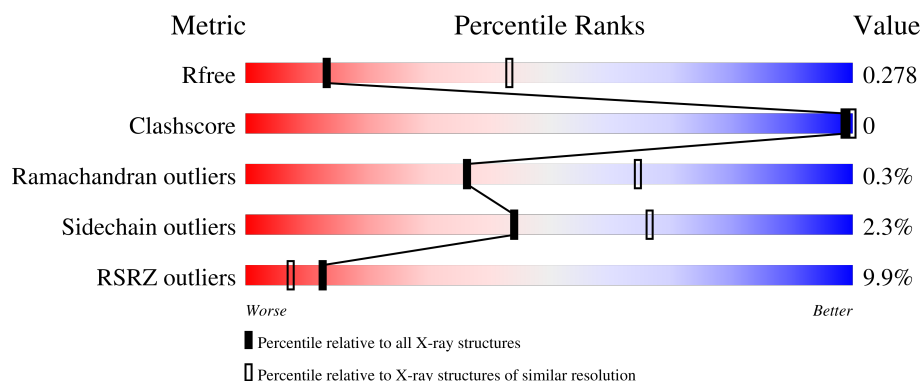
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.15 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	2361 (3.20-3.12)
Clashscore	190562	2486 (3.20-3.12)
Ramachandran outliers	187476	2405 (3.20-3.12)
Sidechain outliers	187428	2404 (3.20-3.12)
RSRZ outliers	180081	2361 (3.20-3.12)

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	226	5% 92% ...
1	C	226	10% 96% .
1	E	226	8% 95% .
1	H	226	18% 93% 6%
2	B	211	4% 95% 5%

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Mol	Chain	Length	Quality of chain
2	D	211	11% 94% 5%
2	F	211	5% 95% 5%
2	L	211	18% 91% 8%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 25500 atoms, of which 12535 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 DH717.1 heavy chain Fab fragment.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	219	Total	C	H	N	O	S	0	0	0
			3257	1037	1615	278	321	6			
1	C	226	Total	C	H	N	O	S	0	0	0
			3362	1066	1668	289	333	6			
1	E	225	Total	C	H	N	O	S	0	0	0
			3348	1062	1661	288	331	6			
1	H	226	Total	C	H	N	O	S	0	0	0
			3362	1066	1668	289	333	6			

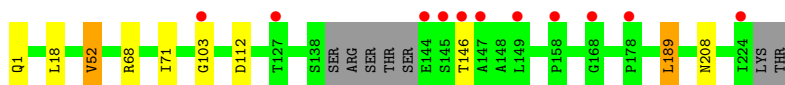
- Molecule 2 is a protein called DH717.1 light chain Fab fragment.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	211	Total	C	H	N	O	S	0	0	0
			3042	972	1480	260	325	5			
2	D	211	Total	C	H	N	O	S	0	0	0
			3044	972	1482	260	325	5			
2	F	211	Total	C	H	N	O	S	0	0	0
			3053	972	1491	260	325	5			
2	L	211	Total	C	H	N	O	S	0	0	0
			3032	972	1470	260	325	5			

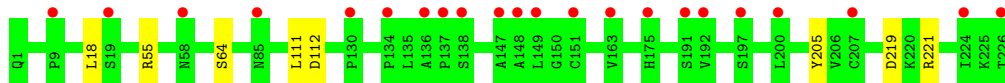
3 Residue-property plots [i](#)

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.

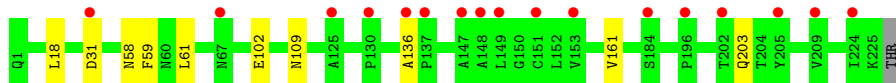
- Molecule 1: DH717.1 heavy chain Fab fragment



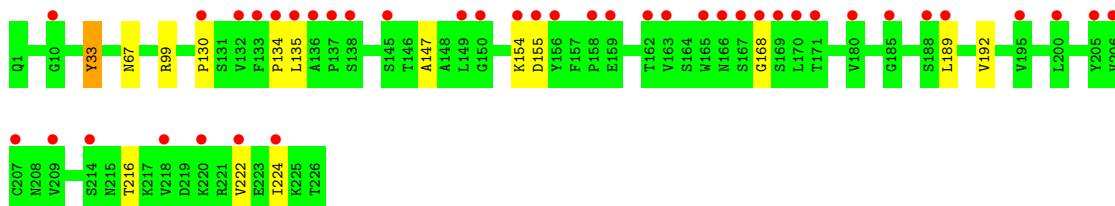
- Molecule 1: DH717.1 heavy chain Fab fragment



- Molecule 1: DH717.1 heavy chain Fab fragment



- Molecule 1: DH717.1 heavy chain Fab fragment

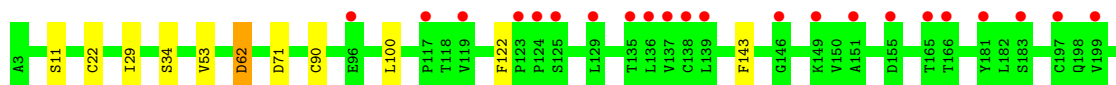


- Molecule 2: DH717.1 light chain Fab fragment





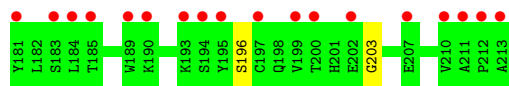
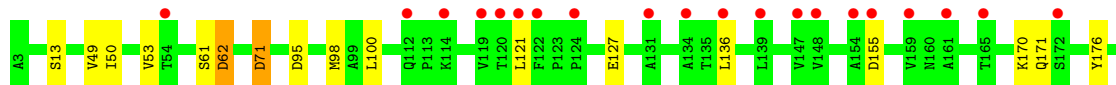
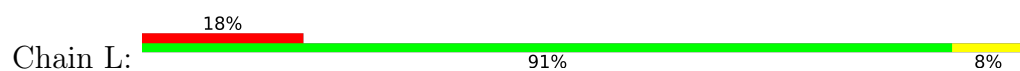
- Molecule 2: DH717.1 light chain Fab fragment



- Molecule 2: DH717.1 light chain Fab fragment



- Molecule 2: DH717.1 light chain Fab fragment



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 2 2	Depositor
Cell constants a, b, c, α , β , γ	201.59Å 201.59Å 154.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.71 – 3.15 41.71 – 3.15	Depositor EDS
% Data completeness (in resolution range)	99.8 (41.71-3.15) 99.8 (41.71-3.15)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.47 (at 3.12Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.245 , 0.282 0.241 , 0.278	Depositor DCC
R_{free} test set	1999 reflections (3.60%)	wwPDB-VP
Wilson B-factor (Å ²)	82.5	Xtriage
Anisotropy	0.012	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 83.3	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	0.90	EDS
Total number of atoms	25500	wwPDB-VP
Average B, all atoms (Å ²)	128.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.42% 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](#)

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	0.73	0/1679	1.32	3/2290 (0.1%)
1	C	0.75	0/1732	1.33	6/2362 (0.3%)
1	E	0.81	0/1725	1.40	6/2352 (0.3%)
1	H	0.83	0/1732	1.50	7/2362 (0.3%)
2	B	0.72	0/1598	1.37	2/2180 (0.1%)
2	D	0.72	0/1598	1.37	7/2180 (0.3%)
2	F	0.74	0/1598	1.36	4/2180 (0.2%)
2	L	0.76	0/1598	1.46	8/2180 (0.4%)
All	All	0.76	0/13260	1.39	43/18086 (0.2%)

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	A	0	1
1	C	0	1
1	H	0	1
2	F	0	1
All	All	0	4

There are no bond length outliers.

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	224	ILE	N-CA-C	7.27	118.37	107.75
1	C	111	LEU	CA-C-N	6.77	129.24	120.44
1	C	111	LEU	C-N-CA	6.77	129.24	120.44
2	F	62	ASP	CA-CB-CG	6.75	119.35	112.60
2	B	49	VAL	CB-CA-C	6.55	117.33	110.91
1	A	112	ASP	CA-CB-CG	6.52	119.12	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	154	LYS	N-CA-C	6.45	118.87	109.07
1	H	134	PRO	CA-C-N	6.42	132.86	121.75
1	H	134	PRO	C-N-CA	6.42	132.86	121.75
2	L	71	ASP	CA-CB-CG	6.10	118.70	112.60
2	D	62	ASP	CA-CB-CG	6.08	118.68	112.60
1	C	219	ASP	CA-CB-CG	6.08	118.68	112.60
1	H	155	ASP	N-CA-C	5.87	120.25	113.38
1	A	146	THR	N-CA-C	5.84	117.32	111.07
2	F	142	ASP	CA-CB-CG	5.78	118.38	112.60
2	L	62	ASP	CA-CB-CG	5.75	118.36	112.60
1	E	136	ALA	N-CA-C	5.74	116.93	109.64
1	C	112	ASP	N-CA-CB	-5.61	101.88	110.01
1	C	221	ARG	CA-C-N	5.58	126.89	121.65
1	C	221	ARG	C-N-CA	5.58	126.89	121.65
2	L	61	SER	CA-C-N	5.46	129.41	120.63
2	L	61	SER	C-N-CA	5.46	129.41	120.63
1	E	109	ASN	OD1-CG-ND2	-5.39	117.21	122.60
2	L	171	GLN	OE1-CD-NE2	-5.32	117.28	122.60
2	D	71	ASP	CA-CB-CG	5.31	117.91	112.60
1	H	154	LYS	CA-C-N	5.25	132.62	123.91
1	H	154	LYS	C-N-CA	5.25	132.62	123.91
2	D	34	SER	CA-C-N	5.21	130.18	122.94
2	D	34	SER	C-N-CA	5.21	130.18	122.94
2	L	127	GLU	CA-C-N	5.12	127.10	120.44
2	L	127	GLU	C-N-CA	5.12	127.10	120.44
1	A	1	GLN	OE1-CD-NE2	-5.12	117.48	122.60
2	B	93	HIS	CB-CG-CD2	-5.10	124.57	131.20
2	L	155	ASP	CA-CB-CG	5.09	117.69	112.60
2	F	53	VAL	CA-C-N	5.08	130.87	121.52
2	F	53	VAL	C-N-CA	5.08	130.87	121.52
1	E	203	GLN	OE1-CD-NE2	-5.07	117.53	122.60
2	D	122	PHE	CA-C-N	5.02	125.55	120.38
2	D	122	PHE	C-N-CA	5.02	125.55	120.38
1	E	59	PHE	CA-CB-CG	5.01	118.81	113.80
1	E	136	ALA	CA-C-N	5.01	125.48	120.52
1	E	136	ALA	C-N-CA	5.01	125.48	120.52
2	D	143	PHE	CA-CB-CG	5.00	118.80	113.80

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	68	ARG	Sidechain
1	C	205	TYR	Sidechain
2	F	144	TYR	Sidechain
1	H	33	TYR	Sidechain

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	1642	1615	1616	2	1
1	C	1694	1668	1670	0	4
1	E	1687	1661	1663	0	6
1	H	1694	1668	1670	3	0
2	B	1562	1480	1504	1	0
2	D	1562	1482	1504	2	3
2	F	1562	1491	1504	2	2
2	L	1562	1470	1504	2	3
All	All	12965	12535	12635	12	11

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 0.

All (12) 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)
2:F:22:CYS:HG	2:F:90:CYS:HG	1.42	0.67
2:D:22:CYS:HG	2:D:90:CYS:HG	1.56	0.54
2:F:22:CYS:SG	2:F:90:CYS:SG	3.01	0.51
1:A:52:VAL:CG2	1:A:71:ILE:HG22	2.44	0.47
2:L:170:LYS:HE3	2:L:176:TYR:CE1	2.51	0.46
2:D:22:CYS:SG	2:D:29:ILE:HD11	2.57	0.44
2:L:170:LYS:HE3	2:L:176:TYR:CZ	2.53	0.44
1:H:33:TYR:CD1	1:H:99:ARG:HD3	2.54	0.42
2:B:20:ILE:HG23	2:B:105:THR:HG21	2.01	0.41
1:H:135:LEU:H	1:H:222:VAL:HG13	1.86	0.41
1:A:189:LEU:C	1:A:189:LEU:HD12	2.46	0.41
1:H:130:PRO:HG2	1:H:216:THR:HG21	2.02	0.41

All (11) 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:E:31:ASP:O	1:E:31:ASP:OD1[7_554]	1.33	0.87
2:F:190:LYS:NZ	2:F:190:LYS:NZ[5_555]	1.42	0.78
1:C:55:ARG:NH2	1:E:58:ASN:HD22[7_554]	1.03	0.57
2:D:11:SER:H	2:L:13:SER:HG[3_454]	1.16	0.44
1:A:103:GLY:HA3	2:F:54:THR:HG21[7_554]	1.21	0.39
1:C:55:ARG:NH2	1:E:58:ASN:ND2[7_554]	1.81	0.39
2:D:205:THR:OG1	2:L:203:GLY:N[3_454]	1.94	0.26
1:C:55:ARG:CZ	1:E:58:ASN:HD22[7_554]	1.41	0.19
1:C:55:ARG:CZ	1:E:58:ASN:ND2[7_554]	2.03	0.17
1:E:31:ASP:OD2	1:E:102:GLU:OE1[7_554]	2.03	0.17
2:D:205:THR:OG1	2:L:203:GLY:CA[3_454]	2.14	0.06

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	215/226 (95%)	202 (94%)	13 (6%)	0	100	100
1	C	224/226 (99%)	209 (93%)	15 (7%)	0	100	100
1	E	223/226 (99%)	210 (94%)	13 (6%)	0	100	100
1	H	224/226 (99%)	203 (91%)	19 (8%)	2 (1%)	14	43
2	B	209/211 (99%)	204 (98%)	5 (2%)	0	100	100
2	D	209/211 (99%)	196 (94%)	12 (6%)	1 (0%)	24	55
2	F	209/211 (99%)	196 (94%)	12 (6%)	1 (0%)	24	55
2	L	209/211 (99%)	188 (90%)	19 (9%)	2 (1%)	12	41
All	All	1722/1748 (98%)	1608 (93%)	108 (6%)	6 (0%)	36	64

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	L	95	ASP
1	H	147	ALA
2	F	26	SER
1	H	168	GLY
2	D	53	VAL
2	L	53	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	186/193 (96%)	182 (98%)	4 (2%)	45	67
1	C	193/193 (100%)	191 (99%)	2 (1%)	68	76
1	E	192/193 (100%)	189 (98%)	3 (2%)	55	71
1	H	193/193 (100%)	190 (98%)	3 (2%)	55	71
2	B	176/176 (100%)	168 (96%)	8 (4%)	24	53
2	D	176/176 (100%)	174 (99%)	2 (1%)	65	75
2	F	176/176 (100%)	173 (98%)	3 (2%)	53	70
2	L	176/176 (100%)	167 (95%)	9 (5%)	21	50
All	All	1468/1476 (100%)	1434 (98%)	34 (2%)	44	66

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	LEU
1	A	52	VAL
1	A	189	LEU
1	A	208	ASN
2	B	25	THR
2	B	49	VAL
2	B	50	ILE
2	B	62	ASP
2	B	100	LEU
2	B	120	THR

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Mol	Chain	Res	Type
2	B	127	GLU
2	B	150	VAL
1	C	18	LEU
1	C	64	SER
2	D	62	ASP
2	D	100	LEU
1	E	18	LEU
1	E	61	LEU
1	E	161	VAL
2	F	25	THR
2	F	49	VAL
2	F	62	ASP
1	H	67	ASN
1	H	189	LEU
1	H	192	VAL
2	L	49	VAL
2	L	50	ILE
2	L	62	ASP
2	L	71	ASP
2	L	98	MET
2	L	100	LEU
2	L	121	LEU
2	L	136	LEU
2	L	196	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	40	GLN
1	A	67	ASN
1	A	210	ASN
2	B	39	GLN
2	B	40	GLN
2	B	41	HIS
1	C	3	GLN
1	C	60	ASN
1	C	109	ASN
1	C	203	GLN
1	C	208	ASN
1	E	67	ASN
1	H	1	GLN
1	H	208	ASN

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Mol	Chain	Res	Type
2	L	171	GLN
2	L	173	ASN

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 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	219/226 (96%)	0.59	11 (5%) 34 20	48, 99, 177, 244	0
1	C	226/226 (100%)	0.89	22 (9%) 13 8	50, 120, 251, 272	0
1	E	225/226 (99%)	0.65	17 (7%) 20 11	39, 93, 242, 260	0
1	H	226/226 (100%)	1.04	41 (18%) 3 2	51, 114, 205, 255	0
2	B	211/211 (100%)	0.70	9 (4%) 40 23	70, 124, 163, 187	0
2	D	211/211 (100%)	0.88	24 (11%) 10 6	64, 141, 217, 241	0
2	F	211/211 (100%)	0.67	11 (5%) 33 19	57, 125, 211, 235	0
2	L	211/211 (100%)	1.10	38 (18%) 3 2	76, 132, 195, 226	0
All	All	1740/1748 (99%)	0.81	173 (9%) 13 7	39, 121, 218, 272	0

All (173) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	135	LEU	6.7
2	L	197	CYS	5.4
2	L	213	ALA	4.9
2	F	213	ALA	4.6
1	E	137	PRO	4.2
2	L	165	THR	4.1
2	L	147	VAL	4.0
1	H	134	PRO	3.9
2	L	120	THR	3.9
1	A	145	SER	3.9
2	L	183	SER	3.9
1	H	155	ASP	3.9
2	L	172	SER	3.9
1	H	205	TYR	3.8
1	H	137	PRO	3.8
1	H	195	VAL	3.8

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Mol	Chain	Res	Type	RSRZ
1	H	136	ALA	3.7
2	L	119	VAL	3.7
1	A	103	GLY	3.6
2	D	197	CYS	3.6
2	L	131	ALA	3.6
1	A	144	GLU	3.5
1	H	222	VAL	3.5
1	H	133	PHE	3.4
1	C	191	SER	3.3
2	D	213	ALA	3.3
1	E	136	ALA	3.3
1	E	184	SER	3.3
1	C	224	ILE	3.3
1	A	149	LEU	3.2
2	L	194	SER	3.2
1	A	224	ILE	3.2
1	E	147	ALA	3.2
1	A	147	ALA	3.2
1	H	207	CYS	3.2
2	D	137	VAL	3.2
2	L	190	LYS	3.1
2	L	139	LEU	3.1
2	D	119	VAL	3.1
2	F	156	GLY	3.1
2	L	184	LEU	3.1
2	F	190	LYS	3.0
1	E	151	CYS	3.0
1	C	149	LEU	3.0
1	H	132	VAL	3.0
1	H	158	PRO	3.0
2	B	190	LYS	3.0
2	B	213	ALA	3.0
1	E	205	TYR	2.9
2	L	121	LEU	2.9
1	H	150	GLY	2.9
1	E	31	ASP	2.9
2	D	124	PRO	2.9
2	L	189	TRP	2.9
1	C	58	ASN	2.9
1	H	166	ASN	2.9
1	H	165	TRP	2.9
1	C	200	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
2	L	195	TYR	2.8
1	H	214	SER	2.8
2	L	212	PRO	2.8
2	L	161	ALA	2.8
1	H	159	GLU	2.7
2	L	200	THR	2.7
1	H	168	GLY	2.6
1	H	218	VAL	2.6
2	L	199	VAL	2.6
2	D	123	PRO	2.6
1	H	10	GLY	2.6
1	E	67	ASN	2.6
2	L	114	LYS	2.6
1	H	185	GLY	2.6
1	H	156	TYR	2.5
1	E	125	ALA	2.5
2	L	207	GLU	2.5
1	C	137	PRO	2.5
1	E	196	PRO	2.5
2	D	146	GLY	2.5
2	L	202	GLU	2.5
1	C	226	THR	2.5
2	L	54	THR	2.5
2	B	212	PRO	2.5
1	H	220	LYS	2.5
2	D	199	VAL	2.5
2	D	183	SER	2.5
2	L	211	ALA	2.5
1	H	130	PRO	2.5
1	C	175	HIS	2.5
2	D	138	CYS	2.4
2	B	133	LYS	2.4
2	L	154	ALA	2.4
1	E	130	PRO	2.4
2	F	212	PRO	2.4
1	E	148	ALA	2.4
1	C	130	PRO	2.4
2	L	181	TYR	2.4
1	H	189	LEU	2.4
1	C	192	VAL	2.4
1	H	206	VAL	2.4
1	A	168	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	H	163	VAL	2.3
2	D	206	VAL	2.3
1	H	138	SER	2.3
1	H	169	SER	2.3
2	D	166	THR	2.3
2	L	155	ASP	2.3
1	E	153	VAL	2.3
2	L	159	VAL	2.3
1	E	224	ILE	2.3
1	H	224	ILE	2.3
2	B	20	ILE	2.3
1	H	171	THR	2.3
2	D	125	SER	2.3
2	D	135	THR	2.3
2	L	185	THR	2.3
2	L	193	LYS	2.3
2	F	20	ILE	2.3
1	H	188	SER	2.3
1	H	154	LYS	2.3
1	C	136	ALA	2.3
1	H	162	THR	2.3
2	D	149	LYS	2.3
1	C	207	CYS	2.2
1	H	209	VAL	2.2
2	L	210	VAL	2.2
1	E	149	LEU	2.2
2	D	151	ALA	2.2
2	D	136	LEU	2.2
1	E	202	THR	2.2
2	B	167	THR	2.2
2	B	125	SER	2.2
2	L	112	GLN	2.2
2	F	107	LEU	2.2
1	A	146	THR	2.2
2	L	148	VAL	2.2
1	C	151	CYS	2.2
2	B	53	VAL	2.1
2	D	129	LEU	2.1
1	A	158	PRO	2.1
1	C	134	PRO	2.1
2	F	119	VAL	2.1
2	D	139	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
2	L	136	LEU	2.1
1	E	209	VAL	2.1
2	F	197	CYS	2.1
2	B	54	THR	2.1
2	D	181	TYR	2.1
2	L	134	ALA	2.1
1	A	178	PRO	2.1
1	H	149	LEU	2.1
1	H	170	LEU	2.1
1	A	127	THR	2.1
1	C	148	ALA	2.1
2	D	117	PRO	2.1
1	C	163	VAL	2.1
1	H	180	VAL	2.0
2	F	210	VAL	2.0
1	H	167	SER	2.0
1	C	147	ALA	2.0
2	D	155	ASP	2.0
2	L	122	PHE	2.0
2	L	124	PRO	2.0
1	C	19	SER	2.0
1	C	138	SER	2.0
1	C	197	SER	2.0
1	H	145	SER	2.0
1	C	85	ASN	2.0
2	D	165	THR	2.0
1	C	9	PRO	2.0
2	F	123	PRO	2.0
2	F	198	GLN	2.0
2	D	96	GLU	2.0
1	H	200	LEU	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

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.