



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 08:29 AM UTC

PDB ID : 8ECZ / pdb_00008ecz
Title : Bovine Fab 4C1
Authors : Stanfield, R.L.; Wilson, I.A.
Deposited on : 2022-09-02
Resolution : 2.82 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

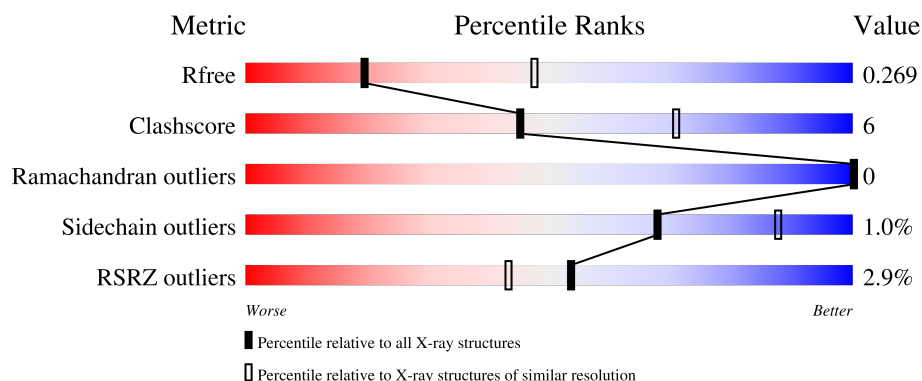
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.82 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	4591 (2.84-2.80)
Clashscore	190562	5010 (2.84-2.80)
Ramachandran outliers	187476	4916 (2.84-2.80)
Sidechain outliers	187428	4918 (2.84-2.80)
RSRZ outliers	180081	4594 (2.84-2.80)

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	216	0% 87% 12% .
1	L	216	0% 82% 16% .
2	B	272	3% 86% 13% .
2	H	272	5% 78% 18% .

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 14019 atoms, of which 6888 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.

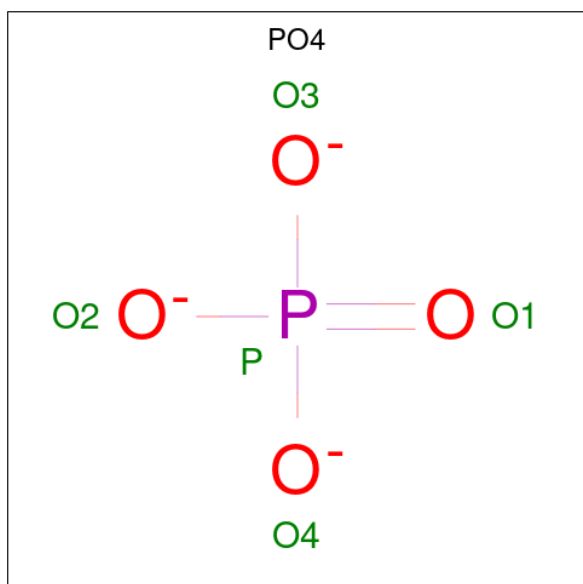
- Molecule 1 is a protein called 4C1 Fab light chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	L	214	Total	C	H	N	O	S	0	0	0
			3068	966	1501	264	332	5			
1	A	213	Total	C	H	N	O	S	0	0	0
			3058	963	1497	263	330	5			

- Molecule 2 is a protein called 4C1 Fab heavy chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	H	261	Total	C	H	N	O	S	0	0	0
			3877	1228	1920	327	394	8			
2	B	271	Total	C	H	N	O	S	0	0	0
			3991	1265	1970	337	410	9			

- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).

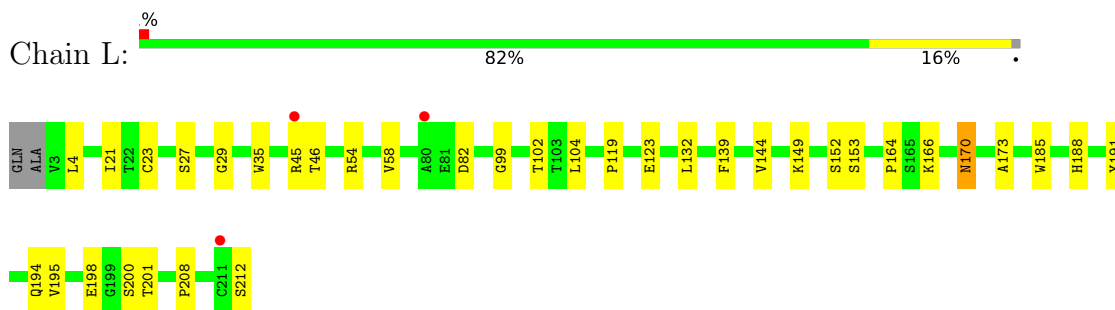


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	H	1	Total	O	P	0	0
			5	4	1		
3	H	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		

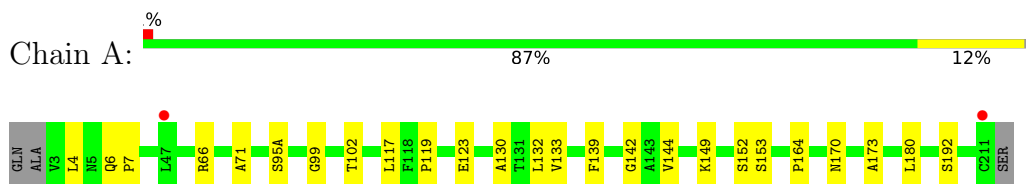
3 Residue-property plots

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.

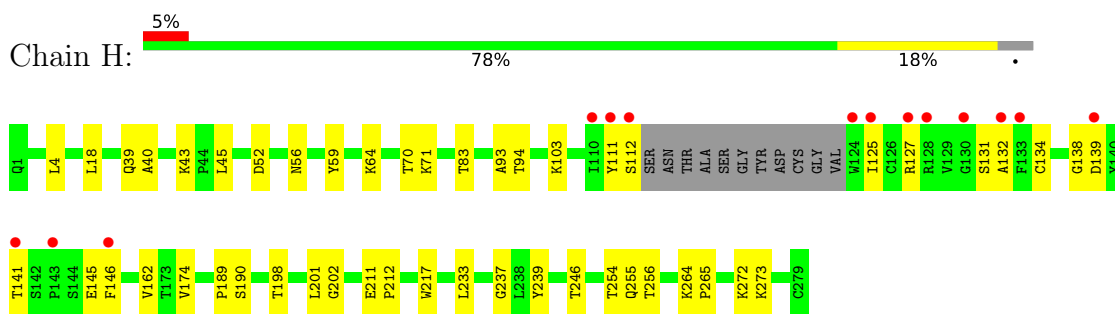
- Molecule 1: 4C1 Fab light chain



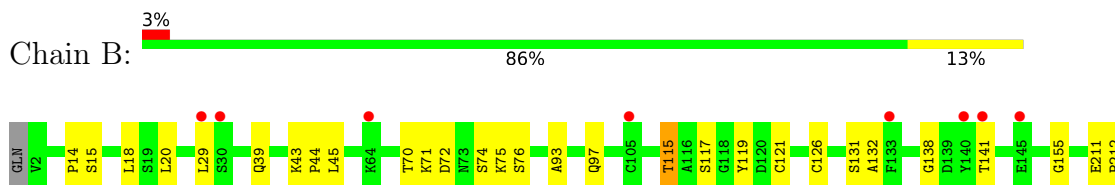
- Molecule 1: 4C1 Fab light chain

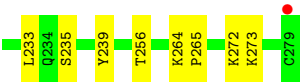


- Molecule 2: 4C1 Fab heavy chain



- Molecule 2: 4C1 Fab heavy chain





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	199.06Å 97.47Å 70.39Å 90.00° 91.44° 90.00°	Depositor
Resolution (Å)	49.75 – 2.82 49.75 – 2.82	Depositor EDS
% Data completeness (in resolution range)	91.9 (49.75-2.82) 91.9 (49.75-2.82)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.61 (at 2.81Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.243 , 0.258 0.255 , 0.269	Depositor DCC
R_{free} test set	1537 reflections (4.71%)	wwPDB-VP
Wilson B-factor (Å ²)	62.2	Xtriage
Anisotropy	0.815	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 39.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.067 for -h,-k,l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	14019	wwPDB-VP
Average B, all atoms (Å ²)	84.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.87% 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: PO4

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	0.19	0/1594	0.40	0/2177
1	L	0.21	0/1600	0.41	0/2185
2	B	0.22	0/2068	0.42	0/2818
2	H	0.21	0/2002	0.43	0/2726
All	All	0.21	0/7264	0.42	0/9906

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	1561	1497	1497	15	0
1	L	1567	1501	1501	23	0
2	B	2021	1970	1970	20	0
2	H	1957	1920	1920	30	0
3	B	15	0	0	0	0
3	H	10	0	0	0	0
All	All	7131	6888	6888	83	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 6.

All (83) 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:7:PRO:O	1:A:102:THR:HG22	1.70	0.92
2:H:127:ARG:NH1	2:H:134:CYS:O	2.22	0.73
2:B:233:LEU:HD13	2:B:239:TYR:CZ	2.30	0.66
2:H:39:GLN:HB2	2:H:45:LEU:HD23	1.82	0.60
2:H:233:LEU:HD13	2:H:239:TYR:CE1	2.37	0.60
1:L:149:LYS:HE2	1:L:152:SER:HA	1.84	0.59
1:L:21:ILE:HD13	1:L:102:THR:HG21	1.85	0.59
2:B:115:THR:HG22	2:B:119:TYR:H	1.67	0.59
2:H:83:THR:C	2:H:174:VAL:HG11	2.28	0.59
2:H:256:THR:HG23	2:H:273:LYS:HE3	1.84	0.59
2:H:59:TYR:HB2	2:H:64:LYS:HD2	1.84	0.58
1:A:117:LEU:HD12	1:A:133:VAL:O	2.04	0.57
1:L:149:LYS:HD2	1:L:194:GLN:NE2	2.21	0.56
2:H:125:ILE:HG12	2:H:141:THR:O	2.06	0.56
2:B:29:LEU:HB3	2:B:71:LYS:HD2	1.87	0.56
2:H:211:GLU:HB3	2:H:212:PRO:HA	1.87	0.55
1:L:185:TRP:CE2	1:L:208:PRO:HB3	2.42	0.54
2:B:131:SER:O	2:B:132:ALA:HB3	2.08	0.54
1:A:130:ALA:HB3	1:A:180:LEU:O	2.08	0.54
2:B:256:THR:HG23	2:B:273:LYS:HE3	1.90	0.53
2:B:126:CYS:HB2	2:B:141:THR:O	2.09	0.53
2:H:40:ALA:HB3	2:H:43:LYS:HG3	1.89	0.53
1:L:119:PRO:HA	1:L:132:LEU:HD23	1.91	0.53
1:A:66:ARG:HA	1:A:71:ALA:HA	1.91	0.52
2:H:111:TYR:O	2:H:112:SER:CB	2.58	0.52
1:L:27:SER:HA	1:L:29:GLY:HA3	1.91	0.51
1:L:195:VAL:O	1:L:201:THR:HA	2.11	0.51
1:L:46:THR:O	1:L:46:THR:HG23	2.11	0.50
2:H:198:THR:CG2	2:H:246:THR:HG23	2.41	0.50
2:H:131:SER:O	2:H:132:ALA:HB3	2.11	0.49
2:H:83:THR:O	2:H:174:VAL:HG11	2.12	0.49
1:L:123:GLU:OE1	2:H:272:LYS:NZ	2.31	0.49
1:L:198:GLU:C	1:L:200:SER:H	2.21	0.49
2:B:43:LYS:HB3	2:B:44:PRO:HD2	1.95	0.48
1:L:21:ILE:HG21	1:L:102:THR:HG21	1.95	0.48
1:L:166:LYS:NZ	1:L:170:ASN:OD1	2.46	0.48
2:H:70:THR:HG22	2:H:71:LYS:N	2.29	0.48
2:H:52:ASP:OD1	2:H:56:ASN:N	2.45	0.47
2:B:39:GLN:HB2	2:B:45:LEU:HD23	1.97	0.47
2:B:115:THR:HG21	2:B:132:ALA:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95(A):SER:HA	2:B:97:GLN:OE1	2.14	0.47
1:L:188:HIS:HD1	1:L:191:TYR:HH	1.61	0.47
1:L:4:LEU:O	1:L:99:GLY:HA2	2.15	0.47
2:H:254:THR:OG1	2:H:255:GLN:N	2.48	0.46
2:H:4:LEU:HD13	2:H:93:ALA:HA	1.98	0.46
2:H:233:LEU:HD11	2:H:237:GLY:O	2.15	0.46
2:B:14:PRO:O	2:B:15:SER:OG	2.28	0.45
2:B:70:THR:HG22	2:B:71:LYS:N	2.31	0.45
1:L:212:SER:C	2:H:190:SER:OG	2.60	0.45
2:H:264:LYS:N	2:H:265:PRO:CD	2.79	0.45
2:B:211:GLU:HB3	2:B:212:PRO:HA	1.97	0.45
2:B:72:ASP:OD1	2:B:74:SER:OG	2.30	0.45
1:A:164:PRO:HA	1:A:173:ALA:O	2.17	0.44
1:A:4:LEU:O	1:A:99:GLY:HA2	2.18	0.44
2:B:264:LYS:N	2:B:265:PRO:CD	2.80	0.44
1:L:54:ARG:HG2	1:L:58:VAL:HB	2.00	0.44
2:B:93:ALA:HB1	2:B:155:GLY:O	2.17	0.44
2:H:18:LEU:HD22	2:H:162:VAL:HG11	2.00	0.44
1:A:149:LYS:O	1:A:192:SER:N	2.51	0.44
2:B:75:LYS:O	2:B:76:SER:OG	2.33	0.43
1:L:82:ASP:O	1:L:104:LEU:HD23	2.18	0.43
1:L:139:PHE:CE2	1:L:144:VAL:HG13	2.53	0.43
1:L:188:HIS:HB2	1:L:191:TYR:CZ	2.53	0.43
2:H:4:LEU:HD11	2:H:94:THR:HG23	2.01	0.43
1:L:164:PRO:HA	1:L:173:ALA:O	2.19	0.43
2:H:103:LYS:HA	2:H:145:GLU:HA	2.01	0.42
1:A:149:LYS:HE2	1:A:152:SER:HA	2.00	0.42
1:A:119:PRO:HA	1:A:132:LEU:HD23	2.01	0.42
1:A:123:GLU:OE1	2:B:272:LYS:NZ	2.52	0.42
1:A:139:PHE:CE2	1:A:144:VAL:HG13	2.54	0.42
1:A:142:GLY:O	1:A:164:PRO:HG2	2.20	0.42
2:H:111:TYR:O	2:H:112:SER:HB2	2.18	0.42
1:A:149:LYS:HA	1:A:153:SER:O	2.20	0.41
2:H:189:PRO:HD3	2:H:201:LEU:HB3	2.02	0.41
2:H:198:THR:HG23	2:H:246:THR:HG23	2.01	0.41
1:A:6:GLN:HB3	1:A:102:THR:CG2	2.49	0.41
1:L:149:LYS:HA	1:L:153:SER:O	2.21	0.41
2:B:18:LEU:HD11	2:B:20:LEU:HD21	2.03	0.41
2:H:202:GLY:HA2	2:H:217:TRP:CZ2	2.56	0.40
1:L:23:CYS:HB2	1:L:35:TRP:CH2	2.56	0.40
2:H:138:GLY:HA3	2:B:138:GLY:HA2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:131:SER:HB2	2:H:139:ASP:HB3	2.04	0.40
1:L:188:HIS:ND1	1:L:191:TYR:OH	2.51	0.40

There are no symmetry-related clashes.

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	211/216 (98%)	200 (95%)	11 (5%)	0	100	100
1	L	212/216 (98%)	201 (95%)	11 (5%)	0	100	100
2	B	269/272 (99%)	251 (93%)	18 (7%)	0	100	100
2	H	257/272 (94%)	241 (94%)	16 (6%)	0	100	100
All	All	949/976 (97%)	893 (94%)	56 (6%)	0	100	100

There are no Ramachandran outliers to report.

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	178/180 (99%)	177 (99%)	1 (1%)	78	92
1	L	179/180 (99%)	177 (99%)	2 (1%)	65	86
2	B	234/235 (100%)	230 (98%)	4 (2%)	53	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	H	227/235 (97%)	226 (100%)	1 (0%)	84	94
All	All	818/830 (99%)	810 (99%)	8 (1%)	68	88

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	45	ARG
1	L	170	ASN
2	H	146	PHE
1	A	170	ASN
2	B	115	THR
2	B	117	SER
2	B	121	CYS
2	B	235	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	126	GLN
2	H	104	ASN
1	A	37	GLN
2	B	16	GLN
2	B	104	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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

5 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	PO4	H	301	-	4,4,4	0.93	0	6,6,6	0.46	0
3	PO4	H	302	-	4,4,4	0.91	0	6,6,6	0.53	0
3	PO4	B	303	-	4,4,4	0.94	0	6,6,6	0.48	0
3	PO4	B	302	-	4,4,4	0.94	0	6,6,6	0.43	0
3	PO4	B	301	-	4,4,4	0.95	0	6,6,6	0.47	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.

No monomer is involved in short contacts.

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	213/216 (98%)	0.29	2 (0%) 81 74	51, 81, 110, 124	0
1	L	214/216 (99%)	0.29	3 (1%) 73 64	45, 76, 108, 125	0
2	B	271/272 (99%)	0.54	9 (3%) 49 39	48, 84, 131, 148	0
2	H	261/272 (95%)	0.46	14 (5%) 31 23	42, 74, 161, 183	0
All	All	959/976 (98%)	0.40	28 (2%) 53 43	42, 78, 130, 183	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	141	THR	4.0
1	L	45	ARG	3.7
1	A	211	CYS	3.6
2	H	111	TYR	3.5
2	H	110	ILE	3.5
2	B	140	TYR	3.5
2	H	133	PHE	3.2
2	H	124	TRP	3.2
2	H	127	ARG	3.0
2	B	133	PHE	3.0
2	H	112	SER	2.9
2	H	125	ILE	2.7
2	H	141	THR	2.7
2	B	29	LEU	2.7
2	H	139	ASP	2.6
2	H	146	PHE	2.6
2	B	145	GLU	2.5
2	B	279	CYS	2.4
1	A	47	LEU	2.4
2	B	64	LYS	2.2
2	H	128	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
2	H	132	ALA	2.1
2	B	105	CYS	2.1
2	B	30	SER	2.0
1	L	211	CYS	2.0
2	H	143	PRO	2.0
2	H	130	GLY	2.0
1	L	80	ALA	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](#)

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	PO4	H	302	5/5	0.70	0.13	70,100,108,110	0
3	PO4	B	302	5/5	0.74	0.10	98,101,125,125	0
3	PO4	B	301	5/5	0.82	0.10	97,103,114,120	0
3	PO4	H	301	5/5	0.86	0.08	67,89,95,96	0
3	PO4	B	303	5/5	0.90	0.25	86,95,113,117	0

6.5 Other polymers [i](#)

There are no such residues in this entry.