



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 24, 2024 – 08:07 PM EDT

PDB ID : 6QNA
Title : Structure of bovine anti-RSV hybrid Fab B13HC-B4LC
Authors : Ren, J.; Nettleship, J.E.; Harris, G.; Mwangi, W.; Rhaman, N.; Grant, C.;
Kotecha, A.; Fry, E.; Charleston, B.; Stuart, D.I.; Hammond, J.; Owens, R.J.
Deposited on : 2019-02-10
Resolution : 2.62 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	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
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)	:	2.37.1

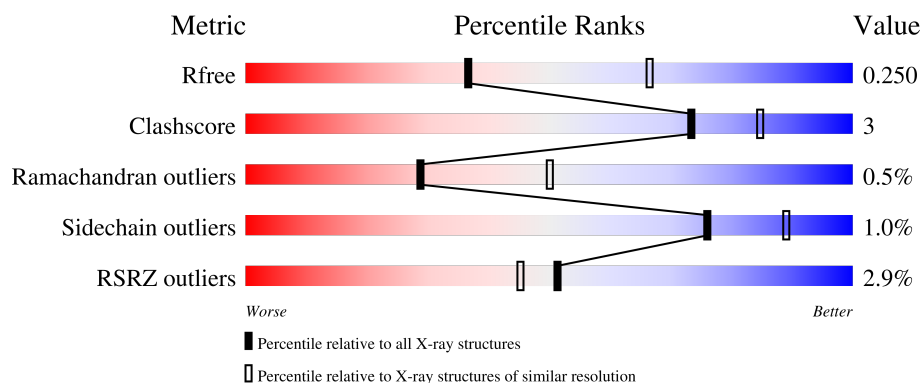
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.62 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	3797 (2.64-2.60)
Clashscore	141614	4168 (2.64-2.60)
Ramachandran outliers	138981	4093 (2.64-2.60)
Sidechain outliers	138945	4093 (2.64-2.60)
RSRZ outliers	127900	3731 (2.64-2.60)

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	243	<div> <div>3%</div> <div>87%</div> <div>7%</div> <div>6%</div> </div>
1	C	243	<div> <div>5%</div> <div>84%</div> <div>9%</div> <div>7%</div> </div>
1	E	243	<div> <div>5%</div> <div>87%</div> <div>6%</div> <div>6%</div> </div>
1	H	243	<div> <div>%</div> <div>84%</div> <div>11%</div> <div>5%</div> </div>
2	B	214	<div> <div>3%</div> <div>90%</div> <div>8%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
2	D	214	<div><div><div></div><div></div><div></div></div><div><div>%</div><div>90%</div><div>9%</div><div>.</div></div></div>
2	F	214	<div><div><div></div><div></div><div></div></div><div><div>2%</div><div>88%</div><div>10%</div><div>.</div></div></div>
2	L	214	<div><div><div></div><div></div><div></div></div><div><div>2%</div><div>89%</div><div>8%</div><div>..</div></div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 13139 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 B13 Heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	232	Total	C	N	O	S	0	0	0
			1727	1084	287	345	11			
1	A	229	Total	C	N	O	S	0	0	0
			1701	1069	280	341	11			
1	C	227	Total	C	N	O	S	0	0	0
			1684	1058	275	340	11			
1	E	228	Total	C	N	O	S	0	0	0
			1686	1059	276	340	11			

- Molecule 2 is a protein called B4 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	211	Total	C	N	O	S	0	0	0
			1571	976	263	326	6			
2	B	211	Total	C	N	O	S	0	0	0
			1571	976	263	326	6			
2	D	211	Total	C	N	O	S	0	0	0
			1571	976	263	326	6			
2	F	211	Total	C	N	O	S	0	0	0
			1571	976	263	326	6			

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			6	3	3		

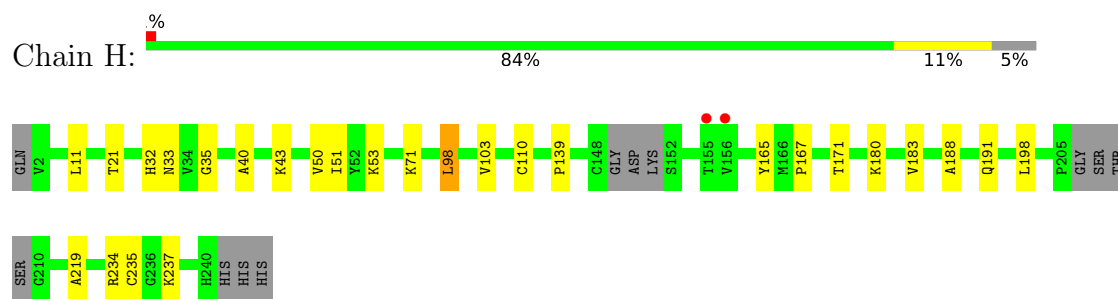
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	H	11	Total	O	0	0
			11	11		
4	L	9	Total	O	0	0
			9	9		
4	A	7	Total	O	0	0
			7	7		
4	B	2	Total	O	0	0
			2	2		
4	C	6	Total	O	0	0
			6	6		
4	D	5	Total	O	0	0
			5	5		
4	E	5	Total	O	0	0
			5	5		
4	F	6	Total	O	0	0
			6	6		

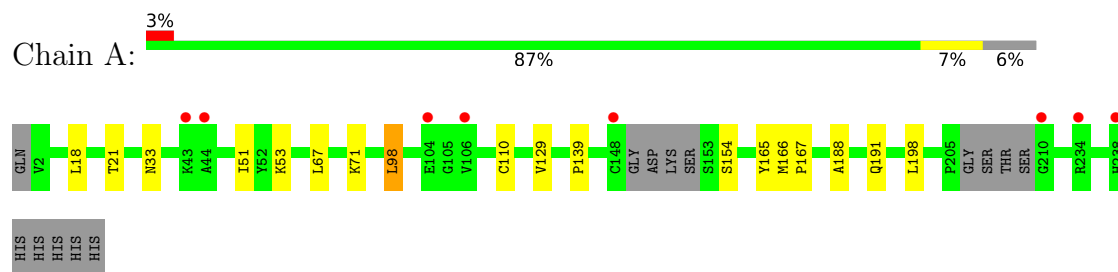
3 Residue-property plots [i](#)

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.

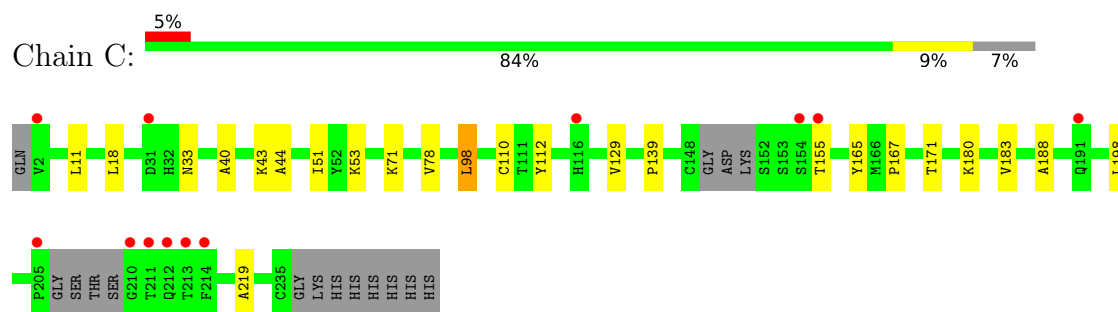
- Molecule 1: B13 Heavy chain



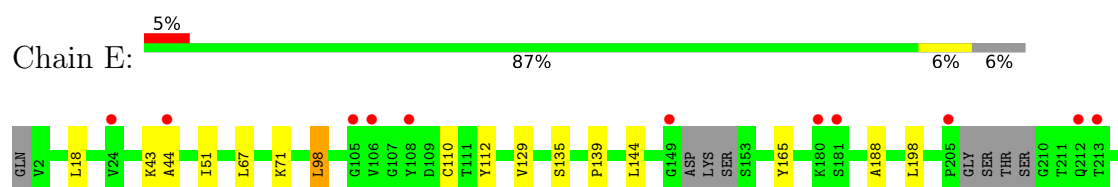
- Molecule 1: B13 Heavy chain

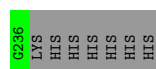


- Molecule 1: B13 Heavy chain

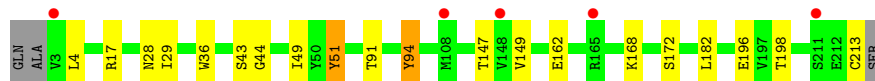
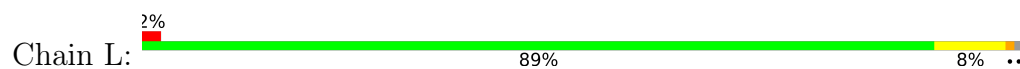


- Molecule 1: B13 Heavy chain

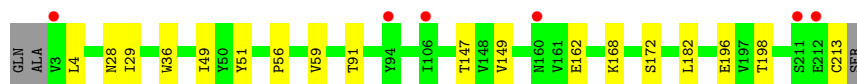
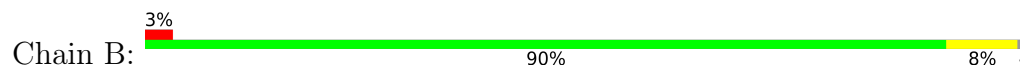




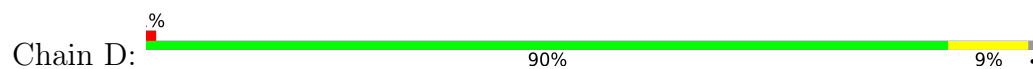
• Molecule 2: B4 light chain



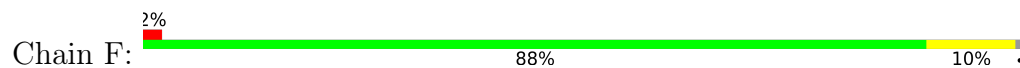
• Molecule 2: B4 light chain



• Molecule 2: B4 light chain



• Molecule 2: B4 light chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	43.44Å 76.27Å 130.03Å 89.66° 87.35° 88.60°	Depositor
Resolution (Å)	65.62 – 2.62 65.89 – 2.62	Depositor EDS
% Data completeness (in resolution range)	98.2 (65.62-2.62) 98.2 (65.89-2.62)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.63 (at 2.62Å)	Xtriage
Refinement program	PHENIX (dev_3386: ???)	Depositor
R, R_{free}	0.220 , 0.250 0.220 , 0.250	Depositor DCC
R_{free} test set	2230 reflections (4.53%)	wwPDB-VP
Wilson B-factor (Å ²)	71.4	Xtriage
Anisotropy	0.362	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 40.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.047 for h,-k,-l 0.066 for -h,k,-l 0.038 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	13139	wwPDB-VP
Average B, all atoms (Å ²)	91.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.11% 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: GOL

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	0.24	0/1738	0.47	0/2372
1	C	0.24	0/1720	0.47	0/2349
1	E	0.24	0/1722	0.47	0/2351
1	H	0.25	0/1766	0.48	0/2410
2	B	0.24	0/1605	0.45	0/2187
2	D	0.24	0/1605	0.45	0/2187
2	F	0.24	0/1605	0.45	0/2187
2	L	0.24	0/1605	0.45	0/2187
All	All	0.24	0/13366	0.46	0/18230

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	1701	0	1664	12	0
1	C	1684	0	1646	13	0
1	E	1686	0	1647	12	0
1	H	1727	0	1683	17	0
2	B	1571	0	1522	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	1571	0	1522	8	0
2	F	1571	0	1522	12	0
2	L	1571	0	1522	10	0
3	B	6	0	8	0	0
4	A	7	0	0	1	0
4	B	2	0	0	0	0
4	C	6	0	0	0	0
4	D	5	0	0	0	0
4	E	5	0	0	2	0
4	F	6	0	0	3	0
4	H	11	0	0	2	0
4	L	9	0	0	0	0
All	All	13139	0	12736	85	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 3.

All (85) 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:21:THR:OG1	4:A:301:HOH:O	2.07	0.72
1:C:11:LEU:HB2	1:C:167:PRO:HG3	1.74	0.69
1:H:11:LEU:HB2	1:H:167:PRO:HG3	1.74	0.68
1:H:21:THR:OG1	4:H:301:HOH:O	2.14	0.64
2:F:153:ASP:N	4:F:301:HOH:O	2.30	0.61
2:L:147:THR:OG1	2:L:198:THR:OG1	2.15	0.60
1:A:139:PRO:HB3	1:A:165:TYR:HB3	1.83	0.60
2:B:147:THR:HG1	2:B:198:THR:HG1	1.50	0.59
2:L:149:VAL:HG23	2:L:196:GLU:HB2	1.86	0.56
1:H:139:PRO:HB3	1:H:165:TYR:HB3	1.86	0.56
2:L:4:LEU:HD11	2:L:91:THR:HG22	1.87	0.56
1:C:139:PRO:HB3	1:C:165:TYR:HB3	1.87	0.56
2:F:55:ARG:NH2	4:F:303:HOH:O	2.35	0.55
2:B:4:LEU:HD11	2:B:91:THR:HG22	1.87	0.55
1:E:139:PRO:HB3	1:E:165:TYR:HB3	1.87	0.54
2:D:4:LEU:HD11	2:D:91:THR:HG22	1.89	0.54
1:A:51:ILE:HD13	1:A:71:LYS:HB3	1.89	0.54
2:F:4:LEU:HD11	2:F:91:THR:HG22	1.90	0.53
1:C:51:ILE:HD13	1:C:71:LYS:HB3	1.92	0.52
2:B:149:VAL:HG23	2:B:196:GLU:HB2	1.90	0.52
1:A:191:GLN:HA	2:B:162:GLU:HG3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:149:VAL:HG23	2:F:196:GLU:HB2	1.90	0.52
2:D:149:VAL:HG23	2:D:196:GLU:HB2	1.91	0.52
2:F:147:THR:HG1	2:F:198:THR:HG1	1.55	0.51
1:H:234:ARG:NH1	1:H:237:LYS:HE3	2.26	0.51
1:H:51:ILE:HD13	1:H:71:LYS:HB3	1.93	0.51
2:D:41:PRO:HG2	2:D:168:LYS:HD2	1.93	0.51
1:E:44:ALA:N	4:E:301:HOH:O	2.21	0.50
1:C:44:ALA:HB2	2:D:101:SER:HA	1.92	0.50
1:C:188:ALA:HA	1:C:198:LEU:HB3	1.94	0.49
1:E:98:LEU:HD22	1:E:110:CYS:HB3	1.94	0.49
1:C:40:ALA:HB3	1:C:43:LYS:HB2	1.94	0.49
1:E:18:LEU:HD13	1:E:129:VAL:HG11	1.95	0.48
2:B:168:LYS:NZ	2:B:172:SER:OG	2.46	0.48
1:C:98:LEU:HD22	1:C:110:CYS:HB3	1.96	0.47
1:A:18:LEU:HD13	1:A:129:VAL:HG11	1.96	0.47
1:C:18:LEU:HD13	1:C:129:VAL:HG21	1.98	0.46
2:B:28:ASN:OD1	2:B:29:ILE:N	2.41	0.46
1:C:71:LYS:HB2	1:C:78:VAL:HG22	1.98	0.46
2:F:28:ASN:OD1	2:F:29:ILE:N	2.42	0.45
2:F:168:LYS:NZ	2:F:172:SER:OG	2.49	0.45
2:F:16:GLN:NE2	4:F:304:HOH:O	2.49	0.45
2:L:36:TRP:CD1	2:L:49:ILE:HD11	2.52	0.45
2:D:28:ASN:OD1	2:D:29:ILE:N	2.41	0.45
1:H:32:HIS:ND1	4:H:302:HOH:O	2.35	0.44
1:A:154:SER:HB3	1:E:135:SER:OG	2.18	0.44
1:E:51:ILE:HD13	1:E:71:LYS:HB3	1.99	0.43
1:A:98:LEU:HD22	1:A:110:CYS:HB3	1.99	0.43
1:E:188:ALA:HA	1:E:198:LEU:HB3	2.00	0.43
1:H:103:VAL:HG21	2:L:51:TYR:CZ	2.54	0.43
1:H:188:ALA:HA	1:H:198:LEU:HB3	2.01	0.43
2:L:43:SER:OG	2:L:44:GLY:N	2.51	0.43
1:A:188:ALA:HA	1:A:198:LEU:HB3	2.01	0.43
2:L:168:LYS:NZ	2:L:172:SER:OG	2.52	0.43
2:B:56:PRO:O	2:B:59:VAL:HG13	2.19	0.43
1:H:180:LYS:O	1:H:183:VAL:HG12	2.19	0.42
1:H:33:ASN:OD1	1:H:53:LYS:HG3	2.19	0.42
1:E:43:LYS:HB3	4:E:301:HOH:O	2.19	0.42
1:H:33:ASN:HB2	1:H:98:LEU:HB3	2.01	0.42
1:H:234:ARG:CZ	1:H:237:LYS:HE3	2.49	0.42
1:A:33:ASN:OD1	1:A:53:LYS:HG3	2.19	0.42
2:D:36:TRP:CD1	2:D:49:ILE:HD11	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:169:GLN:HE21	2:D:175:ALA:HB2	1.84	0.42
1:E:98:LEU:HG	1:E:112:TYR:CE2	2.55	0.42
1:E:67:LEU:HD23	1:E:67:LEU:HA	1.86	0.42
2:L:17:ARG:HD3	2:F:5:THR:HG23	2.01	0.42
1:H:40:ALA:HB3	1:H:43:LYS:HB2	2.02	0.42
1:A:67:LEU:HD23	1:A:67:LEU:HA	1.88	0.42
2:D:56:PRO:O	2:D:59:VAL:HG13	2.20	0.42
1:C:180:LYS:O	1:C:183:VAL:HG12	2.20	0.41
1:H:171:THR:HG23	1:H:219:ALA:HB3	2.02	0.41
1:H:98:LEU:HD22	1:H:110:CYS:HB3	2.01	0.41
2:L:28:ASN:OD1	2:L:29:ILE:N	2.42	0.41
1:C:33:ASN:OD1	1:C:53:LYS:HG3	2.20	0.41
2:F:56:PRO:O	2:F:59:VAL:HG13	2.21	0.41
1:C:98:LEU:HG	1:C:112:TYR:CE2	2.55	0.41
1:H:191:GLN:HA	2:L:162:GLU:HG3	2.02	0.41
1:E:144:LEU:HB3	2:F:120:PHE:CD1	2.55	0.41
1:A:53:LYS:O	1:A:71:LYS:NZ	2.49	0.40
1:E:98:LEU:HD23	1:E:98:LEU:HA	1.96	0.40
1:A:166:MET:HA	1:A:167:PRO:HA	1.84	0.40
2:F:121:PRO:HB3	2:F:208:VAL:HG21	2.03	0.40
1:H:35:GLY:HA2	1:H:50:VAL:HA	2.02	0.40
2:B:36:TRP:CD1	2:B:49:ILE:HD11	2.57	0.40
1:C:171:THR:HG23	1:C:219:ALA:HB3	2.04	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	223/243 (92%)	211 (95%)	12 (5%)	0	100	100
1	C	221/243 (91%)	211 (96%)	9 (4%)	1 (0%)	29	50

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	222/243 (91%)	213 (96%)	9 (4%)	0	100	100
1	H	226/243 (93%)	217 (96%)	9 (4%)	0	100	100
2	B	209/214 (98%)	203 (97%)	5 (2%)	1 (0%)	29	50
2	D	209/214 (98%)	202 (97%)	5 (2%)	2 (1%)	15	30
2	F	209/214 (98%)	203 (97%)	4 (2%)	2 (1%)	15	30
2	L	209/214 (98%)	198 (95%)	9 (4%)	2 (1%)	15	30
All	All	1728/1828 (94%)	1658 (96%)	62 (4%)	8 (0%)	29	50

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	L	51	TYR
2	B	51	TYR
2	L	94	TYR
1	C	155	THR
2	D	51	TYR
2	D	94	TYR
2	F	51	TYR
2	F	94	TYR

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	198/210 (94%)	197 (100%)	1 (0%)	88	95
1	C	197/210 (94%)	196 (100%)	1 (0%)	88	95
1	E	196/210 (93%)	195 (100%)	1 (0%)	88	95
1	H	201/210 (96%)	199 (99%)	2 (1%)	76	89
2	B	182/184 (99%)	180 (99%)	2 (1%)	73	88
2	D	182/184 (99%)	180 (99%)	2 (1%)	73	88
2	F	182/184 (99%)	179 (98%)	3 (2%)	62	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	L	182/184 (99%)	179 (98%)	3 (2%)	62 81
All	All	1520/1576 (96%)	1505 (99%)	15 (1%)	76 89

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	98	LEU
1	H	235	CYS
2	L	94	TYR
2	L	182	LEU
2	L	213	CYS
1	A	98	LEU
2	B	182	LEU
2	B	213	CYS
1	C	98	LEU
2	D	182	LEU
2	D	213	CYS
1	E	98	LEU
2	F	94	TYR
2	F	182	LEU
2	F	213	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	73	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 monosaccharides in this entry.

5.6 Ligand geometry

1 ligand is 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	GOL	B	301	-	5,5,5	0.93	0	5,5,5	0.98	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	B	301	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	301	GOL	C1-C2-C3-O3
3	B	301	GOL	O2-C2-C3-O3

There are no ring outliers.

No monomer is involved in short contacts.

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	229/243 (94%)	-0.17	8 (3%)	44	37	48, 89, 141, 187	0
1	C	227/243 (93%)	-0.01	12 (5%)	26	21	46, 81, 131, 171	0
1	E	228/243 (93%)	0.09	11 (4%)	30	24	60, 93, 148, 161	0
1	H	232/243 (95%)	-0.22	2 (0%)	84	82	46, 72, 138, 174	0
2	B	211/214 (98%)	-0.02	6 (2%)	53	47	63, 98, 143, 159	0
2	D	211/214 (98%)	-0.13	3 (1%)	75	71	58, 88, 129, 153	0
2	F	211/214 (98%)	-0.10	4 (1%)	66	62	65, 101, 134, 149	0
2	L	211/214 (98%)	-0.17	5 (2%)	59	53	50, 86, 125, 141	0
All	All	1760/1828 (96%)	-0.09	51 (2%)	51	45	46, 89, 138, 187	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	155	THR	8.5
1	A	210	GLY	5.7
2	B	211	SER	5.3
1	E	205	PRO	5.1
2	D	3	VAL	4.4
1	C	211	THR	4.3
1	E	106	VAL	4.3
1	A	106	VAL	3.8
1	A	43	LYS	3.6
1	E	212	GLN	3.4
2	B	94	TYR	3.3
1	A	234	ARG	3.2
1	E	180	LYS	3.0
1	E	44	ALA	3.0
2	L	211	SER	2.9
1	E	149	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
1	C	210	GLY	2.8
2	F	160	ASN	2.8
1	A	238	HIS	2.7
1	C	191	GLN	2.7
1	C	155	THR	2.7
1	E	213	THR	2.7
2	L	165	ARG	2.6
1	C	205	PRO	2.6
1	C	116	HIS	2.6
1	E	24	VAL	2.6
2	F	82	GLU	2.5
1	A	104	GLU	2.5
1	A	148	CYS	2.4
1	C	31	ASP	2.4
1	E	105	GLY	2.4
1	E	108	TYR	2.4
2	D	108	MET	2.4
2	D	168	LYS	2.3
2	B	160	ASN	2.3
2	B	212	GLU	2.3
1	H	156	VAL	2.2
2	L	3	VAL	2.2
1	A	44	ALA	2.2
1	C	212	GLN	2.2
1	C	154	SER	2.1
1	E	181	SER	2.1
2	L	148	VAL	2.1
2	B	106	ILE	2.1
1	C	214	PHE	2.1
2	L	108	MET	2.0
2	F	56	PRO	2.0
2	F	159	ARG	2.0
1	C	213	THR	2.0
1	C	2	VAL	2.0
2	B	3	VAL	2.0

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides 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(\AA^2)	Q<0.9
3	GOL	B	301	6/6	0.75	0.15	107,108,109,109	0

6.5 Other polymers [i](#)

There are no such residues in this entry.