



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 06:27 AM UTC

PDB ID : 6P4B / pdb_00006p4b
Title : HyHEL10 fab variant HyHEL10-4x (heavy chain mutations L4F, Y33H, S56N, and Y58F) bound to hen egg lysozyme variant HEL2x-flex (mutations R21Q, R73E, C76S, and C94S)
Authors : Langley, D.B.; Christ, D.
Deposited on : 2019-05-27
Resolution : 1.90 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

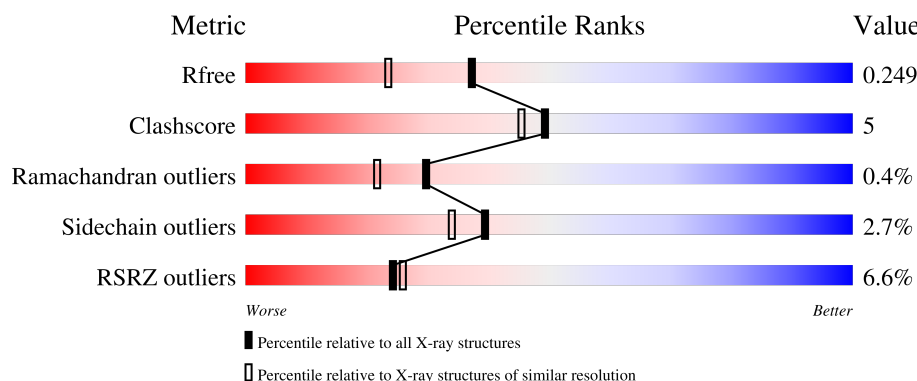
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	214	4% 89% 8% .
1	L	214	6% 80% 17% ..
2	B	223	12% 77% 13% . 9%
2	H	223	7% 79% 12% 8%
3	C	129	4% 90% 9% .

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Mol	Chain	Length	Quality of chain
3	D	129	5% 88% 11%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8755 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 HyHEL10 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	210	Total	C	N	O	S	0	1	0
			1599	998	270	325	6			
1	A	209	Total	C	N	O	S	0	2	0
			1603	997	272	328	6			

- Molecule 2 is a protein called HyHEL10 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	205	Total	C	N	O	S	0	1	0
			1542	984	246	306	6			
2	B	204	Total	C	N	O	S	0	0	0
			1524	971	244	304	5			

- Molecule 3 is a protein called Lysozyme C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	129	Total	C	N	O	S	0	3	0
			1008	617	190	193	8			
3	D	129	Total	C	N	O	S	0	4	0
			1013	620	192	193	8			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	21	GLN	ARG	engineered mutation	UNP P00698
C	73	GLU	ARG	engineered mutation	UNP P00698
C	76	SER	CYS	engineered mutation	UNP P00698
C	94	SER	CYS	engineered mutation	UNP P00698
D	21	GLN	ARG	engineered mutation	UNP P00698
D	73	GLU	ARG	engineered mutation	UNP P00698
D	76	SER	CYS	engineered mutation	UNP P00698
D	94	SER	CYS	engineered mutation	UNP P00698

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	L	5	Total 5	Cl 5	0	0
4	C	2	Total 2	Cl 2	0	0
4	B	1	Total 1	Cl 1	0	0
4	D	1	Total 1	Cl 1	0	0

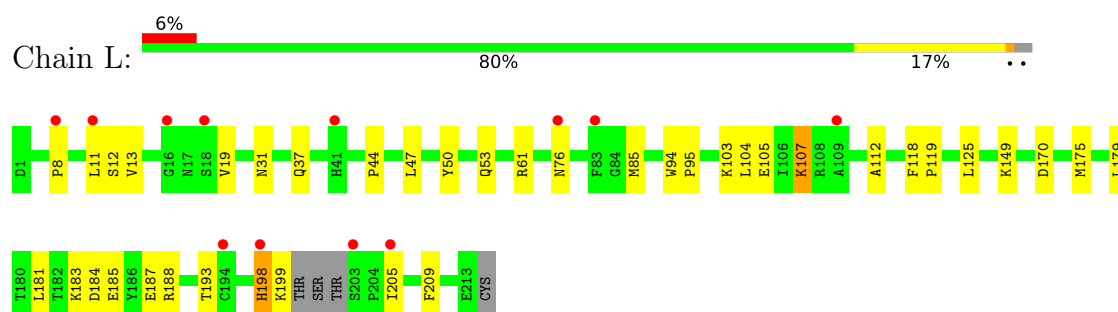
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	L	60	Total 60	O 60	0	0
5	H	71	Total 71	O 71	0	0
5	C	88	Total 88	O 88	0	0
5	A	78	Total 78	O 78	0	0
5	B	68	Total 68	O 68	0	0
5	D	92	Total 92	O 92	0	0

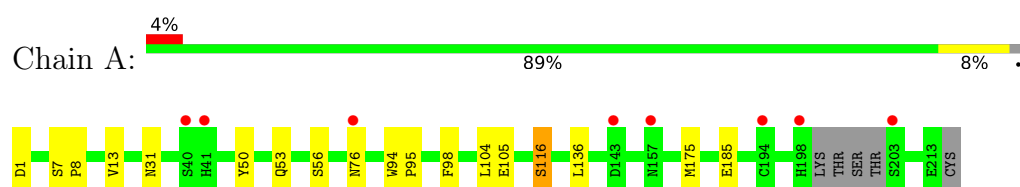
3 Residue-property plots [i](#)

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.

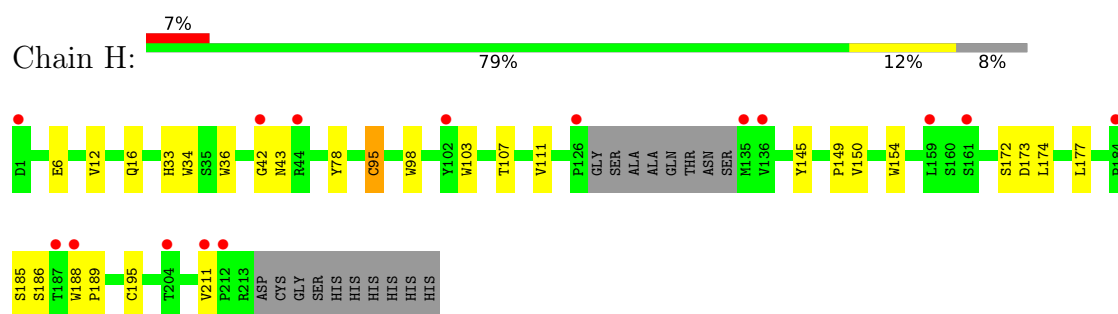
- Molecule 1: HyHEL10 Fab light chain



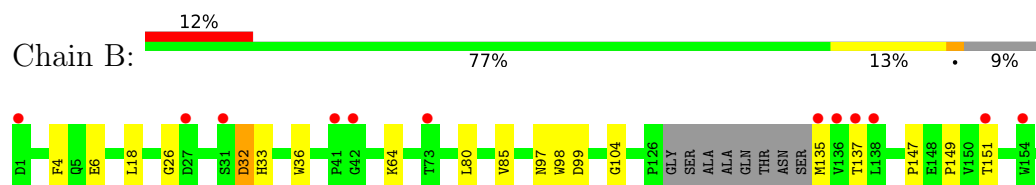
- Molecule 1: HyHEL10 Fab light chain

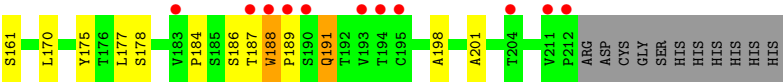


- Molecule 2: HyHEL10 Fab heavy chain

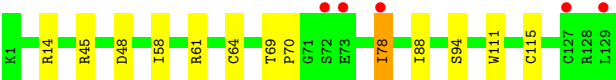
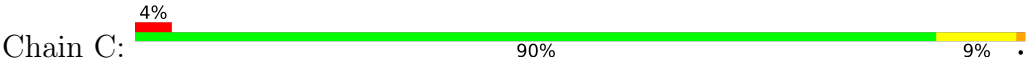


- Molecule 2: HyHEL10 Fab heavy chain

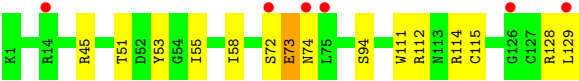
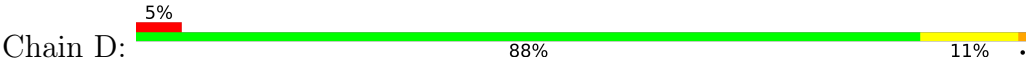




● Molecule 3: Lysozyme C



● Molecule 3: Lysozyme C



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	66.40Å 65.72Å 137.13Å 90.00° 98.48° 90.00°	Depositor
Resolution (Å)	34.91 – 1.90 34.91 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.9 (34.91-1.90) 99.9 (34.91-1.90)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.94 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.203 , 0.244 0.210 , 0.249	Depositor DCC
R_{free} test set	4548 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	25.3	Xtriage
Anisotropy	0.214	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 30.0	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	0.94	EDS
Total number of atoms	8755	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 7.75% 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

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

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	1.09	1/1638 (0.1%)	1.26	2/2228 (0.1%)
1	L	1.06	0/1635	1.29	5/2224 (0.2%)
2	B	1.08	0/1569	1.34	5/2165 (0.2%)
2	H	1.04	0/1587	1.34	3/2187 (0.1%)
3	C	1.16	0/1028	1.34	1/1392 (0.1%)
3	D	1.11	0/1033	1.37	0/1398
All	All	1.09	1/8490 (0.0%)	1.32	16/11594 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	98	PHE	C-O	6.07	1.30	1.23

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	26	GLY	CA-C-O	-7.09	117.34	122.45
1	A	76	ASN	CB-CA-C	6.34	120.46	110.19
2	H	95	CYS	CB-CA-C	6.19	119.88	109.48
2	B	32	ASP	CA-CB-CG	6.14	118.74	112.60
3	C	69	THR	CB-CA-C	5.74	115.85	110.17
2	B	6	GLU	CB-CA-C	-5.65	99.85	109.51
2	H	186	SER	CA-C-N	5.45	127.58	120.28
2	H	186	SER	C-N-CA	5.45	127.58	120.28
2	B	6	GLU	N-CA-CB	5.25	118.97	110.41
1	L	170	ASP	CA-CB-CG	5.22	117.82	112.60
1	L	125	LEU	CA-C-N	5.14	127.42	120.38
1	L	125	LEU	C-N-CA	5.14	127.42	120.38
1	A	53	GLN	CB-CG-CD	5.05	121.19	112.60
1	L	53	GLN	CA-C-N	5.05	128.02	120.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	53	GLN	C-N-CA	5.05	128.02	120.90
2	B	99	ASP	CA-CB-CG	5.03	117.63	112.60

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	1603	0	1492	8	0
1	L	1599	0	1492	24	0
2	B	1524	0	1411	19	0
2	H	1542	0	1446	16	0
3	C	1008	0	948	12	0
3	D	1013	0	950	10	0
4	B	1	0	0	0	0
4	C	2	0	0	1	0
4	D	1	0	0	0	0
4	L	5	0	0	0	0
5	A	78	0	0	1	0
5	B	68	0	0	0	0
5	C	88	0	0	0	0
5	D	92	0	0	0	0
5	H	71	0	0	1	0
5	L	60	0	0	1	0
All	All	8755	0	7739	87	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 5.

All (87) 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)
3:C:78[A]:ILE:CD1	3:C:78[A]:ILE:O	2.29	0.80
3:C:61:ARG:NH1	3:C:70:PRO:O	2.14	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:187:THR:O	2:B:191:GLN:HB2	1.85	0.77
3:C:78[A]:ILE:O	3:C:78[A]:ILE:HD12	1.89	0.73
1:A:1:ASP:HB2	5:A:333:HOH:O	1.90	0.72
3:C:78[A]:ILE:O	3:C:78[A]:ILE:HD13	1.93	0.66
2:B:32:ASP:OD2	2:B:97:ASN:HB2	1.97	0.64
2:H:6:GLU:HB2	2:H:107:THR:HG23	1.83	0.61
3:C:78[A]:ILE:CD1	3:C:78[A]:ILE:C	2.74	0.60
2:B:188:TRP:O	2:B:191:GLN:O	2.22	0.58
2:B:188:TRP:HB3	2:B:189:PRO:HD3	1.86	0.58
1:L:112:ALA:HB1	1:L:205:ILE:HD11	1.86	0.57
2:B:188:TRP:O	2:B:189:PRO:C	2.47	0.57
2:B:177:LEU:C	2:B:177:LEU:HD12	2.29	0.57
1:L:107:LYS:O	5:L:401:HOH:O	2.18	0.56
1:L:13:VAL:HG21	1:L:19:VAL:CG1	2.36	0.56
1:L:11[B]:LEU:C	1:L:11[B]:LEU:HD23	2.31	0.55
3:D:128:ARG:O	3:D:129:LEU:HB2	2.06	0.55
1:L:31:ASN:O	1:L:50:TYR:HA	2.07	0.55
2:H:16:GLN:OE1	5:H:301:HOH:O	2.18	0.55
3:D:58:ILE:HD13	3:D:94:SER:HB2	1.88	0.54
2:H:177:LEU:C	2:H:177:LEU:HD12	2.33	0.54
1:L:11[B]:LEU:HD22	1:L:104:LEU:CD1	2.38	0.53
2:B:151:THR:OG1	2:B:198:ALA:HB3	2.08	0.53
1:L:149:LYS:HB2	1:L:193:THR:HB	1.91	0.53
1:L:11[B]:LEU:HD22	1:L:104:LEU:HD12	1.89	0.53
1:L:37:GLN:HB2	1:L:47:LEU:HD11	1.93	0.51
2:H:42:GLY:O	2:H:43:ASN:HB2	2.11	0.50
1:A:94:TRP:CD2	1:A:95:PRO:HA	2.46	0.50
3:D:51:THR:HB	3:D:53:TYR:CE1	2.48	0.49
1:L:94:TRP:CD2	1:L:95:PRO:HA	2.48	0.49
1:L:185:GLU:OE2	1:L:188:ARG:NH2	2.47	0.47
2:H:34:TRP:HB3	2:H:78:TYR:CZ	2.49	0.47
3:C:111:TRP:CD1	3:C:115:CYS:HB2	2.49	0.47
3:C:64:CYS:HB3	3:C:78[A]:ILE:HD11	1.96	0.47
3:C:78[A]:ILE:HD13	3:C:78[A]:ILE:C	2.39	0.46
3:D:111:TRP:CD1	3:D:115:CYS:HB2	2.51	0.46
3:D:74[A]:ASN:O	3:D:74[A]:ASN:OD1	2.33	0.46
3:D:128:ARG:O	3:D:129:LEU:CB	2.63	0.46
1:A:31:ASN:O	1:A:50:TYR:HA	2.16	0.45
2:B:33:HIS:HB2	2:B:98:TRP:CB	2.47	0.45
1:A:104:LEU:HD23	1:A:104:LEU:C	2.41	0.45
2:H:154:TRP:CZ3	2:H:195:CYS:HB3	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:116:SER:OG	2:B:137:THR:HG21	2.16	0.44
1:L:8:PRO:HG2	1:L:11[A]:LEU:HG	1.99	0.44
2:H:12:VAL:O	2:H:111:VAL:HA	2.17	0.44
2:H:33:HIS:HB2	2:H:98:TRP:HB2	1.99	0.44
2:B:33:HIS:HB2	2:B:98:TRP:HB2	1.97	0.44
2:B:36:TRP:CE2	2:B:80:LEU:HB2	2.53	0.43
2:B:18:LEU:HB2	2:B:85:VAL:HG11	1.99	0.43
1:L:183:LYS:O	1:L:187:GLU:HG2	2.17	0.43
1:L:118:PHE:HA	1:L:119:PRO:HD3	1.90	0.43
3:D:72:SER:OG	3:D:73:GLU:N	2.52	0.43
1:A:136:LEU:HD12	1:A:136:LEU:N	2.34	0.43
3:D:112[B]:ARG:CD	3:D:112[B]:ARG:C	2.92	0.43
1:L:179:LEU:HD11	1:L:181:LEU:HD21	2.01	0.43
1:A:7:SER:HA	1:A:8:PRO:C	2.44	0.43
2:B:170:LEU:HD13	2:B:175:TYR:CZ	2.54	0.43
1:L:85:MET:SD	1:L:103:LYS:HD3	2.59	0.42
1:L:198:HIS:O	1:L:199:LYS:C	2.62	0.42
1:L:61:ARG:HB2	1:L:76:ASN:O	2.19	0.42
2:H:6:GLU:HB2	2:H:107:THR:CG2	2.47	0.42
3:D:74[A]:ASN:OD1	3:D:74[A]:ASN:C	2.62	0.42
1:L:119:PRO:HB3	1:L:209:PHE:CE1	2.55	0.42
1:L:184:ASP:O	1:L:188:ARG:HG3	2.19	0.42
3:C:64:CYS:CB	3:C:78[A]:ILE:CD1	2.97	0.42
3:C:64:CYS:HA	3:C:78[A]:ILE:HD12	2.01	0.42
2:H:188:TRP:CG	2:H:189:PRO:HA	2.54	0.42
3:D:112[B]:ARG:C	3:D:112[B]:ARG:HD3	2.45	0.42
3:C:88:ILE:HG12	4:C:202:CL:CL	2.56	0.41
1:L:112:ALA:HB1	1:L:205:ILE:CD1	2.48	0.41
2:H:154:TRP:CH2	2:H:195:CYS:HB3	2.55	0.41
2:B:188:TRP:CB	2:B:189:PRO:HD3	2.50	0.41
1:L:44:PRO:HG2	2:H:103:TRP:CZ3	2.55	0.41
3:C:58:ILE:HD13	3:C:94:SER:HB2	2.02	0.41
2:H:36:TRP:CZ3	2:H:95:CYS:HB3	2.55	0.41
1:L:11[B]:LEU:HD21	1:L:13:VAL:HB	2.02	0.41
2:B:184:PRO:HB2	2:B:187:THR:HG23	2.02	0.41
2:B:147:PRO:HD2	2:B:201:ALA:CB	2.51	0.41
2:H:145:TYR:CE2	2:H:150:VAL:HG13	2.56	0.41
2:B:4:PHE:O	2:B:104:GLY:HA2	2.20	0.41
2:B:135:MET:CB	2:B:184:PRO:HA	2.51	0.41
2:H:185:SER:O	2:H:188:TRP:O	2.38	0.41
1:A:13:VAL:CG1	1:A:104:LEU:HD21	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:173:ASP:O	2:H:174:LEU:HD23	2.21	0.40
2:B:159:LEU:O	2:B:161:SER:N	2.55	0.40
1:L:13:VAL:HG21	1:L:19:VAL:HG13	2.03	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	207/214 (97%)	197 (95%)	10 (5%)	0	100	100
1	L	207/214 (97%)	198 (96%)	9 (4%)	0	100	100
2	B	200/223 (90%)	192 (96%)	5 (2%)	3 (2%)	8	2
2	H	202/223 (91%)	198 (98%)	4 (2%)	0	100	100
3	C	130/129 (101%)	126 (97%)	4 (3%)	0	100	100
3	D	131/129 (102%)	126 (96%)	4 (3%)	1 (1%)	16	8
All	All	1077/1132 (95%)	1037 (96%)	36 (3%)	4 (0%)	30	22

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	191	GLN
2	B	64	LYS
2	B	188	TRP
3	D	73	GLU

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	179/192 (93%)	174 (97%)	5 (3%)	38	32
1	L	178/192 (93%)	173 (97%)	5 (3%)	38	32
2	B	169/199 (85%)	165 (98%)	4 (2%)	43	38
2	H	173/199 (87%)	170 (98%)	3 (2%)	53	52
3	C	105/105 (100%)	99 (94%)	6 (6%)	18	11
3	D	105/105 (100%)	102 (97%)	3 (3%)	37	31
All	All	909/992 (92%)	883 (97%)	26 (3%)	39	31

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	12	SER
1	L	105	GLU
1	L	107	LYS
1	L	175	MET
1	L	198	HIS
2	H	149	PRO
2	H	172	SER
2	H	211	VAL
3	C	14	ARG
3	C	45	ARG
3	C	48[A]	ASP
3	C	48[B]	ASP
3	C	78[A]	ILE
3	C	78[B]	ILE
1	A	56	SER
1	A	105	GLU
1	A	116	SER
1	A	175	MET
1	A	185	GLU
2	B	149	PRO
2	B	159	LEU
2	B	178	SER
2	B	186	SER
3	D	45	ARG
3	D	55	ILE
3	D	114	ARG

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	198	HIS
2	H	164	HIS
1	A	138	ASN
3	D	44	ASN
3	D	57	GLN

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](#)

Of 9 ligands modelled in this entry, 9 are monoatomic - leaving 0 for Mogul analysis.

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 ⓘ

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	209/214 (97%)	0.54	8 (3%) 44 47	12, 37, 56, 64	2 (0%)
1	L	210/214 (98%)	0.67	12 (5%) 29 31	19, 38, 58, 78	1 (0%)
2	B	204/223 (91%)	0.70	26 (12%) 8 8	15, 35, 71, 90	0
2	H	205/223 (91%)	0.52	15 (7%) 21 22	15, 32, 57, 71	1 (0%)
3	C	129/129 (100%)	0.16	5 (3%) 43 46	14, 23, 39, 60	3 (2%)
3	D	129/129 (100%)	0.13	6 (4%) 36 39	12, 22, 41, 62	4 (3%)
All	All	1086/1132 (95%)	0.50	72 (6%) 24 26	12, 33, 59, 90	11 (1%)

All (72) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	D	75	LEU	4.5
3	D	74[A]	ASN	4.0
3	D	129	LEU	3.9
2	B	159	LEU	3.7
1	A	198	HIS	3.6
2	B	189	PRO	3.6
1	L	198	HIS	3.5
2	B	193	VAL	3.5
2	H	159	LEU	3.4
1	A	41	HIS	3.3
2	B	157	GLY	3.1
1	A	40	SER	3.1
2	B	158	SER	3.0
2	B	136	VAL	2.8
2	B	204	THR	2.8
1	A	194	CYS	2.8
3	D	72	SER	2.8
2	H	135	MET	2.8
2	B	195	CYS	2.7

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Mol	Chain	Res	Type	RSRZ
2	B	151	THR	2.7
2	B	154	TRP	2.7
2	H	126	PRO	2.6
1	L	16	GLY	2.6
2	B	183	VAL	2.6
2	B	187	THR	2.6
3	C	72	SER	2.6
2	H	1	ASP	2.6
2	B	1	ASP	2.6
2	B	138	LEU	2.5
2	B	41	PRO	2.5
2	B	188	TRP	2.5
3	C	129	LEU	2.4
1	L	203	SER	2.4
1	A	143	ASP	2.4
1	A	76	ASN	2.4
2	H	187	THR	2.4
2	H	44	ARG	2.4
2	B	212	PRO	2.4
1	A	203	SER	2.4
3	C	127	CYS	2.4
3	C	73	GLU	2.3
2	H	42	GLY	2.3
2	H	136	VAL	2.3
1	L	83	PHE	2.3
2	B	190	SER	2.3
2	B	73	THR	2.3
1	L	11[A]	LEU	2.3
2	H	102	TYR	2.2
2	H	184	PRO	2.2
3	D	126	GLY	2.2
1	L	41	HIS	2.2
1	A	157	ASN	2.2
2	B	135	MET	2.2
1	L	109	ALA	2.2
2	H	211	VAL	2.2
2	B	27	ASP	2.2
2	H	188	TRP	2.1
2	H	204	THR	2.1
1	L	18	SER	2.1
2	H	161	SER	2.1
1	L	76	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
2	H	212	PRO	2.1
1	L	205	ILE	2.1
2	B	31	SER	2.1
2	B	137	THR	2.1
1	L	194	CYS	2.1
3	C	78[A]	ILE	2.0
2	B	42	GLY	2.0
3	D	14[A]	ARG	2.0
2	B	194	THR	2.0
1	L	8	PRO	2.0
2	B	211	VAL	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(Å ²)	Q<0.9
4	CL	L	304	1/1	0.82	0.17	65,65,65,65	0
4	CL	L	301	1/1	0.84	0.12	56,56,56,56	0
4	CL	C	201	1/1	0.87	0.14	52,52,52,52	0
4	CL	L	303	1/1	0.90	0.14	56,56,56,56	0
4	CL	C	202	1/1	0.90	0.18	49,49,49,49	0
4	CL	L	302	1/1	0.93	0.15	55,55,55,55	0
4	CL	B	301	1/1	0.94	0.10	58,58,58,58	0
4	CL	L	305	1/1	0.96	0.09	36,36,36,36	0
4	CL	D	201	1/1	0.97	0.08	42,42,42,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.