



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 16, 2017 – 10:09 AM EDT

PDB ID : 3D9A
Title : High Resolution Crystal Structure Structure of HyHel10 Fab Complexed to Hen Egg Lysozyme
Authors : DeSantis, M.E.; Li, M.; Shanmuganathan, A.; Acchione, M.; Walter, R.; Wlodawer, A.; Smith-Gill, S.
Deposited on : unknown
Resolution : 1.20 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20030345
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20030345

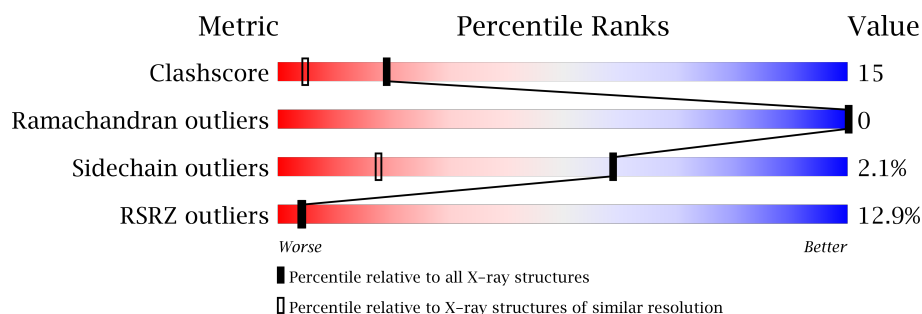
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.20 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))
Clashscore	112137	1201 (1.24-1.16)
Ramachandran outliers	110173	1148 (1.24-1.16)
Sidechain outliers	110143	1147 (1.24-1.16)
RSRZ outliers	101464	1132 (1.24-1.16)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	C	129	<div> <div>12%</div> <div>79%</div> <div>20%</div> <div>.</div> </div>
2	L	213	<div> <div>12%</div> <div>86%</div> <div>12%</div> <div>.</div> </div>
3	H	210	<div> <div>14%</div> <div>80%</div> <div>18%</div> <div>.</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4947 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 Lysozyme C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	129	Total	C	N	O	S	0	0	0
			1001	613	193	185	10			

- Molecule 2 is a protein called Light Chain of HyHel10 Antibody Fragment (Fab).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	213	Total	C	N	O	S	0	2	0
			1655	1029	280	340	6			

- Molecule 3 is a protein called Heavy Chain of HyHel10 Antibody Fragment (Fab).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	210	Total	C	N	O	S	0	1	0
			1608	1016	256	330	6			

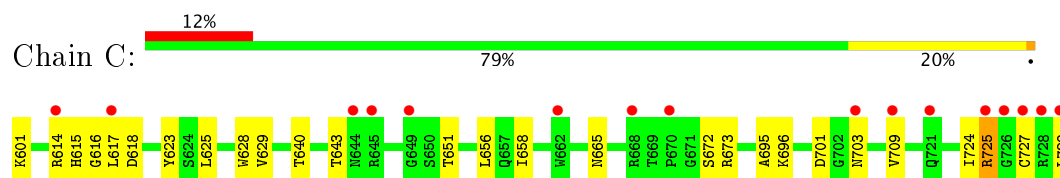
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	155	Total	O	0	0
			155	155		
4	L	268	Total	O	0	0
			268	268		
4	H	260	Total	O	0	0
			260	260		

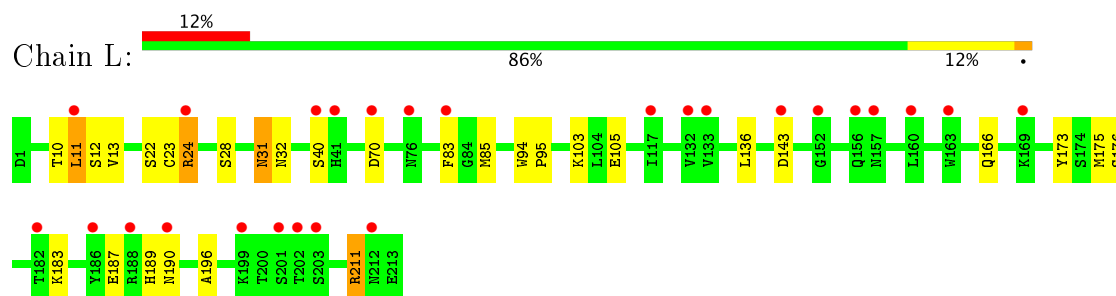
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

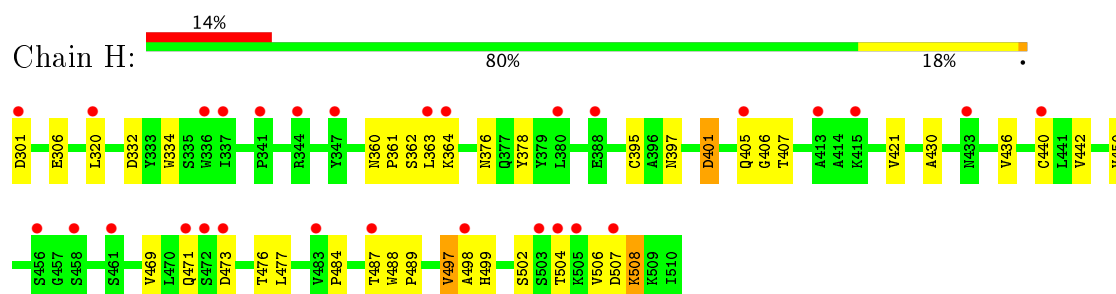
- Molecule 1: Lysozyme C



- Molecule 2: Light Chain of HyHel10 Antibody Fragment (Fab)



- Molecule 3: Heavy Chain of HyHel10 Antibody Fragment (Fab)



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	39.84Å 77.39Å 89.11Å 90.00° 96.66° 90.00°	Depositor
Resolution (Å)	50.00 – 1.20 35.23 – 1.20	Depositor EDS
% Data completeness (in resolution range)	99.3 (50.00-1.20) 94.4 (35.23-1.20)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.99 (at 1.20Å)	Xtriage
Refinement program	REFMAC 5.4.0057	Depositor
R, R_{free}	0.190 , 0.205 0.197 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	14.1	Xtriage
Anisotropy	0.217	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.44 , 53.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4947	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.98% 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

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	C	0.53	0/1021	0.72	0/1379
2	L	0.54	0/1699	0.71	2/2308 (0.1%)
3	H	0.57	0/1655	0.76	1/2272 (0.0%)
All	All	0.55	0/4375	0.73	3/5959 (0.1%)

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
3	H	0	1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	211	ARG	NE-CZ-NH2	7.59	124.09	120.30
3	H	498	ALA	N-CA-C	6.80	129.38	111.00
2	L	211	ARG	NE-CZ-NH1	-5.32	117.64	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	H	497	VAL	Peptide

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	C	1001	0	956	38	0
2	L	1655	0	1582	36	0
3	H	1608	0	1546	52	0
4	C	155	0	0	30	0
4	H	260	0	0	30	1
4	L	268	0	0	15	1
All	All	4947	0	4084	122	1

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 15.

All (122) 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:L:176:SER:HB3	4:L:454:HOH:O	1.09	1.26
3:H:406:GLY:N	4:H:644:HOH:O	1.61	1.24
3:H:376:ASN:HB2	4:H:721:HOH:O	1.34	1.20
1:C:625:LEU:HD12	4:C:814:HOH:O	1.46	1.13
3:H:497:VAL:HG11	4:H:757:HOH:O	1.50	1.09
1:C:617:LEU:O	4:C:805:HOH:O	1.72	1.08
3:H:362:SER:OG	3:H:363:LEU:CD1	2.06	1.04
2:L:189:HIS:O	2:L:211:ARG:HD3	1.56	1.03
3:H:306:GLU:OE1	4:H:644:HOH:O	1.80	1.00
3:H:405:GLN:O	4:H:605:HOH:O	1.87	0.93
3:H:397:ASN:ND2	3:H:401:ASP:OD2	2.04	0.90
3:H:362:SER:OG	3:H:363:LEU:HD12	1.72	0.89
2:L:70:ASP:HB3	4:L:291:HOH:O	1.71	0.89
2:L:28:SER:OG	4:L:366:HOH:O	1.92	0.88
1:C:703:ASN:ND2	4:C:782:HOH:O	2.07	0.87
3:H:484:PRO:O	3:H:487:THR:HG22	1.77	0.84
2:L:176:SER:CB	4:L:454:HOH:O	1.82	0.82
2:L:189:HIS:O	2:L:211:ARG:CD	2.27	0.82
1:C:618:ASP:OD1	4:C:806:HOH:O	1.97	0.81
2:L:11:LEU:HD22	2:L:13:VAL:HG22	1.60	0.80
1:C:703:ASN:OD1	4:C:749:HOH:O	2.00	0.79
2:L:10:THR:HG23	4:L:434:HOH:O	1.83	0.78
3:H:499:HIS:HB3	3:H:504:THR:OG1	1.84	0.78
1:C:724:ILE:CG2	4:C:789:HOH:O	2.31	0.77
1:C:665:ASN:OD1	4:C:868:HOH:O	2.04	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:301:ASP:O	4:H:647:HOH:O	2.03	0.75
3:H:407[A]:THR:HG22	4:H:533:HOH:O	1.86	0.75
1:C:703:ASN:ND2	4:C:749:HOH:O	2.18	0.75
1:C:629:VAL:CG2	4:C:789:HOH:O	2.34	0.74
1:C:625:LEU:HD22	4:C:815:HOH:O	1.87	0.73
1:C:703:ASN:CG	4:C:749:HOH:O	2.26	0.73
3:H:376:ASN:CB	4:H:721:HOH:O	2.07	0.72
1:C:614:ARG:HD3	4:C:847:HOH:O	1.88	0.72
3:H:361:PRO:HA	3:H:364:LYS:HG3	1.70	0.71
2:L:190:ASN:OD1	4:L:346:HOH:O	2.08	0.70
3:H:306:GLU:CG	4:H:533:HOH:O	2.38	0.70
3:H:360:ASN:HB3	3:H:363:LEU:HD13	1.76	0.68
1:C:709:VAL:HG23	4:C:849:HOH:O	1.93	0.67
3:H:320:LEU:HD13	4:H:729:HOH:O	1.93	0.67
2:L:22:SER:OG	2:L:24:ARG:NE	2.23	0.67
2:L:85:MET:SD	2:L:103:LYS:HD3	2.35	0.67
3:H:476:THR:HG23	4:H:603:HOH:O	1.94	0.67
3:H:442:VAL:HG13	4:H:757:HOH:O	1.95	0.66
3:H:376:ASN:CG	4:H:721:HOH:O	2.31	0.65
3:H:363:LEU:N	3:H:363:LEU:HD12	2.11	0.64
1:C:629:VAL:HG23	4:C:789:HOH:O	1.98	0.62
3:H:421:VAL:HG21	3:H:506:VAL:HG21	1.82	0.62
3:H:405:GLN:HG2	4:H:519:HOH:O	1.99	0.62
1:C:696:LYS:NZ	2:L:32:ASN:HD21	1.98	0.61
1:C:656:LEU:HD12	4:C:869:HOH:O	2.01	0.61
3:H:362:SER:C	3:H:363:LEU:HD12	2.20	0.61
1:C:623:TYR:OH	4:C:872:HOH:O	2.01	0.60
3:H:306:GLU:HG2	4:H:533:HOH:O	1.99	0.60
3:H:430:ALA:HB1	4:H:634:HOH:O	2.01	0.60
3:H:421:VAL:HG22	4:H:757:HOH:O	2.01	0.60
3:H:306:GLU:HG3	3:H:395:CYS:SG	2.43	0.57
1:C:696:LYS:NZ	2:L:31:ASN:HD21	2.02	0.57
1:C:629:VAL:HG21	4:C:789:HOH:O	2.03	0.57
2:L:10:THR:CG2	4:L:447:HOH:O	2.52	0.57
1:C:701:ASP:OD2	1:C:703:ASN:ND2	2.37	0.56
2:L:105:GLU:OE2	2:L:173:TYR:OH	2.21	0.56
3:H:421:VAL:HG21	3:H:506:VAL:CG2	2.36	0.55
1:C:673:ARG:HG3	4:C:864:HOH:O	2.07	0.54
3:H:469:VAL:HG23	4:H:746:HOH:O	2.06	0.54
3:H:306:GLU:CD	4:H:533:HOH:O	2.45	0.54
3:H:421:VAL:CG2	4:H:757:HOH:O	2.56	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:658:ILE:HD11	4:C:869:HOH:O	2.06	0.54
3:H:364:LYS:CG	4:H:624:HOH:O	2.55	0.53
2:L:166:GLN:NE2	4:L:426:HOH:O	2.37	0.53
1:C:696:LYS:HZ3	2:L:31:ASN:HD21	1.56	0.53
2:L:83:PHE:CE1	2:L:166:GLN:HB3	2.44	0.53
1:C:615:HIS:HD2	4:C:738:HOH:O	1.92	0.53
3:H:476:THR:HG21	4:H:701:HOH:O	2.09	0.53
3:H:301:ASP:HA	4:H:572:HOH:O	2.08	0.52
3:H:363:LEU:N	3:H:363:LEU:CD1	2.72	0.52
2:L:83:PHE:CZ	2:L:166:GLN:HB3	2.45	0.52
1:C:724:ILE:HG21	4:C:789:HOH:O	2.05	0.52
3:H:502:SER:OG	3:H:504:THR:HG23	2.10	0.52
2:L:10:THR:HG22	4:L:447:HOH:O	2.08	0.52
1:C:618:ASP:O	4:C:745:HOH:O	2.19	0.51
2:L:183:LYS:O	2:L:187:GLU:HG3	2.11	0.50
3:H:334:TRP:HB3	3:H:378:TYR:CZ	2.47	0.50
2:L:94:TRP:CD2	2:L:95:PRO:HA	2.46	0.50
1:C:643:THR:CG2	1:C:651:THR:CG2	2.90	0.49
2:L:40:SER:O	4:L:441:HOH:O	2.19	0.49
1:C:625:LEU:HG	4:C:789:HOH:O	2.12	0.49
1:C:729:LEU:N	1:C:729:LEU:HD23	2.27	0.49
3:H:421:VAL:CG2	3:H:506:VAL:HG21	2.44	0.48
1:C:672:SER:CB	4:C:868:HOH:O	2.61	0.48
2:L:23:CYS:C	2:L:24:ARG:HD3	2.34	0.48
3:H:407[B]:THR:HG23	4:H:533:HOH:O	2.14	0.48
2:L:24:ARG:NE	4:L:311:HOH:O	2.47	0.47
2:L:10:THR:HG21	4:L:447:HOH:O	2.14	0.47
1:C:616:GLY:HA3	2:L:31:ASN:ND2	2.30	0.46
1:C:623:TYR:O	4:C:805:HOH:O	2.20	0.46
3:H:450:VAL:CG2	3:H:477:LEU:HD13	2.46	0.46
3:H:362:SER:OG	3:H:363:LEU:HD13	2.07	0.45
2:L:12:SER:OG	4:L:447:HOH:O	2.20	0.45
2:L:136:LEU:CD2	2:L:196:ALA:HB2	2.48	0.44
2:L:31:ASN:HD22	2:L:31:ASN:H	1.65	0.44
1:C:727:CYS:HB3	4:C:787:HOH:O	2.17	0.43
3:H:471:GLN:NE2	4:H:701:HOH:O	2.50	0.43
2:L:136:LEU:HD23	2:L:196:ALA:HB2	1.99	0.43
3:H:362:SER:OG	3:H:363:LEU:HD11	2.10	0.43
3:H:436:VAL:HB	4:H:645:HOH:O	2.18	0.43
1:C:628:TRP:HB2	4:C:814:HOH:O	2.19	0.42
3:H:487:THR:HG21	4:H:752:HOH:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:24:ARG:HD3	2:L:24:ARG:N	2.34	0.42
1:C:601:LYS:N	1:C:640:THR:HG1	2.16	0.42
1:C:695:ALA:HB2	4:C:869:HOH:O	2.18	0.42
3:H:362:SER:CB	3:H:363:LEU:HD12	2.48	0.42
3:H:488:TRP:CD1	3:H:489:PRO:HA	2.54	0.42
3:H:507:ASP:O	3:H:508:LYS:HD2	2.19	0.42
1:C:725:ARG:NE	4:C:764:HOH:O	2.49	0.42
1:C:672:SER:HB3	4:C:868:HOH:O	2.20	0.42
2:L:103:LYS:HD2	4:L:303:HOH:O	2.19	0.42
2:L:11:LEU:CD2	2:L:13:VAL:HG22	2.42	0.41
3:H:477:LEU:HA	4:H:655:HOH:O	2.21	0.41
3:H:487:THR:HG23	4:H:577:HOH:O	2.21	0.41
3:H:364:LYS:HG2	4:H:624:HOH:O	2.19	0.40
2:L:136:LEU:HD13	2:L:175:MET:HG2	2.04	0.40
2:L:187:GLU:HG2	4:L:362:HOH:O	2.21	0.40

All (1) 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)
4:L:469:HOH:O	4:H:538:HOH:O[2_656]	1.98	0.22

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	C	127/129 (98%)	125 (98%)	2 (2%)	0	100	100
2	L	213/213 (100%)	210 (99%)	3 (1%)	0	100	100
3	H	209/210 (100%)	205 (98%)	4 (2%)	0	100	100
All	All	549/552 (100%)	540 (98%)	9 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	C	105/105 (100%)	104 (99%)	1 (1%)	80	48
2	L	193/191 (101%)	189 (98%)	4 (2%)	59	18
3	H	188/187 (100%)	183 (97%)	5 (3%)	50	10
All	All	486/483 (101%)	476 (98%)	10 (2%)	59	18

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	725	ARG
2	L	11	LEU
2	L	24	ARG
2	L	31	ASN
2	L	143	ASP
3	H	332	ASP
3	H	401	ASP
3	H	440	CYS
3	H	473	ASP
3	H	508	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	615	HIS
1	C	637	ASN
1	C	677	ASN
1	C	693	ASN
1	C	713	ASN
1	C	721	GLN
2	L	31	ASN
2	L	32	ASN

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Mol	Chain	Res	Type
2	L	53	GLN
2	L	92	ASN
2	L	190	ASN
3	H	303	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 carbohydrates 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	C	129/129 (100%)	0.86	16 (12%) 4 5	12, 16, 25, 39	0
2	L	213/213 (100%)	0.93	26 (12%) 5 5	10, 19, 27, 31	0
3	H	210/210 (100%)	0.99	29 (13%) 3 4	11, 19, 27, 34	0
All	All	552/552 (100%)	0.94	71 (12%) 4 4	10, 18, 27, 39	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	729	LEU	10.4
1	C	728	ARG	8.3
2	L	41	HIS	6.8
1	C	670	PRO	6.2
2	L	202	THR	6.1
2	L	83	PHE	6.0
3	H	415	LYS	4.1
1	C	649	GLY	4.1
3	H	473	ASP	4.0
1	C	703	ASN	4.0
3	H	505	LYS	3.8
2	L	156	GLN	3.8
3	H	503	SER	3.8
1	C	645	ARG	3.7
3	H	440	CYS	3.6
1	C	726	GLY	3.5
2	L	157	ASN	3.3
3	H	405	GLN	3.3
1	C	662	TRP	3.2
3	H	504	THR	3.1
1	C	727	CYS	3.1
3	H	301	ASP	3.0
3	H	344	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
2	L	163	TRP	2.9
2	L	40	SER	2.9
1	C	725	ARG	2.8
2	L	203	SER	2.8
2	L	160	LEU	2.8
2	L	190	ASN	2.7
3	H	337	ILE	2.7
3	H	433	ASN	2.7
1	C	709	VAL	2.7
2	L	133	VAL	2.6
2	L	199	LYS	2.6
2	L	11	LEU	2.6
2	L	132	VAL	2.6
2	L	188	ARG	2.5
3	H	341	PRO	2.5
3	H	336	TRP	2.5
3	H	471	GLN	2.5
1	C	668	ARG	2.4
2	L	24	ARG	2.4
1	C	617	LEU	2.4
1	C	614	ARG	2.4
3	H	487	THR	2.4
3	H	380	LEU	2.4
2	L	70	ASP	2.4
2	L	186	TYR	2.4
2	L	169	LYS	2.3
3	H	458	SER	2.3
3	H	363	LEU	2.3
3	H	364	LYS	2.3
2	L	212	ASN	2.3
3	H	472	SER	2.2
2	L	117	ILE	2.2
1	C	721	GLN	2.2
3	H	461	SER	2.2
3	H	320	LEU	2.2
2	L	182	THR	2.1
2	L	143	ASP	2.1
3	H	507	ASP	2.1
3	H	498	ALA	2.1
2	L	76	ASN	2.1
3	H	347	TYR	2.1
2	L	201	SER	2.1

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Mol	Chain	Res	Type	RSRZ
2	L	152	GLY	2.1
1	C	644	ASN	2.0
3	H	456	SER	2.0
3	H	483	VAL	2.0
3	H	413	ALA	2.0
3	H	388	GLU	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 carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.