



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 07:34 PM UTC

PDB ID : 8PMX / pdb_00008pmx
Title : rat HEV P domain in complex with glycan-sensitive nAb p60.12
Authors : Ssebyatika, G.; Krey, T.
Deposited on : 2023-06-29
Resolution : 3.92 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
Xtrriage (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

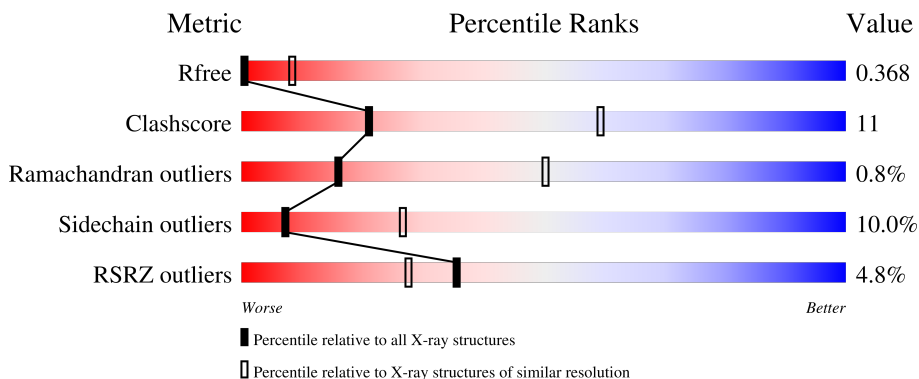
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.92 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	1033 (4.10-3.74)
Clashscore	190562	1070 (4.10-3.74)
Ramachandran outliers	187476	1017 (4.10-3.74)
Sidechain outliers	187428	1010 (4.10-3.74)
RSRZ outliers	180081	1033 (4.10-3.74)

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	165	 12% 67% 22% 7%
1	B	165	 5% 65% 25% 7%
2	H	233	 68% 21% 8%
3	L	217	 3% 76% 20% 1%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5572 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 Pro-secreted protein ORF2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	154	1194	766	197	228	3	0	0	0
1	B	154	1194	766	197	228	3	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	450	GLY	-	expression tag	UNP E0XL23
A	451	ASP	-	expression tag	UNP E0XL23
A	452	ASP	-	expression tag	UNP E0XL23
A	453	ASP	-	expression tag	UNP E0XL23
A	454	ASP	-	expression tag	UNP E0XL23
A	455	LYS	-	expression tag	UNP E0XL23
B	450	GLY	-	expression tag	UNP E0XL23
B	451	ASP	-	expression tag	UNP E0XL23
B	452	ASP	-	expression tag	UNP E0XL23
B	453	ASP	-	expression tag	UNP E0XL23
B	454	ASP	-	expression tag	UNP E0XL23
B	455	LYS	-	expression tag	UNP E0XL23

- Molecule 2 is a protein called Fab p60.12-HC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	H	214	1602	1011	271	313	7	0	0	0

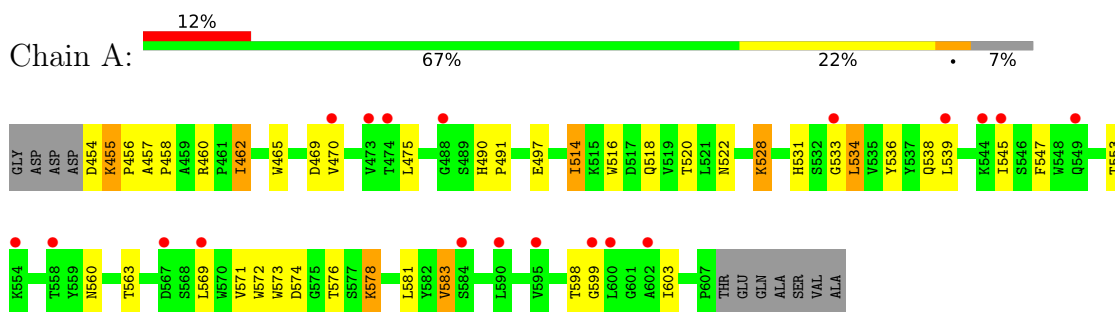
- Molecule 3 is a protein called Fab p60.12-LC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	L	213	1582	988	261	328	5	0	1	0

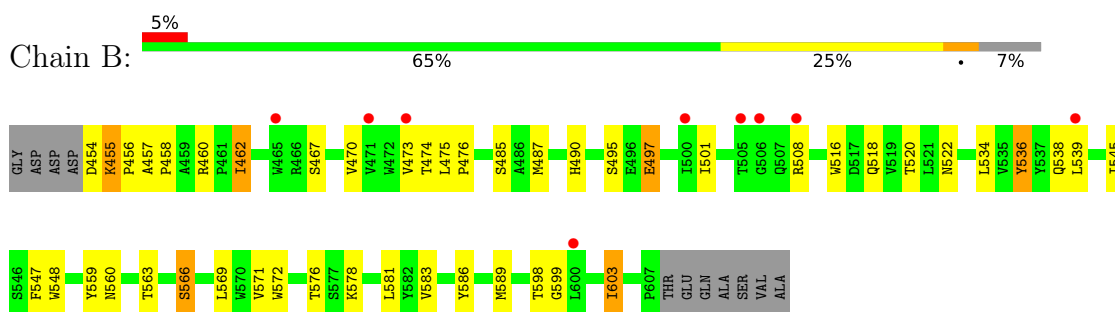
3 Residue-property plots [i](#)

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.

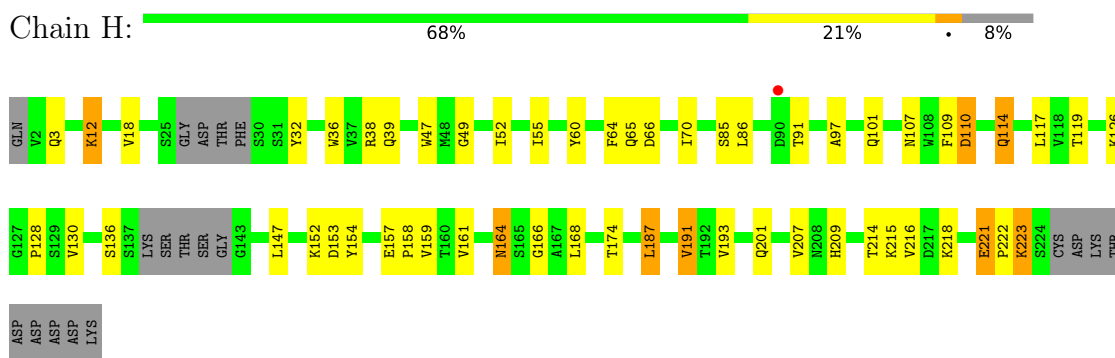
- Molecule 1: Pro-secreted protein ORF2



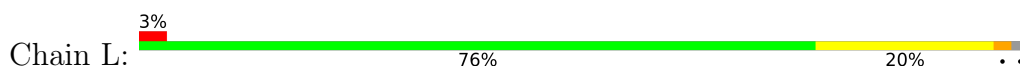
- Molecule 1: Pro-secreted protein ORF2

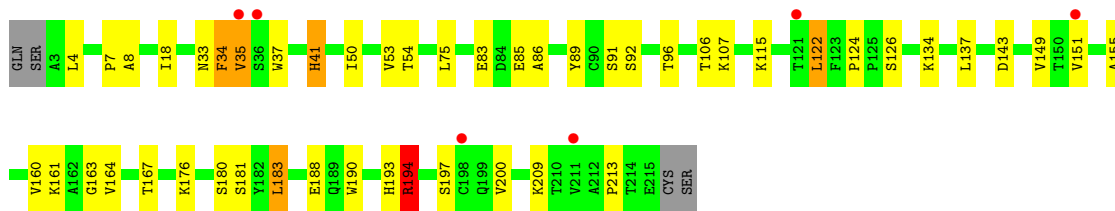


- Molecule 2: Fab p60.12-HC



- Molecule 3: Fab p60.12-LC





4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	112.86Å 112.86Å 184.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.68 – 3.92 48.68 – 3.92	Depositor EDS
% Data completeness (in resolution range)	99.8 (48.68-3.92) 99.8 (48.68-3.92)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.39 (at 3.88Å)	Xtrriage
Refinement program	BUSTER 2.10.4	Depositor
R, R_{free}	0.300 , 0.361 0.294 , 0.368	Depositor DCC
R_{free} test set	562 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	171.8	Xtrriage
Anisotropy	0.025	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 265.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	5572	wwPDB-VP
Average B, all atoms (Å ²)	196.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.10% 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	0.68	0/1232	1.05	0/1690
1	B	0.73	1/1232 (0.1%)	1.04	1/1690 (0.1%)
2	H	0.66	0/1638	0.93	1/2233 (0.0%)
3	L	0.67	1/1627 (0.1%)	0.93	3/2223 (0.1%)
All	All	0.68	2/5729 (0.0%)	0.98	5/7836 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	460	ARG	CA-C	7.08	1.60	1.52
3	L	96	THR	CA-C	5.15	1.58	1.53

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	34	PHE	CA-CB-CG	6.37	120.17	113.80
3	L	35	VAL	N-CA-C	5.51	115.51	108.12
1	B	536	TYR	N-CA-C	5.20	118.22	109.95
3	L	91	SER	N-CA-C	5.12	116.51	107.61
2	H	97	ALA	N-CA-C	5.00	116.45	107.80

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	1194	0	1148	29	0
1	B	1194	0	1148	24	0
2	H	1602	0	1588	44	0
3	L	1582	0	1524	37	0
All	All	5572	0	5408	121	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 11.

All (121) 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:H:223:LYS:HA	3:L:126:SER:HA	1.35	1.07
2:H:157:GLU:HG2	2:H:158:PRO:HA	1.40	1.02
2:H:130:VAL:HB	2:H:218:LYS:HG2	1.39	1.01
1:A:534:LEU:HD12	1:A:572:TRP:CD1	2.01	0.95
2:H:126:LYS:HZ1	2:H:153:ASP:HB3	1.30	0.94
2:H:152:LYS:HZ2	3:L:134:LYS:HB3	1.31	0.94
2:H:136:SER:HA	2:H:222:PRO:HB3	1.52	0.92
2:H:130:VAL:HB	2:H:218:LYS:CG	2.02	0.89
1:A:534:LEU:HD12	1:A:572:TRP:CG	2.09	0.88
2:H:152:LYS:NZ	3:L:134:LYS:HB3	1.90	0.86
3:L:190:TRP:NE1	3:L:213:PRO:HB3	1.89	0.86
2:H:126:LYS:NZ	2:H:153:ASP:HB3	1.89	0.86
3:L:190:TRP:HE1	3:L:213:PRO:HB3	1.41	0.85
2:H:52:ILE:HB	2:H:55:ILE:HG22	1.64	0.80
3:L:143:ASP:HA	3:L:176:LYS:HB3	1.64	0.78
1:A:528:LYS:HZ3	1:A:536:TYR:H	1.32	0.76
1:B:467:SER:HA	1:B:603:ILE:HG22	1.71	0.71
2:H:36:TRP:CD1	2:H:70:ILE:HD13	2.25	0.71
2:H:223:LYS:HA	3:L:126:SER:CA	2.16	0.71
2:H:157:GLU:HG2	2:H:158:PRO:CA	2.16	0.71
1:B:534:LEU:HD12	1:B:572:TRP:NE1	2.05	0.70
2:H:126:LYS:HZ3	2:H:153:ASP:C	2.01	0.68
1:A:460:ARG:NH2	1:A:469:ASP:OD2	2.28	0.67
1:A:514:ILE:HG22	1:A:516:TRP:NE1	2.11	0.66
3:L:8:ALA:HA	3:L:106:THR:HA	1.78	0.65
3:L:37:TRP:CD2	3:L:75:LEU:HD13	2.31	0.65
2:H:47:TRP:NE1	2:H:49:GLY:O	2.29	0.65
3:L:161:LYS:NZ	3:L:164:VAL:HB	2.13	0.64
1:A:470:VAL:HG11	1:B:470:VAL:HG11	1.79	0.63
1:A:528:LYS:NZ	1:A:536:TYR:H	1.97	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:216:VAL:HB	2:H:218:LYS:NZ	2.14	0.62
3:L:151:VAL:HB	3:L:181:SER:HB2	1.82	0.62
3:L:53:VAL:HG12	3:L:54:THR:HG23	1.80	0.61
3:L:122:LEU:HG	3:L:137:LEU:HB3	1.81	0.61
2:H:107:ASN:HB2	3:L:34:PHE:HB3	1.83	0.60
3:L:161:LYS:HZ3	3:L:164:VAL:HB	1.66	0.59
1:A:514:ILE:HG21	1:A:516:TRP:CE2	2.37	0.59
1:A:545:ILE:HD13	1:A:583:VAL:HG23	1.84	0.59
3:L:35:VAL:HG22	3:L:92:SER:HB2	1.84	0.59
2:H:223:LYS:NZ	3:L:124:PRO:HB2	2.18	0.59
1:A:514:ILE:HG22	1:A:516:TRP:CD1	2.38	0.58
1:B:560:ASN:HB3	1:B:563:THR:OG1	2.03	0.58
3:L:8:ALA:HB1	3:L:107:LYS:HG2	1.86	0.58
1:A:514:ILE:CG2	1:A:516:TRP:CE2	2.85	0.58
1:A:516:TRP:CE2	1:A:571:VAL:HG11	2.38	0.58
2:H:223:LYS:CA	3:L:126:SER:HA	2.24	0.58
3:L:193:HIS:ND1	3:L:194:ARG:NH2	2.52	0.58
1:B:545:ILE:HD13	1:B:583:VAL:HG23	1.86	0.58
1:A:475:LEU:HD21	1:A:581:LEU:HD22	1.85	0.57
1:A:560:ASN:HB3	1:A:563:THR:OG1	2.04	0.57
1:B:516:TRP:CE2	1:B:571:VAL:HG11	2.40	0.57
2:H:164:ASN:HB2	2:H:168:LEU:HB2	1.87	0.55
1:B:586:TYR:OH	3:L:54:THR:O	2.24	0.55
2:H:174:THR:HG23	2:H:187:LEU:HD22	1.89	0.54
3:L:50[B]:ILE:HG13	3:L:75:LEU:HD11	1.89	0.54
3:L:37:TRP:CG	3:L:75:LEU:HD13	2.43	0.54
3:L:50[A]:ILE:HG13	3:L:75:LEU:HD11	1.89	0.53
2:H:128:PRO:HD2	2:H:209:HIS:HB2	1.90	0.53
3:L:151:VAL:HB	3:L:181:SER:CB	2.38	0.53
2:H:168:LEU:HG	2:H:193:VAL:HG11	1.89	0.53
1:A:569:LEU:HD22	1:A:581:LEU:HD21	1.91	0.53
2:H:91:THR:HG23	2:H:119:THR:HA	1.93	0.51
1:B:569:LEU:HD22	1:B:581:LEU:HD21	1.92	0.50
1:B:534:LEU:HD12	1:B:572:TRP:HE1	1.77	0.49
2:H:109:PHE:O	2:H:110:ASP:HB2	2.13	0.49
1:B:473:VAL:HG11	1:B:581:LEU:HD22	1.95	0.48
1:B:536:TYR:CE2	1:B:572:TRP:HB2	2.47	0.48
1:A:462:ILE:HD12	1:A:462:ILE:H	1.77	0.48
1:B:474:THR:HG22	1:B:598:THR:HG22	1.96	0.48
1:A:465:TRP:CE3	1:A:603:ILE:HD11	2.49	0.47
1:A:516:TRP:HD1	1:A:573:TRP:CD1	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:216:VAL:HB	2:H:218:LYS:HZ1	1.80	0.46
3:L:7:PRO:O	3:L:106:THR:OG1	2.28	0.46
2:H:12:LYS:HD2	2:H:18:VAL:HB	1.97	0.46
3:L:167:THR:OG1	3:L:180:SER:OG	2.30	0.46
2:H:130:VAL:HG22	2:H:207:VAL:HB	1.96	0.46
2:H:126:LYS:HG2	2:H:154:TYR:HA	1.97	0.46
2:H:152:LYS:HZ2	3:L:134:LYS:CB	2.16	0.46
1:A:574:ASP:CG	1:A:578:LYS:HB3	2.41	0.46
2:H:38:ARG:HE	2:H:64:PHE:HZ	1.64	0.45
2:H:126:LYS:HZ3	2:H:154:TYR:N	2.13	0.45
3:L:41:HIS:ND1	3:L:86:ALA:HB2	2.31	0.45
2:H:221:GLU:HG2	2:H:222:PRO:HD2	1.99	0.45
2:H:223:LYS:NZ	3:L:124:PRO:CB	2.80	0.44
3:L:143:ASP:HA	3:L:176:LYS:HD2	1.98	0.44
1:B:476:PRO:HD2	1:B:497:GLU:O	2.18	0.44
1:B:589:MET:HE2	1:B:589:MET:HB3	1.90	0.44
2:H:157:GLU:CG	2:H:158:PRO:HA	2.28	0.44
3:L:37:TRP:HA	3:L:89:TYR:O	2.17	0.44
1:B:457:ALA:HA	1:B:458:PRO:HD3	1.90	0.44
2:H:216:VAL:HB	2:H:218:LYS:HZ2	1.82	0.44
1:B:490:HIS:NE2	1:B:559:TYR:CD2	2.87	0.43
1:B:462:ILE:HD12	1:B:462:ILE:H	1.82	0.43
2:H:18:VAL:HG12	2:H:86:LEU:HD11	1.99	0.43
2:H:159:VAL:HG12	2:H:209:HIS:ND1	2.33	0.43
1:A:514:ILE:HG22	1:A:516:TRP:CE2	2.53	0.43
1:B:487:MET:HG3	1:B:490:HIS:HB2	2.00	0.43
1:B:547:PHE:HA	1:B:599:GLY:HA2	2.00	0.43
2:H:126:LYS:NZ	2:H:154:TYR:N	2.66	0.43
1:A:457:ALA:HA	1:A:458:PRO:HD3	1.94	0.42
1:A:553:THR:HB	1:B:566:SER:HB2	2.00	0.42
1:A:533:GLY:C	1:A:534:LEU:HD23	2.44	0.42
2:H:223:LYS:HZ2	3:L:124:PRO:HB2	1.82	0.42
2:H:114:GLN:H	2:H:114:GLN:HG3	1.59	0.42
2:H:191:VAL:HG22	2:H:193:VAL:HG13	2.01	0.42
1:B:548:TRP:NE1	1:B:598:THR:OG1	2.52	0.42
2:H:130:VAL:CB	2:H:218:LYS:HG2	2.28	0.42
1:A:547:PHE:HA	1:A:599:GLY:HA2	2.02	0.41
1:A:528:LYS:HZ3	1:A:536:TYR:N	2.10	0.41
1:B:501:ILE:HG23	1:B:508:ARG:HB3	2.02	0.41
3:L:164:VAL:HG13	3:L:183:LEU:HA	2.01	0.41
3:L:149:VAL:HG23	3:L:200:VAL:HG11	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:455:LYS:HZ2	1:A:456:PRO:HD2	1.86	0.41
1:A:528:LYS:HE3	1:A:528:LYS:HB3	1.84	0.41
1:B:475:LEU:HB3	1:B:495:SER:HB2	2.02	0.41
3:L:155:ALA:HA	3:L:197:SER:HB2	2.02	0.41
1:A:465:TRP:CE3	1:A:603:ILE:CD1	3.05	0.40
1:B:455:LYS:HZ2	1:B:456:PRO:HD2	1.86	0.40
2:H:161:VAL:HG22	2:H:207:VAL:HA	2.04	0.40
1:A:490:HIS:HA	1:A:491:PRO:HD3	1.89	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	152/165 (92%)	128 (84%)	24 (16%)	0	100	100
1	B	152/165 (92%)	135 (89%)	16 (10%)	1 (1%)	18	53
2	H	208/233 (89%)	171 (82%)	34 (16%)	3 (1%)	9	38
3	L	212/217 (98%)	175 (82%)	35 (16%)	2 (1%)	14	47
All	All	724/780 (93%)	609 (84%)	109 (15%)	6 (1%)	16	50

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	110	ASP
2	H	214	THR
3	L	194	ARG
1	B	603	ILE
2	H	166	GLY
3	L	163	GLY

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	127/135 (94%)	110 (87%)	17 (13%)	4	18
1	B	127/135 (94%)	114 (90%)	13 (10%)	7	25
2	H	183/200 (92%)	164 (90%)	19 (10%)	7	25
3	L	182/185 (98%)	169 (93%)	13 (7%)	13	39
All	All	619/655 (94%)	557 (90%)	62 (10%)	7	27

All (62) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	454	ASP
1	A	455	LYS
1	A	462	ILE
1	A	497	GLU
1	A	514	ILE
1	A	518	GLN
1	A	520	THR
1	A	522	ASN
1	A	528	LYS
1	A	531	HIS
1	A	534	LEU
1	A	538	GLN
1	A	539	LEU
1	A	576	THR
1	A	578	LYS
1	A	583	VAL
1	A	598	THR
1	B	454	ASP
1	B	455	LYS
1	B	462	ILE
1	B	485	SER
1	B	497	GLU
1	B	518	GLN
1	B	520	THR

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Mol	Chain	Res	Type
1	B	522	ASN
1	B	538	GLN
1	B	539	LEU
1	B	566	SER
1	B	576	THR
1	B	578	LYS
2	H	3	GLN
2	H	12	LYS
2	H	32	TYR
2	H	39	GLN
2	H	60	TYR
2	H	65	GLN
2	H	66	ASP
2	H	85	SER
2	H	101	GLN
2	H	114	GLN
2	H	117	LEU
2	H	147	LEU
2	H	164	ASN
2	H	187	LEU
2	H	191	VAL
2	H	201	GLN
2	H	215	LYS
2	H	221	GLU
2	H	223	LYS
3	L	4	LEU
3	L	18	ILE
3	L	33	ASN
3	L	41	HIS
3	L	83	GLU
3	L	85	GLU
3	L	115	LYS
3	L	122	LEU
3	L	160	VAL
3	L	183	LEU
3	L	188	GLU
3	L	194	ARG
3	L	209	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	538	GLN
1	B	464	ASN
1	B	538	GLN
1	B	550	GLN
2	H	3	GLN
2	H	77	ASN
2	H	103	GLN
2	H	180	GLN
3	L	172	GLN
3	L	189	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](#)

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	154/165 (93%)	0.49	19 (12%) 8 11	52, 125, 227, 280	0
1	B	154/165 (93%)	0.13	9 (5%) 29 24	50, 123, 208, 279	0
2	H	214/233 (91%)	-0.08	1 (0%) 87 72	141, 257, 296, 300	1 (0%)
3	L	213/217 (98%)	0.17	6 (2%) 55 39	64, 274, 300, 300	1 (0%)
All	All	735/780 (94%)	0.15	35 (4%) 35 27	50, 200, 300, 300	2 (0%)

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	584	SER	5.9
1	A	590	LEU	5.3
1	A	539	LEU	4.0
1	A	545	ILE	3.8
1	A	473	VAL	3.7
1	A	567	ASP	3.6
1	A	599	GLY	3.6
3	L	36	SER	3.5
1	B	506	GLY	3.2
1	A	600	LEU	3.2
1	A	595	VAL	3.2
1	B	600	LEU	3.2
3	L	35	VAL	3.1
1	A	544	LYS	3.1
1	B	505	THR	3.1
1	A	569	LEU	3.0
1	A	558	THR	2.9
1	A	549	GLN	2.8
3	L	198	CYS	2.8
3	L	151	VAL	2.8
1	B	500	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	539	LEU	2.7
1	B	508	ARG	2.7
2	H	90	ASP	2.6
1	A	474	THR	2.5
1	B	473	VAL	2.5
1	A	533	GLY	2.3
1	A	488	GLY	2.3
1	A	470	VAL	2.3
1	B	465	TRP	2.2
1	A	554	LYS	2.2
1	A	602	ALA	2.2
1	B	471	VAL	2.1
3	L	211	VAL	2.1
3	L	121	THR	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.