



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 21, 2024 – 01:09 pm BST

PDB ID : 8RRN  
Title : Crystal structure of the SARS-CoV-2 S RBD in complex with pT1616 Fab  
Authors : Hansen, G.; Krey, T.  
Deposited on : 2024-01-23  
Resolution : 3.11 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](mailto: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>.

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

MolProbity : 4.02b-467  
Xtriage (Phenix) : 1.13  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.003 (Gargrove)  
Density-Fitness : 1.0.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

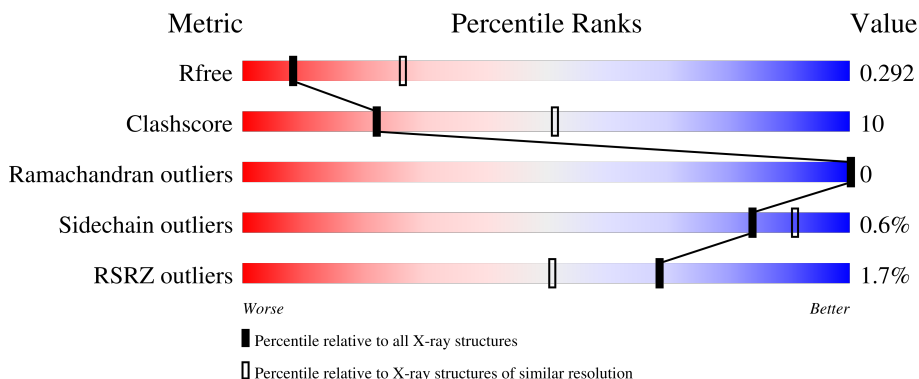
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.11 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.



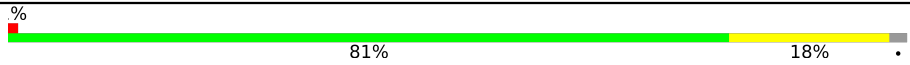
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	164625	1668 (3.14-3.10)
Clashscore	180529	1788 (3.14-3.10)
Ramachandran outliers	177936	1696 (3.14-3.10)
Sidechain outliers	177891	1696 (3.14-3.10)
RSRZ outliers	164620	1668 (3.14-3.10)

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  $\geq 3$ , 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	199	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 76%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 21%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 1%; height: 10px; background-color: grey; margin-right: 5px;"></div> <div style="width: 1%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center;">2% 76% 21% .</p>
1	B	199	<div style="display: flex; align-items: center;"> <div style="width: 0%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 79%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 19%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 1%; height: 10px; background-color: grey; margin-right: 5px;"></div> <div style="width: 1%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center;">% 79% 19% ..</p>
2	C	235	<div style="display: flex; align-items: center;"> <div style="width: 3%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 74%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 20%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: grey; margin-right: 5px;"></div> <div style="width: 1%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center;">3% 74% 20% 5%</p>
2	H	235	<div style="display: flex; align-items: center;"> <div style="width: 0%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 66%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 29%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 1%; height: 10px; background-color: grey; margin-right: 5px;"></div> <div style="width: 1%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center;">% 66% 29% . 5%</p>
3	D	217	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 82%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 16%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 1%; height: 10px; background-color: grey; margin-right: 5px;"></div> <div style="width: 1%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center;">2% 82% 16% .</p>

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Mol	Chain	Length	Quality of chain
3	L	217	 <p>A horizontal bar chart representing the quality of the chain. The bar is divided into two segments: a green segment on the left representing 81% and a yellow segment on the right representing 18%. A small red square is at the beginning of the bar, and a small grey square is at the end. A percentage sign (%) is located above the bar on the left side.</p>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 18717 atoms, of which 9200 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 Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	193	2975	981	1447	254	285	8	0	0	0
1	B	195	3001	989	1457	257	290	8	0	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	528	ASP	-	expression tag	UNP P0DTC2
A	529	ASP	-	expression tag	UNP P0DTC2
A	530	ASP	-	expression tag	UNP P0DTC2
A	531	ASP	-	expression tag	UNP P0DTC2
A	532	LYS	-	expression tag	UNP P0DTC2
B	528	ASP	-	expression tag	UNP P0DTC2
B	529	ASP	-	expression tag	UNP P0DTC2
B	530	ASP	-	expression tag	UNP P0DTC2
B	531	ASP	-	expression tag	UNP P0DTC2
B	532	LYS	-	expression tag	UNP P0DTC2

- Molecule 2 is a protein called pT1616 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
2	H	224	3280	1040	1629	276	328	7	0	0	0
2	C	223	3264	1035	1620	275	327	7	0	0	0

- Molecule 3 is a protein called pT1616 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
3	L	213	3098	982	1523	266	323	4	0	0	0

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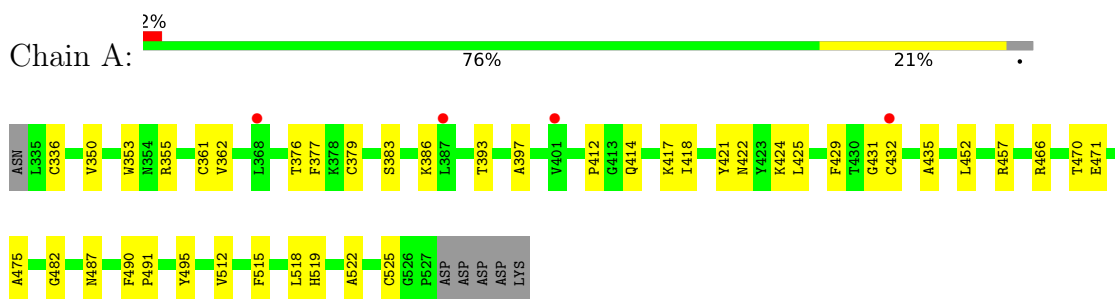
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
3	D	213	3099	982	1524	266	323	4	0	0	0

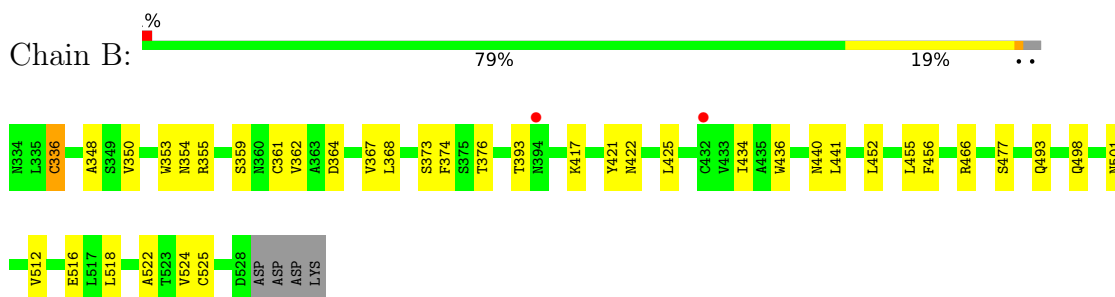
### 3 Residue-property plots [i](#)

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.

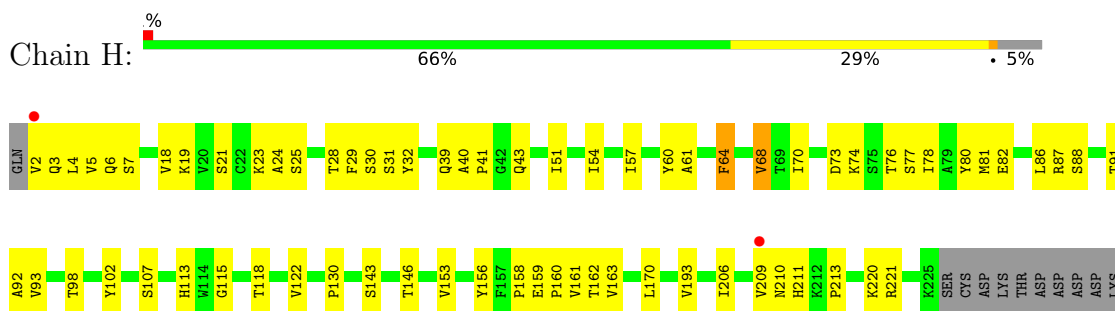
- Molecule 1: Spike protein S1



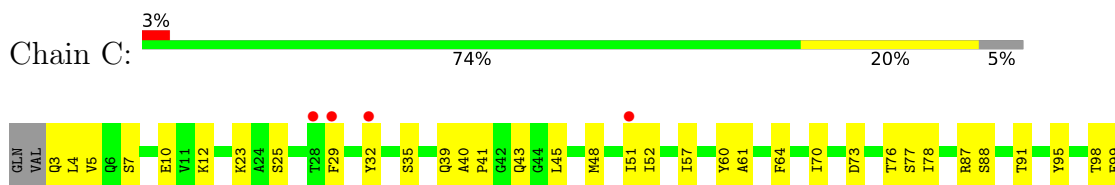
- Molecule 1: Spike protein S1

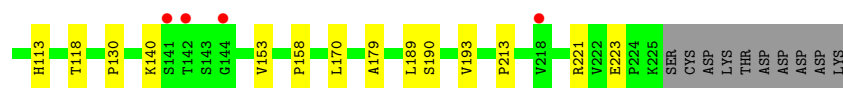


- Molecule 2: pT1616 Fab heavy chain

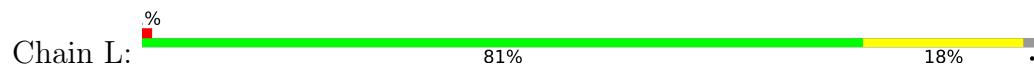


- Molecule 2: pT1616 Fab heavy chain

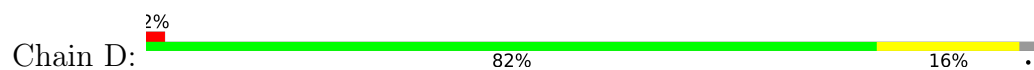




- Molecule 3: pT1616 Fab light chain



- Molecule 3: pT1616 Fab light chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	173.10Å 59.06Å 152.03Å 90.00° 95.45° 90.00°	Depositor
Resolution (Å)	45.62 – 3.11 45.62 – 3.12	Depositor EDS
% Data completeness (in resolution range)	99.5 (45.62-3.11) 99.6 (45.62-3.12)	Depositor EDS
$R_{merge}$	0.41	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.45 (at 3.12Å)	Xtrriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, $R_{free}$	0.243 , 0.291 0.251 , 0.292	Depositor DCC
$R_{free}$ test set	1393 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	96.6	Xtrriage
Anisotropy	0.459	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 79.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.26$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	18717	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	119.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.47% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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	0.40	0/1572	0.54	0/2140
1	B	0.41	0/1588	0.57	0/2162
2	C	0.44	0/1682	0.62	0/2290
2	H	0.41	0/1689	0.59	0/2300
3	D	0.39	0/1613	0.57	0/2206
3	L	0.38	0/1613	0.55	0/2206
All	All	0.41	0/9757	0.57	0/13304

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	1528	1447	1447	25	0
1	B	1544	1457	1457	24	0
2	C	1644	1620	1620	39	0
2	H	1651	1629	1629	65	0
3	D	1575	1524	1523	22	0
3	L	1575	1523	1523	30	0
All	All	9517	9200	9199	196	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 10.

All (196) 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:D:3:VAL:HA	3:D:101:LEU:HD21	1.55	0.87
2:H:3:GLN:O	2:H:4:LEU:HD23	1.73	0.87
3:D:20:ILE:HG21	3:D:106:THR:HG21	1.61	0.82
2:H:23:LYS:HG2	2:H:78:ILE:HD12	1.64	0.80
3:L:7:PRO:O	3:L:106:THR:HG22	1.80	0.80
2:H:51:ILE:HD11	2:H:70:ILE:HB	1.62	0.80
3:L:113:GLN:HG2	3:L:114:PRO:HD2	1.65	0.79
2:C:170:LEU:HD21	2:C:193:VAL:HG21	1.69	0.76
2:H:19:LYS:HD2	2:H:80:TYR:HB3	1.69	0.74
2:H:19:LYS:HE2	2:H:82:GLU:HB2	1.70	0.74
3:L:3:VAL:HA	3:L:101:LEU:HD21	1.70	0.73
2:H:5:VAL:HG22	2:H:23:LYS:HB2	1.70	0.73
3:L:6:GLN:NE2	3:L:90:CYS:SG	2.62	0.71
1:B:350:VAL:HG22	1:B:422:ASN:HB3	1.75	0.69
2:C:4:LEU:HA	2:C:25:SER:HB3	1.74	0.68
2:C:88:SER:O	2:C:91:THR:HG22	1.95	0.66
1:A:393:THR:HG21	1:A:518:LEU:HB3	1.77	0.66
3:L:113:GLN:HG2	3:L:114:PRO:CD	2.26	0.66
2:H:40:ALA:HB1	2:H:41:PRO:HD2	1.79	0.65
2:H:91:THR:HG22	2:H:122:VAL:H	1.60	0.65
1:B:455:LEU:HD22	1:B:493:GLN:HG3	1.80	0.64
1:A:470:THR:O	2:H:31:SER:HB3	1.98	0.63
2:H:170:LEU:HD21	2:H:193:VAL:HG21	1.79	0.63
2:H:158:PRO:HD2	2:H:213:PRO:CB	2.28	0.63
2:H:6:GLN:HA	2:H:21:SER:O	2.00	0.62
3:L:35:VAL:HG21	3:L:73:ALA:HB1	1.82	0.62
2:C:51:ILE:HD13	2:C:70:ILE:HG22	1.81	0.61
1:B:348:ALA:HB2	1:B:354:ASN:OD1	2.00	0.61
1:B:359:SER:HA	1:B:524:VAL:HG22	1.83	0.61
1:B:452:LEU:HD21	2:C:57:ILE:HD13	1.83	0.60
1:A:482:GLY:O	2:H:30:SER:HB2	2.02	0.59
3:L:6:GLN:OE1	3:L:106:THR:HG23	2.00	0.59
2:C:10:GLU:OE2	2:C:12:LYS:NZ	2.29	0.59
3:L:26:ASN:HA	3:L:30:GLY:HA3	1.84	0.59
2:H:220:LYS:NZ	3:L:128:GLU:OE1	2.30	0.58
2:H:3:GLN:HB3	2:H:113:HIS:HB3	1.85	0.58
2:C:130:PRO:HB2	2:C:153:VAL:HG13	1.84	0.58
2:H:4:LEU:HD11	2:H:98:THR:HG23	1.85	0.58
3:D:35:VAL:HG21	3:D:73:ALA:HB1	1.86	0.57
2:C:190:SER:OG	3:D:182:TYR:OH	2.23	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:26:ASN:HA	3:D:30:GLY:HA3	1.86	0.57
2:C:158:PRO:HD2	2:C:213:PRO:CB	2.34	0.56
2:H:61:ALA:O	2:H:64:PHE:HB3	2.06	0.56
3:L:85:GLU:OE1	3:L:171:LYS:NZ	2.37	0.56
2:C:40:ALA:HB1	2:C:41:PRO:HD2	1.88	0.56
3:D:118:PRO:HB3	3:D:144:PHE:HB3	1.87	0.56
2:C:23:LYS:HG2	2:C:78:ILE:HG23	1.87	0.56
2:C:179:ALA:HB2	2:C:189:LEU:HB3	1.86	0.56
2:H:2:VAL:HG12	2:H:3:GLN:OE1	2.06	0.56
3:L:153:TRP:HB2	3:L:160:VAL:HG11	1.87	0.56
3:L:20:ILE:HG23	3:L:106:THR:HG21	1.86	0.56
1:A:353:TRP:O	1:A:466:ARG:NH1	2.40	0.55
2:H:60:TYR:HB2	2:H:64:PHE:CD1	2.41	0.55
2:H:64:PHE:CD2	2:H:68:VAL:HG13	2.41	0.55
2:H:40:ALA:HB3	2:H:43:GLN:HB3	1.89	0.55
2:H:130:PRO:HB2	2:H:153:VAL:HG13	1.88	0.54
2:H:60:TYR:HB3	2:H:64:PHE:CG	2.42	0.54
1:A:490:PHE:CD1	2:H:54:ILE:HD12	2.43	0.54
1:A:518:LEU:HD23	1:A:519:HIS:N	2.22	0.53
3:L:6:GLN:NE2	3:L:90:CYS:H	2.06	0.53
2:C:130:PRO:CB	2:C:153:VAL:HG13	2.38	0.53
1:A:355:ARG:HA	1:A:397:ALA:O	2.08	0.53
2:H:163:VAL:HG22	2:H:209:VAL:HG22	1.90	0.53
2:C:23:LYS:HG2	2:C:78:ILE:HD12	1.90	0.53
2:H:5:VAL:CG2	2:H:23:LYS:HB2	2.37	0.53
2:H:158:PRO:HD2	2:H:213:PRO:HB2	1.90	0.53
2:H:87:ARG:HG3	2:H:88:SER:H	1.74	0.52
1:A:518:LEU:HD23	1:A:519:HIS:C	2.29	0.52
1:A:350:VAL:HG22	1:A:422:ASN:HB3	1.90	0.52
1:A:425:LEU:HD21	1:A:512:VAL:HG11	1.92	0.52
2:H:64:PHE:HD2	2:H:68:VAL:HG13	1.74	0.52
2:H:70:ILE:HG22	2:H:81:MET:HB2	1.92	0.52
1:B:368:LEU:O	1:B:374:PHE:HE2	1.92	0.52
1:B:336:CYS:HA	1:B:361:CYS:HB2	1.91	0.52
3:L:41:LEU:HD23	3:L:86:ALA:HB2	1.90	0.52
2:H:4:LEU:HD22	2:H:24:ALA:HA	1.93	0.51
2:C:52:ILE:HD12	2:C:57:ILE:HD12	1.93	0.51
2:H:156:TYR:CZ	2:H:161:VAL:HG11	2.46	0.51
1:B:393:THR:HA	1:B:522:ALA:HA	1.91	0.51
2:H:18:VAL:HG12	2:H:86:LEU:HD11	1.92	0.51
2:H:3:GLN:O	2:H:25:SER:HB3	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:113:GLN:OE1	3:L:145:TYR:CG	2.64	0.50
3:L:164:VAL:HG22	3:L:183:LEU:HD13	1.93	0.50
2:H:91:THR:CG2	2:H:122:VAL:H	2.22	0.50
2:C:76:THR:O	2:C:77:SER:HB3	2.11	0.50
3:D:149:VAL:HG13	3:D:200:VAL:HG13	1.93	0.50
1:A:418:ILE:HD11	1:A:495:TYR:OH	2.12	0.50
2:H:4:LEU:O	2:H:115:GLY:HA2	2.11	0.50
3:L:115:LYS:N	3:L:115:LYS:HD3	2.26	0.50
2:C:32:TYR:HB3	2:C:99:GLU:O	2.11	0.50
2:C:190:SER:HG	3:D:182:TYR:HH	1.51	0.50
2:H:60:TYR:CE2	2:H:70:ILE:HG12	2.47	0.50
3:D:20:ILE:CG2	3:D:106:THR:HG21	2.36	0.50
2:H:130:PRO:CB	2:H:153:VAL:HG13	2.42	0.49
3:D:154:LYS:HA	3:D:159:PRO:HA	1.93	0.49
1:B:355:ARG:O	3:D:95:SER:OG	2.29	0.49
2:H:156:TYR:HD2	2:H:211:HIS:HE2	1.61	0.49
2:H:51:ILE:HG12	2:H:70:ILE:HG13	1.94	0.49
2:H:76:THR:O	2:H:77:SER:HB3	2.12	0.49
3:L:149:VAL:HG12	3:L:202:HIS:HB2	1.95	0.49
2:C:3:GLN:HB3	2:C:113:HIS:HB3	1.95	0.49
2:C:73:ASP:HB2	2:C:76:THR:OG1	2.12	0.49
2:H:73:ASP:HB2	2:H:76:THR:OG1	2.13	0.48
1:A:376:THR:OG1	1:A:435:ALA:HB3	2.12	0.48
2:H:39:GLN:O	2:H:92:ALA:HB1	2.13	0.48
1:A:431:GLY:HA2	1:A:515:PHE:CD2	2.49	0.48
2:C:221:ARG:NH1	2:C:223:GLU:OE2	2.46	0.48
2:C:40:ALA:HB3	2:C:43:GLN:HB2	1.95	0.48
1:B:362:VAL:HA	1:B:525:CYS:O	2.13	0.48
3:D:88:TYR:HB2	3:D:106:THR:HG23	1.95	0.47
3:D:18:VAL:HG23	3:D:80:LEU:HD11	1.96	0.47
3:D:41:LEU:HD23	3:D:86:ALA:HB2	1.96	0.47
1:B:425:LEU:HD21	1:B:512:VAL:HG11	1.95	0.47
2:C:45:LEU:HD12	2:C:45:LEU:N	2.29	0.47
2:H:39:GLN:HB3	2:H:93:VAL:HG23	1.96	0.47
1:A:362:VAL:HA	1:A:525:CYS:O	2.15	0.46
1:A:393:THR:HA	1:A:522:ALA:HA	1.98	0.46
3:D:141:ILE:HG22	3:D:144:PHE:CD2	2.51	0.46
3:D:153:TRP:HB2	3:D:160:VAL:CG2	2.45	0.46
1:B:373:SER:O	1:B:436:TRP:CB	2.63	0.46
2:H:7:SER:O	2:H:118:THR:HG22	2.15	0.46
1:A:336:CYS:HA	1:A:361:CYS:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:373:SER:O	1:B:436:TRP:HB3	2.16	0.46
3:L:20:ILE:HD13	3:L:106:THR:OG1	2.16	0.46
3:L:35:VAL:HG21	3:L:73:ALA:CB	2.45	0.46
2:C:158:PRO:HD2	2:C:213:PRO:HB2	1.96	0.46
2:H:158:PRO:HD2	2:H:213:PRO:HB3	1.96	0.45
1:B:353:TRP:O	1:B:466:ARG:NH1	2.49	0.45
1:B:440:ASN:C	1:B:441:LEU:HD12	2.37	0.45
2:H:60:TYR:HB2	2:H:64:PHE:CE1	2.52	0.45
3:L:30:GLY:HA2	3:L:71:THR:HG22	1.99	0.45
3:D:38:TYR:HE2	3:D:91:GLN:HB3	1.82	0.45
3:L:27:SER:HB2	3:L:94:ASP:OD1	2.17	0.45
1:A:383:SER:HB3	1:A:386:LYS:HB2	1.99	0.45
2:C:60:TYR:CE1	2:C:70:ILE:HD12	2.52	0.45
1:B:417:LYS:O	1:B:421:TYR:HB2	2.17	0.45
2:H:23:LYS:HG2	2:H:78:ILE:HG23	1.99	0.45
1:B:477:SER:O	1:B:477:SER:OG	2.28	0.44
2:H:143:SER:HB3	2:H:146:THR:HB	1.98	0.44
2:H:162:THR:CG2	2:H:210:ASN:HB3	2.46	0.44
2:C:4:LEU:CA	2:C:25:SER:HB3	2.43	0.44
3:D:115:LYS:HG3	3:D:116:ALA:N	2.31	0.44
1:A:417:LYS:O	1:A:421:TYR:HB2	2.18	0.44
2:H:61:ALA:O	2:H:64:PHE:HD1	1.99	0.44
2:C:4:LEU:HD11	2:C:98:THR:HG23	1.99	0.44
3:L:6:GLN:HE22	3:L:90:CYS:N	2.16	0.44
3:L:113:GLN:OE1	3:L:145:TYR:CD1	2.71	0.44
2:C:35:SER:OG	2:C:99:GLU:OE2	2.35	0.44
1:B:498:GLN:HB3	1:B:501:ASN:ND2	2.32	0.44
1:B:376:THR:O	1:B:434:ILE:HA	2.17	0.44
2:H:29:PHE:CE1	2:H:74:LYS:HG3	2.53	0.44
2:H:102:TYR:CE2	2:H:107:SER:HA	2.53	0.43
2:C:61:ALA:HB3	2:C:64:PHE:HD1	1.83	0.43
1:B:364:ASP:O	1:B:367:VAL:HG22	2.18	0.43
3:D:171:LYS:HE2	3:D:177:TYR:OH	2.19	0.43
2:H:162:THR:O	2:H:209:VAL:HA	2.17	0.43
3:D:18:VAL:O	3:D:76:VAL:HA	2.18	0.43
1:A:471:GLU:O	1:A:491:PRO:HD3	2.18	0.43
2:H:41:PRO:HD3	2:H:91:THR:O	2.18	0.43
1:B:440:ASN:N	1:B:440:ASN:OD1	2.52	0.43
3:D:81:GLN:O	3:D:110:VAL:HG21	2.19	0.43
3:D:87:ASP:N	3:D:87:ASP:OD1	2.52	0.43
2:H:60:TYR:CB	2:H:64:PHE:CG	3.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:68:VAL:HA	2:H:82:GLU:O	2.19	0.42
2:H:159:GLU:N	2:H:160:PRO:CD	2.82	0.42
3:L:118:PRO:HB3	3:L:144:PHE:HB3	2.01	0.42
1:B:516:GLU:HG2	1:B:518:LEU:HG	2.00	0.42
2:H:28:THR:O	2:H:29:PHE:CG	2.73	0.42
2:C:221:ARG:CZ	2:C:223:GLU:OE2	2.68	0.42
1:A:412:PRO:HG3	1:A:429:PHE:HB3	2.00	0.42
2:C:7:SER:O	2:C:118:THR:HG22	2.20	0.42
2:H:206:ILE:HG12	2:H:221:ARG:HG2	2.01	0.42
3:L:153:TRP:CB	3:L:160:VAL:HG11	2.49	0.42
1:B:455:LEU:HD23	1:B:456:PHE:CE2	2.55	0.41
2:H:32:TYR:CD1	2:H:98:THR:HB	2.56	0.41
3:L:145:TYR:HA	3:L:146:PRO:C	2.40	0.41
2:C:48:MET:HG2	2:C:64:PHE:CE1	2.55	0.41
2:H:60:TYR:CD2	2:H:64:PHE:CE2	3.08	0.41
1:A:452:LEU:HD21	2:H:57:ILE:HD13	2.03	0.41
2:H:5:VAL:HG23	2:H:5:VAL:O	2.20	0.41
2:H:19:LYS:HD3	2:H:81:MET:O	2.20	0.41
1:A:475:ALA:O	1:A:487:ASN:HB3	2.20	0.41
2:C:4:LEU:HD22	2:C:23:LYS:O	2.21	0.41
2:C:5:VAL:HG23	2:C:25:SER:HB2	2.03	0.41
1:A:379:CYS:HA	1:A:432:CYS:HA	2.03	0.41
2:C:25:SER:C	2:C:29:PHE:HE1	2.24	0.41
2:C:140:LYS:N	2:C:140:LYS:HD2	2.36	0.41
1:A:421:TYR:CD1	1:A:457:ARG:HB3	2.57	0.40
2:C:39:GLN:HE21	2:C:95:TYR:HE2	1.68	0.40
3:L:36:HIS:ND1	3:L:51:TYR:HA	2.36	0.40
3:L:172:GLN:OE1	3:L:178:ALA:HB2	2.20	0.40
2:C:87:ARG:HA	2:C:87:ARG:HD2	1.86	0.40
3:L:88:TYR:O	3:L:105:GLY:HA2	2.21	0.40
2:C:3:GLN:O	2:C:25:SER:C	2.60	0.40
1:A:414:GLN:O	1:A:424:LYS:NZ	2.54	0.40
1:B:498:GLN:HB3	1:B:501:ASN:HD21	1.86	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	191/199 (96%)	176 (92%)	15 (8%)	0	100	100
1	B	193/199 (97%)	177 (92%)	16 (8%)	0	100	100
2	C	221/235 (94%)	211 (96%)	10 (4%)	0	100	100
2	H	222/235 (94%)	209 (94%)	13 (6%)	0	100	100
3	D	211/217 (97%)	199 (94%)	12 (6%)	0	100	100
3	L	211/217 (97%)	201 (95%)	10 (5%)	0	100	100
All	All	1249/1302 (96%)	1173 (94%)	76 (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	166/172 (96%)	165 (99%)	1 (1%)	84	91
1	B	168/172 (98%)	167 (99%)	1 (1%)	84	91
2	C	185/197 (94%)	185 (100%)	0	100	100
2	H	186/197 (94%)	184 (99%)	2 (1%)	70	83
3	D	177/181 (98%)	175 (99%)	2 (1%)	70	83
3	L	177/181 (98%)	177 (100%)	0	100	100
All	All	1059/1100 (96%)	1053 (99%)	6 (1%)	84	91

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	377	PHE
1	B	336	CYS
2	H	64	PHE
2	H	68	VAL
3	D	87	ASP
3	D	93	TYR

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

Mol	Chain	Res	Type
2	H	116	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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	193/199 (96%)	0.20	4 (2%) 63 45	74, 116, 158, 184	0
1	B	195/199 (97%)	0.07	2 (1%) 79 64	77, 110, 150, 175	0
2	C	223/235 (94%)	0.23	8 (3%) 46 29	69, 119, 181, 229	0
2	H	224/235 (95%)	0.14	2 (0%) 81 66	80, 117, 156, 208	0
3	D	213/217 (98%)	0.21	4 (1%) 66 48	80, 130, 173, 205	0
3	L	213/217 (98%)	0.10	2 (0%) 81 66	85, 114, 147, 171	0
All	All	1261/1302 (96%)	0.16	22 (1%) 69 51	69, 117, 165, 229	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	209	VAL	3.6
3	D	108	LEU	3.3
3	D	118	PRO	3.0
3	D	20	ILE	2.8
1	A	368	LEU	2.7
2	C	32	TYR	2.7
3	D	179	ALA	2.7
2	H	2	VAL	2.6
2	C	51	ILE	2.6
3	L	53	ASN	2.5
2	C	28	THR	2.4
1	A	432	CYS	2.4
1	B	432	CYS	2.3
3	L	49	LEU	2.3
1	A	401	VAL	2.2
2	C	141	SER	2.2
2	C	142	THR	2.2
2	C	218	VAL	2.2
1	B	394	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
2	C	144	GLY	2.1
2	C	29	PHE	2.1
1	A	387	LEU	2.1

## 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 monosaccharides 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.