



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 26, 2026 – 09:28 AM EDT

PDB ID : 7WN2 / pdb_00007wn2
Title : Crystal structure of SARS-CoV-2 spike receptor-binding domain (RBD) in complex with NCV2SG53 Fab
Authors : Yamamoto, A.; Higashiura, A.
Deposited on : 2022-01-17
Resolution : 2.35 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
Mogul : 2022.3.0, CSD as543be (2022)
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

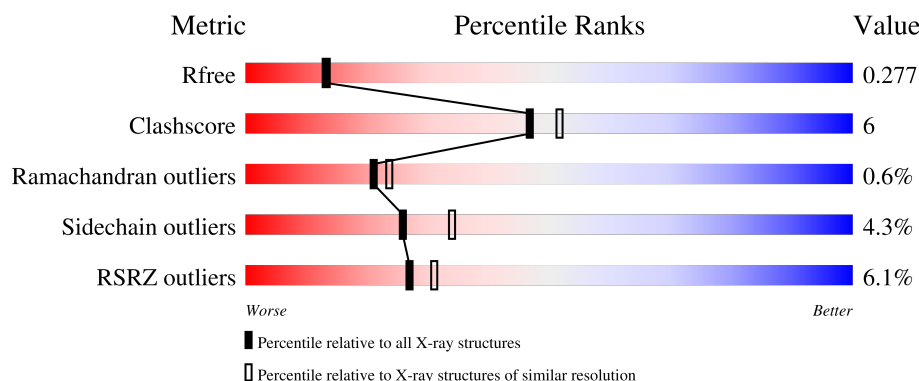
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	224	11% 74% 14% 12%
1	R	224	10% 68% 18% 12%
2	B	227	5% 80% 16% • •
2	H	227	2% 78% 16% • •
3	C	214	4% 87% 11% •

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Mol	Chain	Length	Quality of chain
3	L	214	% 88% 10%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9987 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 Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	R	196	Total	C	N	O	S	13	0	0
			1552	995	259	290	8			
1	A	197	Total	C	N	O	S	11	0	0
			1561	1001	261	291	8			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	537	THR	-	expression tag	UNP P0DTC2
R	538	GLY	-	expression tag	UNP P0DTC2
R	539	HIS	-	expression tag	UNP P0DTC2
R	540	HIS	-	expression tag	UNP P0DTC2
R	541	HIS	-	expression tag	UNP P0DTC2
R	542	HIS	-	expression tag	UNP P0DTC2
R	543	HIS	-	expression tag	UNP P0DTC2
R	544	HIS	-	expression tag	UNP P0DTC2
A	537	THR	-	expression tag	UNP P0DTC2
A	538	GLY	-	expression tag	UNP P0DTC2
A	539	HIS	-	expression tag	UNP P0DTC2
A	540	HIS	-	expression tag	UNP P0DTC2
A	541	HIS	-	expression tag	UNP P0DTC2
A	542	HIS	-	expression tag	UNP P0DTC2
A	543	HIS	-	expression tag	UNP P0DTC2
A	544	HIS	-	expression tag	UNP P0DTC2

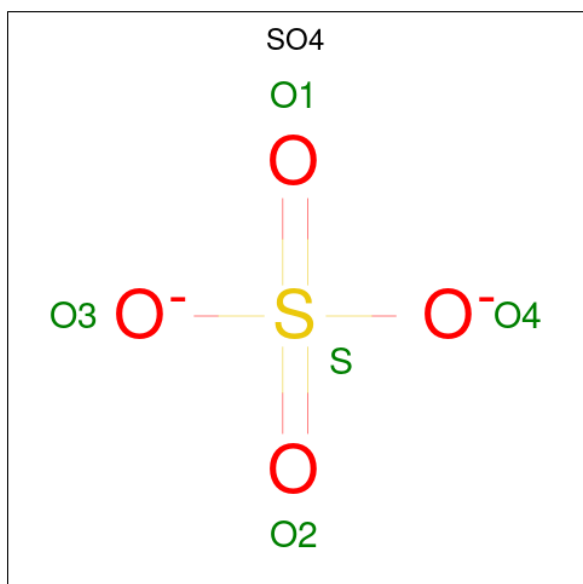
- Molecule 2 is a protein called Fab Heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	218	Total	C	N	O	S	0	1	0
			1644	1042	274	319	9			
2	B	223	Total	C	N	O	S	2	0	0
			1671	1057	279	326	9			

- Molecule 3 is a protein called Fab Light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	213	Total	C	N	O	S	0	1	0
			1627	1021	273	329	4			
3	C	213	Total	C	N	O	S	0	1	0
			1625	1020	270	331	4			

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	R	1	Total	O	S	0	0
			5	4	1		
4	R	1	Total	O	S	0	0
			5	4	1		
4	H	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	R	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		

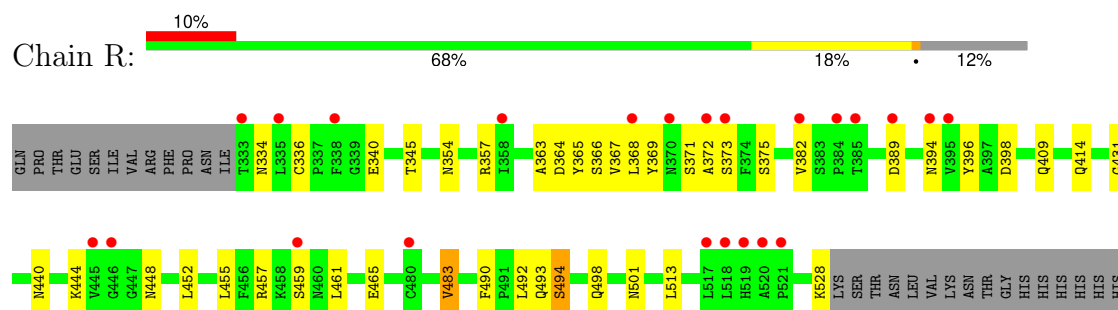
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	R	33	Total	O	0	0
			33	33		
6	H	33	Total	O	0	0
			33	33		
6	L	57	Total	O	0	0
			57	57		
6	A	26	Total	O	0	0
			26	26		
6	B	34	Total	O	0	0
			34	34		
6	C	61	Total	O	0	0
			61	61		

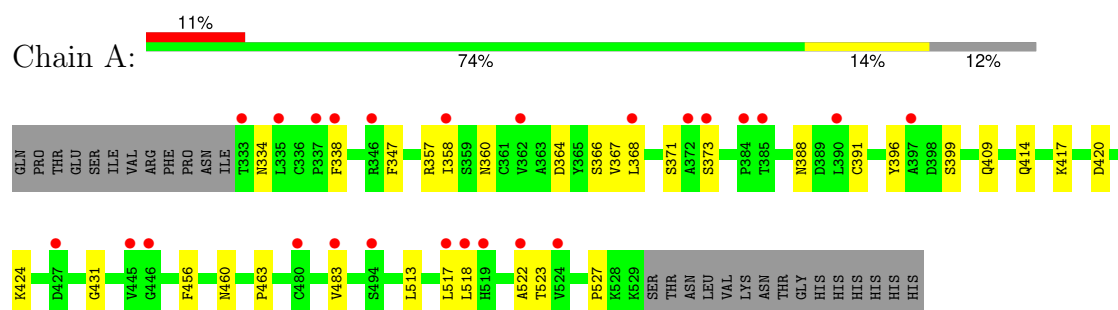
3 Residue-property plots [i](#)

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.

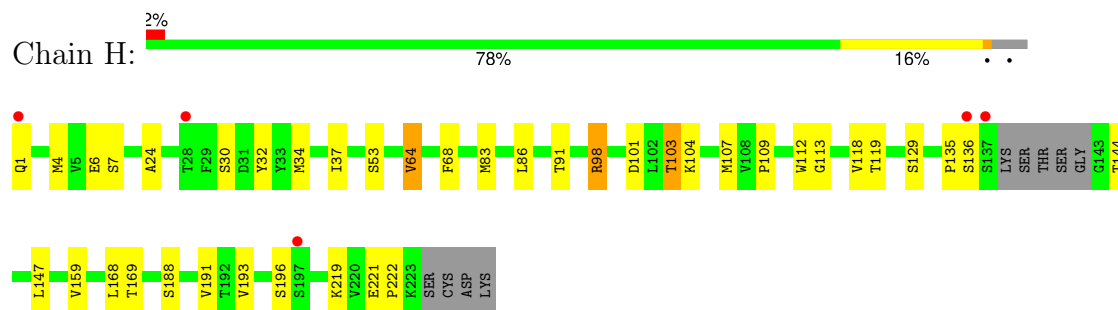
• Molecule 1: Spike protein S1



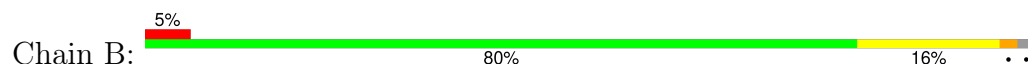
• Molecule 1: Spike protein S1

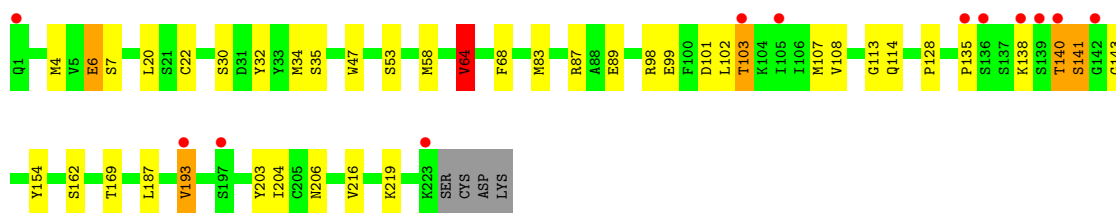


• Molecule 2: Fab Heavy chain

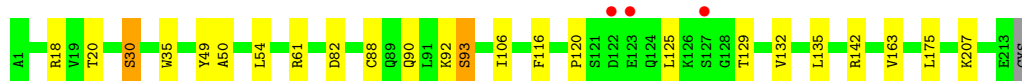
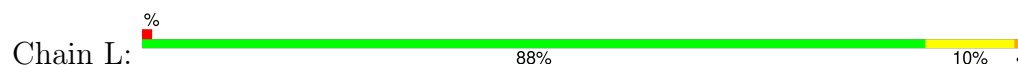


• Molecule 2: Fab Heavy chain

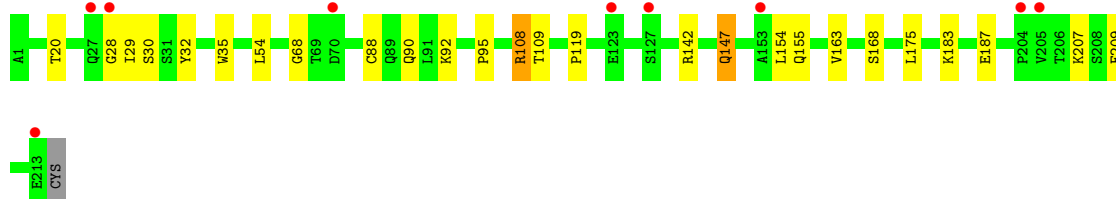
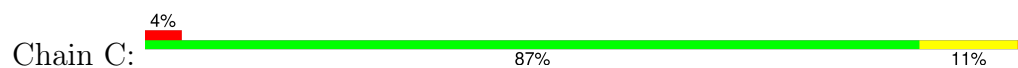




• Molecule 3: Fab Light chain



• Molecule 3: Fab Light chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	76.27Å 118.19Å 196.29Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.71 – 2.35 46.71 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.2 (46.71-2.35) 99.2 (46.71-2.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.39 (at 2.34Å)	Xtriage
Refinement program	PHENIX (1.19.1_4122: ???)	Depositor
R, R_{free}	0.228 , 0.279 0.228 , 0.277	Depositor DCC
R_{free} test set	3699 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	44.7	Xtriage
Anisotropy	0.874	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 35.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9987	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 43.26 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.8090e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: SO4, NAG

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	0.43	0/1605	0.61	0/2183
1	R	0.40	0/1596	0.63	2/2172 (0.1%)
2	B	0.38	0/1711	0.62	1/2326 (0.0%)
2	H	0.36	0/1686	0.61	0/2292
3	C	0.37	0/1662	0.56	0/2258
3	L	0.36	0/1664	0.57	0/2260
All	All	0.38	0/9924	0.60	3/13491 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	140	THR	N-CA-C	-6.41	105.59	113.41
1	R	365	TYR	CA-C-N	-5.45	113.45	120.65
1	R	365	TYR	C-N-CA	-5.45	113.45	120.65

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	1561	0	1485	16	0
1	R	1552	0	1472	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1671	0	1651	23	0
2	H	1644	0	1623	20	0
3	C	1625	0	1594	15	0
3	L	1627	0	1601	15	0
4	A	5	0	0	0	0
4	B	5	0	0	0	0
4	C	10	0	0	0	0
4	H	5	0	0	0	0
4	R	10	0	0	0	0
5	A	14	0	13	0	0
5	R	14	0	13	0	0
6	A	26	0	0	1	0
6	B	34	0	0	0	0
6	C	61	0	0	1	0
6	H	33	0	0	0	0
6	L	57	0	0	1	0
6	R	33	0	0	2	0
All	All	9987	0	9452	108	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 6.

All (108) 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:409:GLN:HA	1:A:414:GLN:HG2	1.58	0.85
2:B:107:MET:HE1	3:C:32:TYR:HA	1.62	0.81
2:B:4:MET:HE1	2:B:34:MET:HE1	1.63	0.80
1:A:417:LYS:H	1:A:417:LYS:HE2	1.50	0.76
1:R:409:GLN:HA	1:R:414:GLN:HG2	1.72	0.71
1:A:391:CYS:HB3	1:A:522:ALA:HB1	1.72	0.71
2:H:107:MET:HG2	3:L:50:ALA:HB2	1.75	0.67
2:H:4:MET:HE1	2:H:34:MET:HE1	1.79	0.65
1:R:444:LYS:HG3	1:R:448:ASN:HB2	1.79	0.63
1:R:457:ARG:NH1	1:R:459:SER:O	2.28	0.61
1:R:440:ASN:ND2	1:R:440:ASN:H	2.00	0.60
3:L:18:ARG:HG2	3:L:18:ARG:HH11	1.67	0.59
2:B:64:VAL:HG13	2:B:68:PHE:HB2	1.85	0.58
2:H:135:PRO:HB3	2:H:147:LEU:HB3	1.86	0.57
1:R:364:ASP:O	1:R:367:VAL:HG12	2.06	0.56
1:R:440:ASN:H	1:R:440:ASN:HD22	1.52	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:204:ILE:HD13	2:B:219:LYS:HA	1.87	0.56
2:H:83:MET:HB3	2:H:86:LEU:HD21	1.89	0.55
1:R:389:ASP:HB3	1:R:528:LYS:HD3	1.88	0.55
1:A:424:LYS:HB3	1:A:463:PRO:HA	1.89	0.55
3:C:108:ARG:HG2	3:C:109:THR:N	2.21	0.55
1:R:357:ARG:HG3	1:R:396:TYR:HE1	1.73	0.54
3:L:61:ARG:NH2	3:L:82:ASP:OD1	2.40	0.54
2:H:91:THR:HG23	2:H:119:THR:HA	1.90	0.54
3:C:90:GLN:OE1	3:C:92:LYS:N	2.41	0.53
1:A:388:ASN:HB3	1:A:527:PRO:HD2	1.91	0.53
2:H:32:TYR:CD1	2:H:98:ARG:HD2	2.45	0.53
3:C:119:PRO:HB3	3:C:209:PHE:CZ	2.43	0.52
2:H:101:ASP:OD1	2:H:103:THR:HB	2.10	0.52
1:R:371:SER:O	1:R:373:SER:N	2.32	0.51
2:B:30:SER:O	2:B:53:SER:HB3	2.10	0.51
2:B:98:ARG:O	2:B:98:ARG:HG3	2.10	0.51
3:L:18:ARG:HG2	3:L:18:ARG:NH1	2.24	0.51
1:R:357:ARG:HH21	1:R:394:ASN:ND2	2.08	0.51
3:C:35:TRP:CZ3	3:C:88:CYS:HB3	2.46	0.50
3:L:90:GLN:OE1	3:L:92:LYS:N	2.44	0.50
2:H:6:GLU:OE2	2:H:113:GLY:HA3	2.12	0.50
2:H:135:PRO:HD2	2:H:222:PRO:HA	1.94	0.50
3:C:183:LYS:O	3:C:187:GLU:HG2	2.11	0.50
1:R:336:CYS:SG	1:R:363:ALA:HB2	2.52	0.50
1:R:490:PHE:CE2	1:R:492:LEU:HB2	2.46	0.50
1:R:357:ARG:HH21	1:R:394:ASN:HD21	1.59	0.49
2:B:87:ARG:HB3	2:B:89:GLU:OE1	2.12	0.49
1:A:456:PHE:HE2	2:B:102:LEU:HD11	1.78	0.49
2:H:4:MET:HE3	2:H:24:ALA:HB2	1.94	0.48
2:B:89:GLU:H	2:B:89:GLU:CD	2.21	0.48
2:H:219:LYS:HE3	2:H:221:GLU:OE1	2.14	0.48
2:B:128:PRO:HB3	2:B:154:TYR:HB3	1.96	0.47
1:A:364:ASP:OD2	1:A:367:VAL:HG23	2.15	0.47
3:C:163:VAL:HG22	3:C:175:LEU:HD12	1.96	0.47
1:A:460:ASN:N	6:A:706:HOH:O	2.47	0.47
1:R:357:ARG:HE	1:R:394:ASN:ND2	2.14	0.46
3:L:142[A]:ARG:CZ	3:L:163:VAL:HG21	2.44	0.46
1:A:431:GLY:HA3	1:A:513:LEU:O	2.15	0.46
1:A:368:LEU:HD12	1:A:368:LEU:HA	1.67	0.46
1:R:452:LEU:HD23	1:R:494:SER:HA	1.97	0.46
2:H:109:PRO:HD3	3:L:49:TYR:CE2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:32:TYR:CD1	2:B:98:ARG:HD2	2.50	0.46
2:H:103:THR:HG22	2:H:104:LYS:HG3	1.98	0.46
2:B:58:MET:HE2	2:B:58:MET:HB3	1.90	0.45
2:B:6:GLU:OE2	2:B:113:GLY:HA3	2.17	0.45
3:C:142:ARG:CZ	3:C:163:VAL:HG21	2.46	0.45
1:R:431:GLY:HA3	1:R:513:LEU:O	2.16	0.45
2:B:162:SER:OG	2:B:206:ASN:OD1	2.35	0.45
2:H:168:LEU:HD21	2:H:191:VAL:HG11	1.99	0.45
2:B:6:GLU:H	2:B:114:GLN:HE22	1.63	0.45
1:A:338:PHE:HE1	1:A:358:ILE:HG13	1.81	0.45
2:H:64:VAL:HG13	2:H:68:PHE:HB2	1.97	0.44
1:R:354:ASN:O	1:R:398:ASP:HA	2.18	0.44
1:R:357:ARG:HG3	1:R:396:TYR:CE1	2.52	0.44
1:A:357:ARG:HD2	1:A:396:TYR:HE1	1.83	0.44
1:R:340:GLU:HB3	6:R:714:HOH:O	2.17	0.43
1:A:420:ASP:HA	1:A:424:LYS:NZ	2.33	0.43
1:R:498:GLN:HB2	1:R:501:ASN:OD1	2.18	0.43
3:L:30:SER:HB3	6:L:353:HOH:O	2.17	0.43
1:R:444:LYS:NZ	6:R:708:HOH:O	2.51	0.43
3:L:54:LEU:HD12	3:L:54:LEU:HA	1.69	0.43
1:A:360:ASN:HA	1:A:523:THR:HG22	1.99	0.43
1:A:456:PHE:CE2	2:B:102:LEU:HD11	2.53	0.43
2:B:20:LEU:HG	2:B:83:MET:HE2	1.99	0.43
2:B:35:SER:HB2	2:B:99:GLU:OE2	2.19	0.43
3:C:54:LEU:HA	3:C:54:LEU:HD12	1.82	0.43
3:L:35:TRP:CZ3	3:L:88:CYS:HB3	2.54	0.43
3:L:125:LEU:HA	3:L:125:LEU:HD23	1.87	0.43
3:L:163:VAL:HG22	3:L:175:LEU:HD12	2.01	0.43
2:H:30:SER:O	2:H:53:SER:HB3	2.18	0.43
3:L:116:PHE:CD1	3:L:135:LEU:HD23	2.54	0.43
1:R:461:LEU:HD22	1:R:465:GLU:HB3	2.01	0.42
1:A:347:PHE:CE2	1:A:399:SER:HB2	2.54	0.42
2:B:101:ASP:OD1	2:B:103:THR:HB	2.19	0.42
3:L:120:PRO:HD3	3:L:132:VAL:HG22	2.02	0.42
2:H:4:MET:HE2	2:H:4:MET:HB3	1.72	0.42
2:B:4:MET:HE3	2:B:22:CYS:SG	2.59	0.42
3:C:119:PRO:HB3	3:C:209:PHE:CE1	2.55	0.42
3:C:147:GLN:HG2	3:C:154:LEU:HD13	2.01	0.41
3:C:207:LYS:HE2	6:C:435:HOH:O	2.19	0.41
3:C:154:LEU:HD12	3:C:155:GLN:N	2.35	0.41
2:B:141:SER:C	2:B:143:GLY:H	2.29	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:68:PHE:CE2	2:H:83:MET:HG2	2.55	0.41
2:B:47:TRP:CZ3	3:C:95:PRO:HB3	2.55	0.41
1:R:368:LEU:HD23	1:R:368:LEU:HA	1.82	0.41
1:R:455:LEU:HB2	1:R:493:GLN:HG2	2.03	0.41
1:R:483:VAL:CG1	3:L:93:SER:HB2	2.51	0.41
2:B:193:VAL:HG21	2:B:203:TYR:CE1	2.55	0.41
1:R:366:SER:O	1:R:369:TYR:N	2.54	0.41
3:C:28:GLY:HA2	3:C:68:GLY:O	2.20	0.41
2:H:37:ILE:HD13	2:H:112:TRP:CZ2	2.56	0.40
2:H:68:PHE:CD1	2:H:68:PHE:N	2.89	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	195/224 (87%)	184 (94%)	11 (6%)	0	100	100
1	R	194/224 (87%)	178 (92%)	14 (7%)	2 (1%)	12	12
2	B	221/227 (97%)	206 (93%)	13 (6%)	2 (1%)	14	14
2	H	215/227 (95%)	204 (95%)	10 (5%)	1 (0%)	24	27
3	C	212/214 (99%)	202 (95%)	9 (4%)	1 (0%)	24	27
3	L	212/214 (99%)	203 (96%)	8 (4%)	1 (0%)	24	27
All	All	1249/1330 (94%)	1177 (94%)	65 (5%)	7 (1%)	21	24

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	R	372	ALA
2	H	136	SER

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Mol	Chain	Res	Type
2	B	135	PRO
3	L	30	SER
1	R	382	VAL
2	B	64	VAL
3	C	29	ILE

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	170/196 (87%)	163 (96%)	7 (4%)	27	36
1	R	169/196 (86%)	164 (97%)	5 (3%)	36	48
2	B	189/193 (98%)	177 (94%)	12 (6%)	16	19
2	H	186/193 (96%)	173 (93%)	13 (7%)	14	15
3	C	185/185 (100%)	180 (97%)	5 (3%)	39	52
3	L	185/185 (100%)	180 (97%)	5 (3%)	39	52
All	All	1084/1148 (94%)	1037 (96%)	47 (4%)	26	34

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	R	334	ASN
1	R	345	THR
1	R	375	SER
1	R	483	VAL
1	R	494	SER
2	H	1	GLN
2	H	7	SER
2	H	64	VAL
2	H	98	ARG
2	H	103	THR
2	H	118	VAL
2	H	129	SER
2	H	144	THR

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Mol	Chain	Res	Type
2	H	159	VAL
2	H	169	THR
2	H	188	SER
2	H	193	VAL
2	H	196	SER
3	L	20	THR
3	L	93	SER
3	L	106	ILE
3	L	129	THR
3	L	207	LYS
1	A	334	ASN
1	A	366	SER
1	A	371	SER
1	A	373	SER
1	A	483	VAL
1	A	517	LEU
1	A	518	LEU
2	B	6	GLU
2	B	7	SER
2	B	64	VAL
2	B	103	THR
2	B	108	VAL
2	B	138	LYS
2	B	140	THR
2	B	141	SER
2	B	169	THR
2	B	187	LEU
2	B	193	VAL
2	B	216	VAL
3	C	20	THR
3	C	30	SER
3	C	108	ARG
3	C	147	GLN
3	C	168	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	R	388	ASN
1	R	394	ASN
1	R	440	ASN
1	R	450	ASN

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Mol	Chain	Res	Type
2	H	180	GLN
2	H	213	ASN
3	L	79	GLN
1	A	474	GLN
3	C	199	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

9 ligands are 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	$\# Z > 2$
4	SO4	R	602	-	4,4,4	0.28	0	6,6,6	0.19	0
4	SO4	C	301	-	4,4,4	0.24	0	6,6,6	0.16	0
4	SO4	A	601	-	4,4,4	0.27	0	6,6,6	0.21	0
5	NAG	A	602	1	14,14,15	0.54	0	17,19,21	0.90	1 (5%)
4	SO4	B	301	-	4,4,4	0.23	0	6,6,6	0.17	0
4	SO4	H	301	-	4,4,4	0.22	0	6,6,6	0.24	0
5	NAG	R	603	1	14,14,15	0.87	1 (7%)	17,19,21	0.71	0
4	SO4	C	302	-	4,4,4	0.28	0	6,6,6	0.20	0
4	SO4	R	601	-	4,4,4	0.21	0	6,6,6	0.24	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
5	NAG	A	602	1	-	0/6/23/26	0/1/1/1
5	NAG	R	603	1	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	R	603	NAG	O5-C1	2.84	1.48	1.43

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	602	NAG	C1-O5-C5	3.43	116.78	112.19

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 [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	197/224 (87%)	1.01	25 (12%) 8 9	42, 57, 96, 140	3 (1%)
1	R	196/224 (87%)	1.03	23 (11%) 9 11	41, 54, 99, 123	3 (1%)
2	B	223/227 (98%)	0.58	12 (5%) 31 37	39, 50, 76, 132	1 (0%)
2	H	218/227 (96%)	0.52	5 (2%) 61 66	34, 49, 68, 97	1 (0%)
3	C	213/214 (99%)	0.47	9 (4%) 40 46	28, 45, 61, 106	1 (0%)
3	L	213/214 (99%)	0.45	3 (1%) 73 78	27, 45, 65, 91	1 (0%)
All	All	1260/1330 (94%)	0.67	77 (6%) 27 31	27, 49, 86, 140	10 (0%)

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	372	ALA	7.0
2	B	136	SER	5.2
1	R	372	ALA	4.6
2	B	140	THR	4.5
1	A	446	GLY	4.4
1	R	518	LEU	4.3
1	R	519	HIS	3.9
2	B	139	SER	3.8
1	R	385	THR	3.7
1	R	335	LEU	3.5
1	R	445	VAL	3.5
1	R	520	ALA	3.4
1	A	390	LEU	3.4
2	H	136	SER	3.4
1	R	384	PRO	3.3
1	R	373	SER	3.3
1	A	518	LEU	3.3
1	R	517	LEU	3.2
1	R	333	THR	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	358	ILE	3.2
1	A	338	PHE	3.1
1	A	517	LEU	3.0
2	B	135	PRO	3.0
1	A	373	SER	2.9
1	A	335	LEU	2.9
1	A	522	ALA	2.9
1	A	333	THR	2.9
1	A	524	VAL	2.8
3	L	127	SER	2.8
2	B	197	SER	2.8
2	H	1	GLN	2.8
1	R	382	VAL	2.8
3	C	204	PRO	2.7
1	R	521	PRO	2.7
1	R	338	PHE	2.7
3	C	205	VAL	2.7
1	R	389	ASP	2.6
1	R	480	CYS	2.6
1	R	370	ASN	2.6
1	A	397	ALA	2.5
3	C	28	GLY	2.5
2	B	223	LYS	2.5
1	A	519	HIS	2.5
1	A	362	VAL	2.5
1	R	368	LEU	2.4
3	L	122	ASP	2.4
1	A	445	VAL	2.4
2	B	193	VAL	2.4
2	B	105	ILE	2.4
1	A	385	THR	2.4
1	R	394	ASN	2.3
2	B	103	THR	2.3
2	H	137	SER	2.3
3	L	123	GLU	2.3
1	A	337	PRO	2.2
3	C	213	GLU	2.2
1	R	358	ILE	2.2
3	C	123	GLU	2.2
1	A	346	ARG	2.2
3	C	70	ASP	2.2
1	A	384	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
1	R	459	SER	2.2
2	H	28	THR	2.2
1	A	368	LEU	2.2
1	A	494	SER	2.2
1	A	480	CYS	2.1
3	C	127	SER	2.1
1	R	395	VAL	2.1
3	C	153	ALA	2.1
2	H	197	SER	2.1
1	A	427	ASP	2.1
2	B	1	GLN	2.1
1	A	483	VAL	2.1
2	B	138	LYS	2.0
1	R	446	GLY	2.0
2	B	142	GLY	2.0
3	C	27	GLN	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
5	NAG	R	603	14/15	0.64	0.14	59,77,83,83	0
5	NAG	A	602	14/15	0.67	0.13	66,77,83,83	0
4	SO4	C	301	5/5	0.71	0.11	86,92,98,107	0
4	SO4	R	601	5/5	0.74	0.15	95,106,116,122	0
4	SO4	C	302	5/5	0.74	0.12	96,98,117,125	0
4	SO4	H	301	5/5	0.79	0.10	78,89,105,106	0
4	SO4	R	602	5/5	0.81	0.16	90,105,114,128	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	SO4	A	601	5/5	0.85	0.17	101,105,112,126	0
4	SO4	B	301	5/5	0.89	0.08	80,87,99,99	0

6.5 Other polymers [i](#)

There are no such residues in this entry.