



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 11:16 PM UTC

PDB ID : 7P19 / pdb_00007p19
Title : Crystal structure of SARS-CoV-2 RBD Q498Y complexed with human ACE2
Authors : Erausquin, E.; Lopez-Sagaseta, J.
Deposited on : 2021-07-01
Resolution : 3.24 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

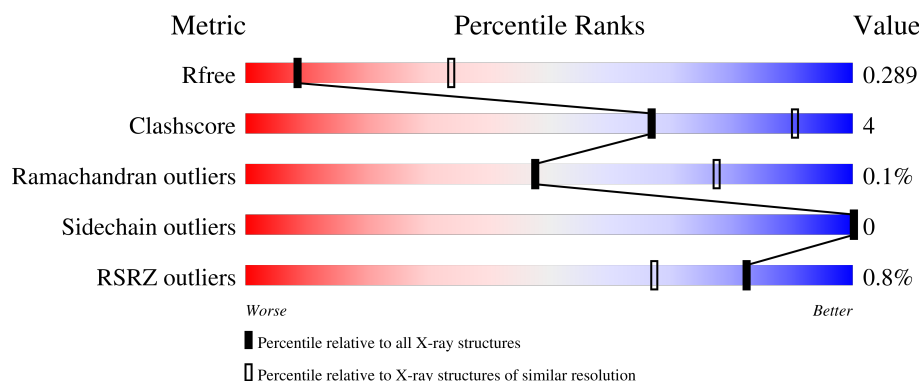
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.24 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	2153 (3.28-3.20)
Clashscore	190562	2275 (3.28-3.20)
Ramachandran outliers	187476	2233 (3.28-3.20)
Sidechain outliers	187428	2232 (3.28-3.20)
RSRZ outliers	180081	2153 (3.28-3.20)

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	599	2% 90% 10%
1	B	599	88% 11%
2	C	210	80% 6% 13%
2	E	210	2% 76% 8% 16%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	CL	E	602	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 12614 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 Processed angiotensin-converting enzyme 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	597	Total	C	N	O	S	0	2	0
			4810	3087	797	897	29			
1	B	594	Total	C	N	O	S	0	1	0
			4849	3104	804	912	29			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	17	GLY	-	expression tag	UNP Q9BYF1
A	18	PRO	-	expression tag	UNP Q9BYF1
B	17	GLY	-	expression tag	UNP Q9BYF1
B	18	PRO	-	expression tag	UNP Q9BYF1

- Molecule 2 is a protein called Spike protein S1.

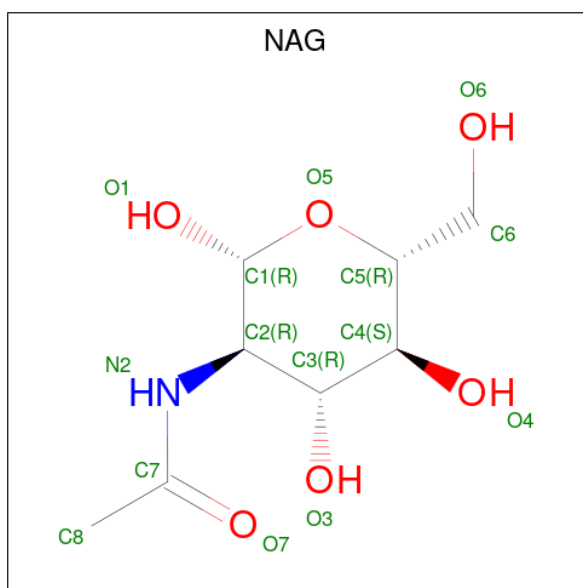
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	176	Total	C	N	O	S	0	0	0
			1395	894	234	262	5			
2	C	182	Total	C	N	O	S	0	0	0
			1451	933	240	271	7			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	332	GLY	-	expression tag	UNP P0DTC2
E	333	PRO	-	expression tag	UNP P0DTC2
E	498	TYR	GLN	engineered mutation	UNP P0DTC2
C	332	GLY	-	expression tag	UNP P0DTC2
C	333	PRO	-	expression tag	UNP P0DTC2
C	498	TYR	GLN	engineered mutation	UNP P0DTC2

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula:

C₈H₁₅NO₆).



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

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Zn	0	0
			1	1		
4	B	1	Total	Zn	0	0
			1	1		

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		

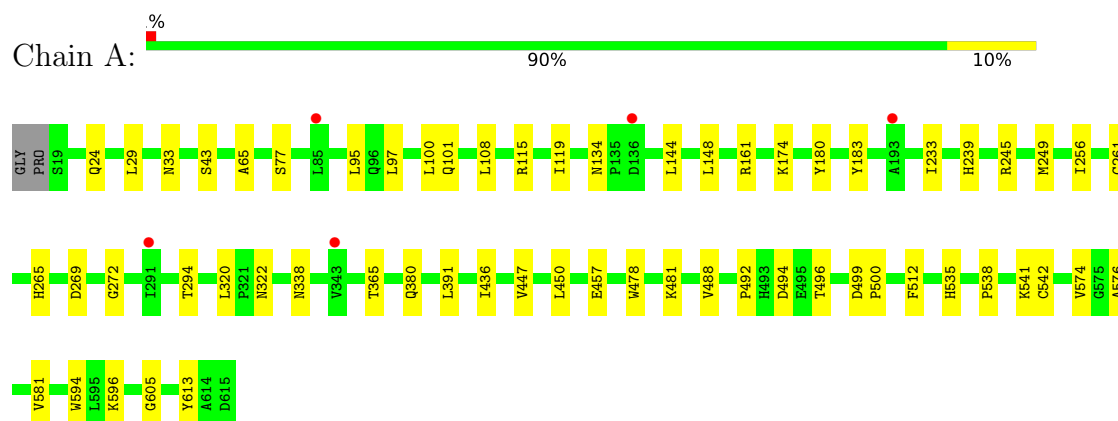
- Molecule 6 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	E	1	Total	Cl	0	0
			1	1		

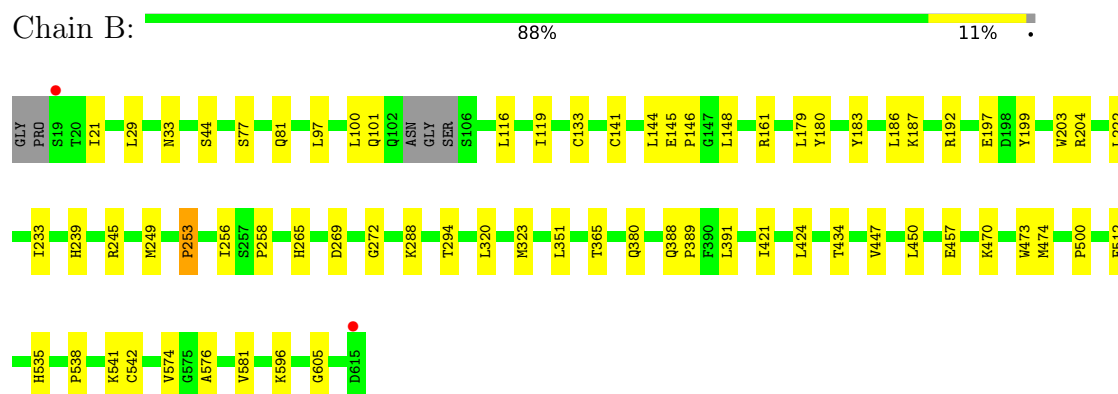
3 Residue-property plots [i](#)

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.

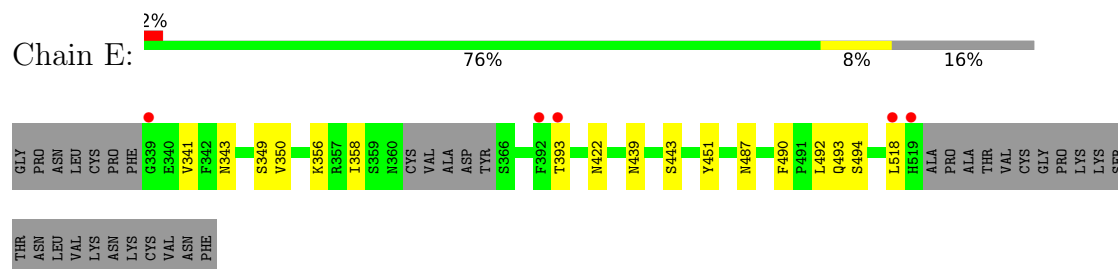
• Molecule 1: Processed angiotensin-converting enzyme 2



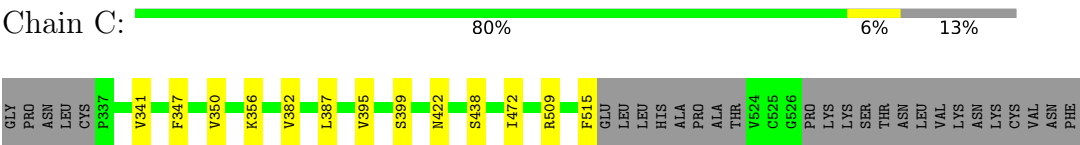
• Molecule 1: Processed angiotensin-converting enzyme 2



• Molecule 2: Spike protein S1



● Molecule 2: Spike protein S1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	60.59Å 165.04Å 228.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	93.99 – 3.24 93.99 – 3.24	Depositor EDS
% Data completeness (in resolution range)	99.4 (93.99-3.24) 99.5 (93.99-3.24)	Depositor EDS
R_{merge}	0.26	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.51 (at 3.26Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.231 , 0.288 0.230 , 0.289	Depositor DCC
R_{free} test set	1853 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	85.1	Xtriage
Anisotropy	0.729	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 60.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	12614	wwPDB-VP
Average B, all atoms (Å ²)	97.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.24% 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](#)

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

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	0.09	0/4949	0.28	0/6731
1	B	0.09	0/4988	0.28	0/6776
2	C	0.08	0/1492	0.27	0/2026
2	E	0.09	0/1432	0.31	0/1945
All	All	0.09	0/12861	0.28	0/17478

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	4810	0	4547	35	0
1	B	4849	0	4626	39	0
2	C	1451	0	1368	8	0
2	E	1395	0	1314	11	0
3	A	28	0	26	0	0
3	B	42	0	39	1	0
3	C	14	0	13	0	0
3	E	14	0	13	1	0
4	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	1	0	0	0	0
5	A	4	0	6	0	0
5	B	4	0	6	0	0
6	E	1	0	0	2	0
All	All	12614	0	11958	92	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 4.

All (92) 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:B:81:GLN:HG3	1:B:101:GLN:HB2	1.79	0.65
2:E:451:TYR:HB3	6:E:602:CL:CL	2.34	0.65
1:B:192:ARG:NH1	1:B:197:GLU:O	2.31	0.64
2:E:341:VAL:HG21	2:E:358:ILE:HD11	1.79	0.62
1:B:269:ASP:OD1	1:B:272:GLY:N	2.33	0.61
1:A:294:THR:HG23	1:A:365:THR:HA	1.82	0.61
2:E:341:VAL:HG12	2:E:356:LYS:HD3	1.84	0.59
1:A:269:ASP:OD1	1:A:272:GLY:N	2.34	0.59
1:B:320:LEU:HD13	1:B:380:GLN:HG2	1.85	0.59
1:B:100:LEU:HG	1:B:391:LEU:HD11	1.86	0.58
1:A:77:SER:OG	1:A:100:LEU:O	2.18	0.58
1:B:233:ILE:HG12	1:B:581:VAL:HG21	1.85	0.58
1:A:239:HIS:CE1	1:A:596:LYS:HG3	2.41	0.56
1:A:457:GLU:HG2	1:A:512:PHE:HB3	1.88	0.55
1:B:21:ILE:HD12	1:B:21:ILE:H	1.72	0.54
1:A:320:LEU:HD13	1:A:380:GLN:HG2	1.88	0.54
1:B:133:CYS:HA	1:B:141:CYS:HA	1.89	0.54
1:B:144:LEU:HA	1:B:148:LEU:HB2	1.88	0.54
1:B:245:ARG:NH2	1:B:605:GLY:O	2.41	0.54
1:B:421:ILE:HG22	3:B:703:NAG:H62	1.88	0.54
1:B:239:HIS:CE1	1:B:596:LYS:HG3	2.43	0.53
1:A:24:GLN:OE1	2:E:487:ASN:ND2	2.42	0.53
1:B:457:GLU:HG2	1:B:512:PHE:HB3	1.90	0.53
1:A:144:LEU:HA	1:A:148:LEU:HB2	1.91	0.52
1:B:29:LEU:O	1:B:33:ASN:ND2	2.43	0.51
2:E:439:ASN:O	2:E:443:SER:OG	2.26	0.50
1:B:294:THR:HG23	1:B:365:THR:HA	1.93	0.50
2:E:393:THR:HG23	2:E:518:LEU:HD23	1.93	0.50
1:A:574:VAL:HG23	1:A:576:ALA:H	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:44:SER:HB3	1:B:351:LEU:HD23	1.94	0.49
2:C:382:VAL:HG13	2:C:387:LEU:HD23	1.94	0.49
2:C:341:VAL:HG12	2:C:356:LYS:HD2	1.94	0.49
1:B:288:LYS:HD3	1:B:434:THR:HG23	1.93	0.49
1:B:535:HIS:CD2	1:B:542:CYS:HB2	2.48	0.49
1:A:29:LEU:O	1:A:33:ASN:ND2	2.43	0.48
2:E:349:SER:HA	6:E:602:CL:CL	2.50	0.48
1:B:77:SER:OG	1:B:100:LEU:O	2.23	0.48
2:E:493:GLN:HG3	2:E:494:SER:N	2.29	0.48
1:B:574:VAL:HG23	1:B:576:ALA:H	1.78	0.48
1:A:180:TYR:HA	1:A:183:TYR:HB3	1.96	0.47
1:A:161:ARG:NE	1:A:265:HIS:O	2.37	0.47
1:B:116:LEU:HB2	1:B:186:LEU:HD13	1.96	0.47
2:E:350:VAL:HG22	2:E:422:ASN:HB3	1.95	0.47
1:B:447:VAL:HA	1:B:450:LEU:HD12	1.96	0.47
1:A:322:ASN:OD1	1:A:322:ASN:N	2.48	0.47
1:A:338:ASN:O	1:A:338:ASN:ND2	2.38	0.46
1:A:100:LEU:HG	1:A:391:LEU:HD11	1.98	0.46
1:A:436:ILE:HD13	1:A:594:TRP:CD1	2.51	0.46
1:A:538:PRO:HD2	1:A:541:LYS:HD3	1.98	0.46
1:B:187:LYS:HB3	1:B:199:TYR:CG	2.50	0.46
2:C:350:VAL:HG22	2:C:422:ASN:HB3	1.96	0.46
2:E:490:PHE:CE2	2:E:492:LEU:HB2	2.50	0.45
1:A:245:ARG:NH2	1:A:605:GLY:O	2.50	0.45
1:A:478:TRP:HA	1:A:481:LYS:HB2	1.98	0.45
1:A:492:PRO:HD3	1:A:613:TYR:CG	2.52	0.45
1:A:249:MET:HG3	1:A:256:ILE:HB	1.99	0.44
1:A:499:ASP:N	1:A:500:PRO:HD2	2.33	0.44
1:A:174:LYS:HG2	1:A:496:THR:O	2.18	0.44
2:C:472:ILE:H	2:C:472:ILE:HD12	1.82	0.44
1:A:97:LEU:O	1:A:101:GLN:HG2	2.18	0.44
1:B:180:TYR:HA	1:B:183:TYR:HB3	1.99	0.44
1:A:134:ASN:OD1	1:A:134:ASN:N	2.51	0.43
1:B:470:LYS:HA	1:B:473:TRP:CD1	2.53	0.43
1:A:261:CYS:HB2	1:A:488:VAL:HB	1.99	0.43
1:B:249:MET:O	1:B:253:PRO:HA	2.19	0.43
1:B:204:ARG:HG2	1:B:222:LEU:HD23	2.00	0.43
1:A:115:ARG:O	1:A:119:ILE:HG13	2.19	0.43
2:C:395:VAL:HG22	2:C:515:PHE:HD1	1.84	0.43
1:A:447:VAL:HA	1:A:450:LEU:HD12	2.01	0.42
1:A:43:SER:HA	1:A:65:ALA:HB1	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:474:MET:HE1	1:B:500:PRO:HD3	2.00	0.42
1:B:538:PRO:HD2	1:B:541:LYS:HD3	2.02	0.42
1:A:95:LEU:HD23	1:A:95:LEU:HA	1.92	0.42
2:E:343:ASN:ND2	3:E:601:NAG:O5	2.53	0.42
1:B:161:ARG:NE	1:B:265:HIS:O	2.45	0.42
1:A:97:LEU:HD23	1:A:97:LEU:HA	1.90	0.41
1:B:388:GLN:OE1	1:B:389:PRO:HD2	2.20	0.41
1:B:97:LEU:HD23	1:B:97:LEU:HA	1.88	0.41
2:C:347:PHE:CE2	2:C:399:SER:HB2	2.56	0.41
1:A:535:HIS:CD2	1:A:542:CYS:HB2	2.56	0.41
1:B:145:GLU:HA	1:B:146:PRO:HA	1.85	0.41
1:B:203:TRP:CE3	1:B:203:TRP:HA	2.55	0.41
1:B:245:ARG:HD2	1:B:258:PRO:HA	2.02	0.41
1:B:424:LEU:HD12	1:B:424:LEU:HA	1.95	0.41
1:A:233:ILE:HG12	1:A:581:VAL:HG21	2.03	0.41
2:C:472:ILE:HD12	2:C:472:ILE:N	2.36	0.41
1:A:494:ASP:OD1	1:A:496:THR:HG22	2.22	0.40
2:C:438:SER:HB3	2:C:509:ARG:HG3	2.02	0.40
1:B:119:ILE:HG23	1:B:179:LEU:HD22	2.03	0.40
1:A:108:LEU:HD23	1:A:108:LEU:HA	1.86	0.40
1:B:323:MET:HA	1:B:323:MET:HE2	2.03	0.40
1:B:249:MET:HG3	1:B:256:ILE:HB	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	597/599 (100%)	577 (97%)	20 (3%)	0	100	100
1	B	591/599 (99%)	571 (97%)	19 (3%)	1 (0%)	43	72
2	C	178/210 (85%)	168 (94%)	10 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	E	172/210 (82%)	163 (95%)	9 (5%)	0	100	100
All	All	1538/1618 (95%)	1479 (96%)	58 (4%)	1 (0%)	48	77

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	253	PRO

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	506/528 (96%)	506 (100%)	0	100	100
1	B	524/528 (99%)	524 (100%)	0	100	100
2	C	157/182 (86%)	157 (100%)	0	100	100
2	E	149/182 (82%)	149 (100%)	0	100	100
All	All	1336/1420 (94%)	1336 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	64	ASN
1	A	101	GLN
1	A	239	HIS
1	A	417	HIS
1	A	599	ASN
2	E	481	ASN
1	B	51	ASN
1	B	239	HIS
1	B	380	GLN
1	B	524	GLN

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Mol	Chain	Res	Type
1	B	599	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 3 are monoatomic - leaving 9 for Mogul analysis.

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	$\# Z > 2$
5	EDO	A	704	-	3,3,3	0.43	0	2,2,2	0.39	0
3	NAG	A	703	-	14,14,15	0.18	0	17,19,21	0.48	0
3	NAG	B	703	-	14,14,15	0.16	0	17,19,21	0.49	0
5	EDO	B	704	-	3,3,3	0.43	0	2,2,2	0.36	0
3	NAG	C	601	-	14,14,15	0.18	0	17,19,21	0.58	0
3	NAG	A	701	1	14,14,15	0.24	0	17,19,21	0.44	0
3	NAG	E	601	-	14,14,15	0.16	0	17,19,21	0.59	0
3	NAG	B	705	-	14,14,15	0.22	0	17,19,21	0.41	0
3	NAG	B	701	-	14,14,15	0.23	0	17,19,21	0.43	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	EDO	A	704	-	-	1/1/1/1	-
3	NAG	A	703	-	-	0/6/23/26	0/1/1/1
3	NAG	B	703	-	-	0/6/23/26	0/1/1/1
5	EDO	B	704	-	-	0/1/1/1	-
3	NAG	C	601	-	-	4/6/23/26	0/1/1/1
3	NAG	A	701	1	-	3/6/23/26	0/1/1/1
3	NAG	E	601	-	-	1/6/23/26	0/1/1/1
3	NAG	B	705	-	-	0/6/23/26	0/1/1/1
3	NAG	B	701	-	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	701	NAG	C8-C7-N2-C2
3	A	701	NAG	O7-C7-N2-C2
3	C	601	NAG	C8-C7-N2-C2
3	C	601	NAG	O7-C7-N2-C2
3	C	601	NAG	C4-C5-C6-O6
3	A	701	NAG	O5-C5-C6-O6
3	E	601	NAG	O5-C5-C6-O6
3	B	701	NAG	O5-C5-C6-O6
3	C	601	NAG	O5-C5-C6-O6
5	A	704	EDO	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	703	NAG	1	0
3	E	601	NAG	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [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, 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	597/599 (99%)	-0.08	5 (0%) 82 67	40, 84, 116, 199	2 (0%)
1	B	594/599 (99%)	-0.13	2 (0%) 90 81	53, 97, 145, 216	1 (0%)
2	C	182/210 (86%)	0.16	0 100 100	82, 109, 182, 207	0
2	E	176/210 (83%)	0.07	5 (2%) 55 36	65, 89, 133, 189	0
All	All	1549/1618 (95%)	-0.06	12 (0%) 82 67	40, 93, 146, 216	3 (0%)

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	615	ASP	3.6
1	A	136	ASP	3.2
2	E	519	HIS	3.1
2	E	339	GLY	2.9
2	E	392	PHE	2.7
2	E	393	THR	2.6
1	A	85	LEU	2.4
1	A	193	ALA	2.2
1	A	343	VAL	2.0
2	E	518	LEU	2.0
1	A	291	ILE	2.0
1	B	19	SER	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
3	NAG	E	601	14/15	0.34	0.12	150,160,165,167	0
3	NAG	A	703	14/15	0.36	0.18	102,117,125,128	0
5	EDO	B	704	4/4	0.55	0.21	68,76,77,82	0
6	CL	E	602	1/1	0.58	0.20	97,97,97,97	0
3	NAG	B	703	14/15	0.63	0.19	141,165,178,180	0
5	EDO	A	704	4/4	0.68	0.26	60,63,70,71	0
3	NAG	B	705	14/15	0.74	0.12	139,159,171,173	0
3	NAG	C	601	14/15	0.79	0.10	136,141,147,150	0
3	NAG	A	701	14/15	0.80	0.10	96,99,105,108	0
3	NAG	B	701	14/15	0.80	0.12	98,103,111,120	0
4	ZN	B	702	1/1	0.94	0.07	100,100,100,100	0
4	ZN	A	702	1/1	0.96	0.07	91,91,91,91	0

6.5 Other polymers [i](#)

There are no such residues in this entry.