



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 06:14 AM UTC

PDB ID : 6E0V / pdb_00006e0v
Title : Apo crystal structure of the colanidase tailspike protein gp150 of Phage Phi92
Authors : Leiman, P.G.; Browning, C.; Gerardy-Schahn, R.; Shneider, M.M.; Plattner, M.; Schwarzer, D.
Deposited on : 2018-07-07
Resolution : 1.75 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

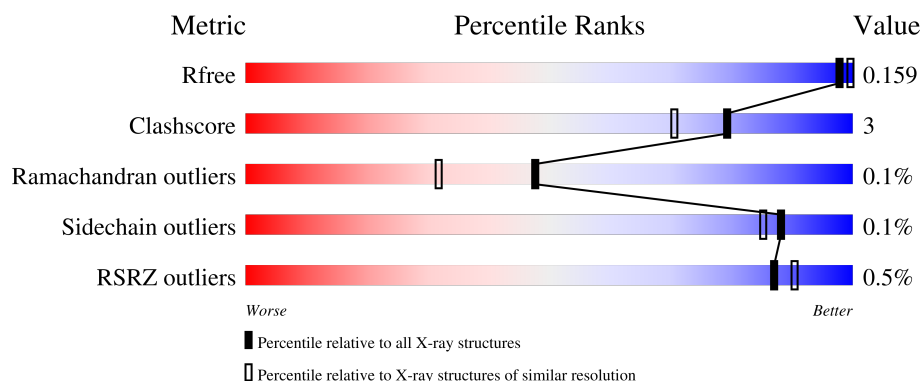
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	3183 (1.76-1.76)
Clashscore	190562	3299 (1.76-1.76)
Ramachandran outliers	187476	3274 (1.76-1.76)
Sidechain outliers	187428	3274 (1.76-1.76)
RSRZ outliers	180081	3183 (1.76-1.76)

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	626	
1	B	626	
1	C	626	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 30024 atoms, of which 13426 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 Bacteriophage Phi92 gp150.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	602	Total	C	H	N	O	S	0	9	0
			9052	2895	4438	782	912	25			
1	B	602	Total	C	H	N	O	S	0	11	0
			9067	2902	4443	781	916	25			
1	C	602	Total	C	H	N	O	S	0	10	0
			9057	2898	4433	782	919	25			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	179	SER	-	expression tag	UNP I7I026
B	179	SER	-	expression tag	UNP I7I026
C	179	SER	-	expression tag	UNP I7I026

- Molecule 2 is STRONTIUM ION (CCD ID: SR) (formula: Sr).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	7	Total	Sr	0	0
			7	7		
2	B	9	Total	Sr	0	0
			9	9		
2	C	8	Total	Sr	0	0
			8	8		

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

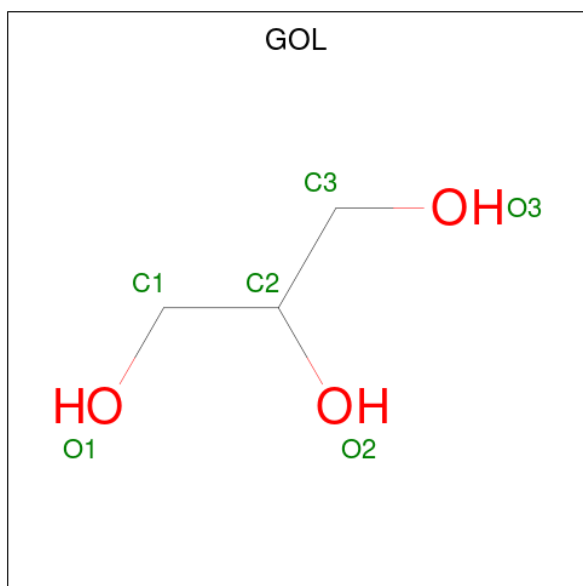
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total	Cl	0	0
			3	3		
3	B	3	Total	Cl	0	0
			3	3		

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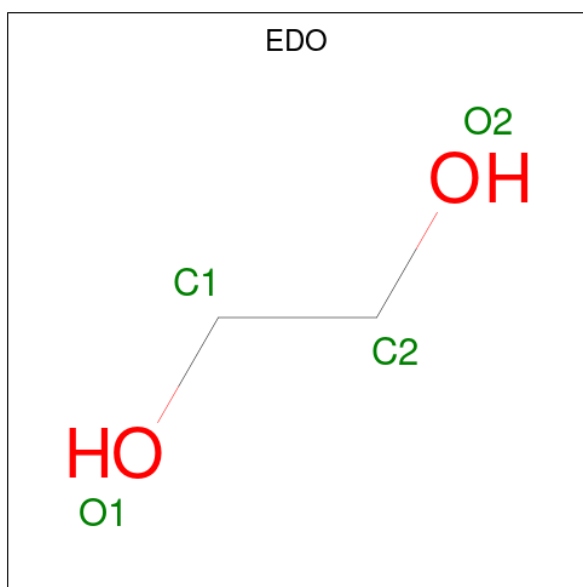
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	3	Total	Cl		0	0
			3	3			

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			14	3	8	3		
4	A	1	Total	C	H	O	0	0
			14	3	8	3		
4	A	1	Total	C	H	O	0	0
			14	3	8	3		
4	B	1	Total	C	H	O	0	0
			14	3	8	3		
4	B	1	Total	C	H	O	0	0
			14	3	8	3		
4	B	1	Total	C	H	O	0	0
			14	3	8	3		
4	C	1	Total	C	H	O	0	0
			14	3	8	3		
4	C	1	Total	C	H	O	0	0
			14	3	8	3		

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	H	O	0	0
			10	2	6	2		
5	A	1	Total	C	H	O	0	0
			10	2	6	2		
5	B	1	Total	C	H	O	0	0
			10	2	6	2		
5	B	1	Total	C	H	O	0	0
			10	2	6	2		
5	B	1	Total	C	H	O	0	0
			10	2	6	2		
5	C	1	Total	C	H	O	0	0
			10	2	6	2		
5	C	1	Total	C	H	O	0	0
			10	2	6	2		
5	C	1	Total	C	H	O	0	0
			10	2	6	2		

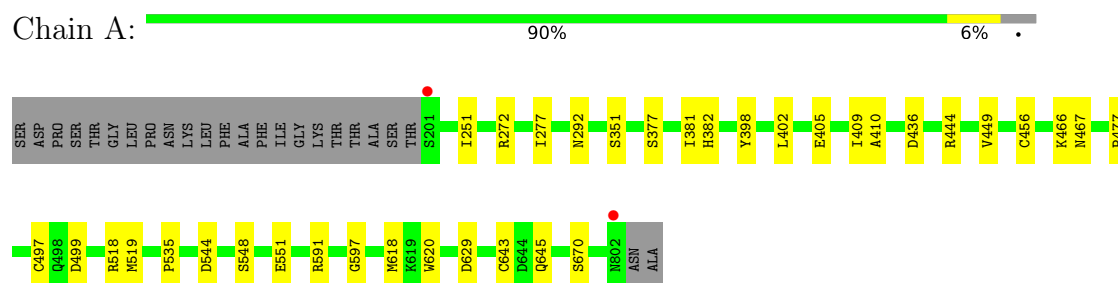
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	977	Total	O	0	0
			977	977		
6	B	908	Total	O	0	0
			908	908		
6	C	738	Total	O	0	0
			738	738		

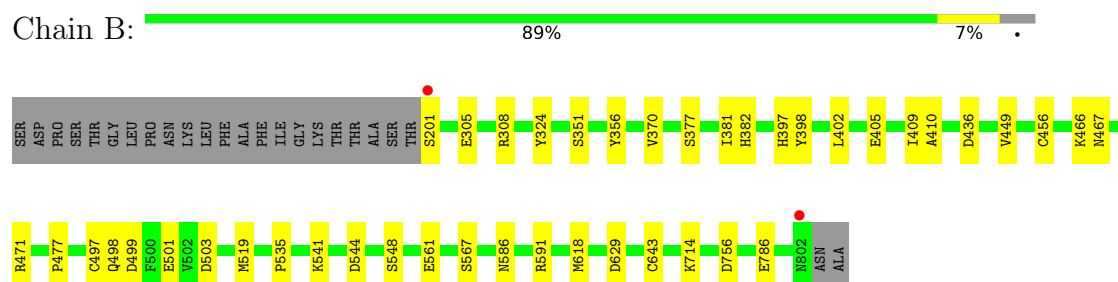
3 Residue-property plots [i](#)

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.

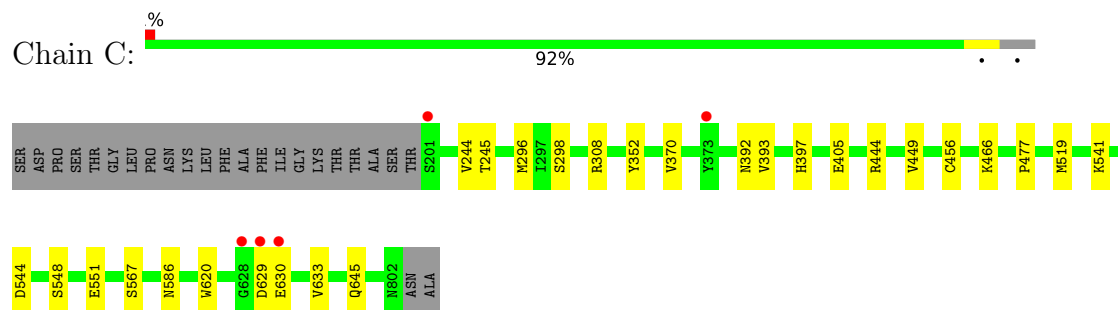
• Molecule 1: Bacteriophage Phi92 gp150



• Molecule 1: Bacteriophage Phi92 gp150



• Molecule 1: Bacteriophage Phi92 gp150



4 Data and refinement statistics

Property	Value	Source
Space group	P 3	Depositor
Cell constants a, b, c, α , β , γ	118.40Å 118.40Å 140.17Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.15 – 1.75 48.15 – 1.75	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.15-1.75) 100.0 (48.15-1.75)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.74 (at 1.75Å)	Xtriage
Refinement program	PHENIX (dev_3092: ???)	Depositor
R, R_{free}	0.134 , 0.163 0.131 , 0.159	Depositor DCC
R_{free} test set	4441 reflections (2.00%)	wwPDB-VP
Wilson B-factor (Å ²)	19.0	Xtriage
Anisotropy	0.263	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 64.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.010 for -h,-k,l 0.027 for h,-h-k,-l 0.016 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	30024	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.90% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	0.50	0/4739	0.61	0/6443
1	B	0.45	0/4755	0.57	0/6464
1	C	0.39	0/4731	0.53	0/6435
All	All	0.45	0/14225	0.57	0/19342

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

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	4614	4438	4438	25	0
1	B	4624	4443	4431	27	0
1	C	4624	4433	4430	22	0
2	A	7	0	0	0	0
2	B	9	0	0	0	0
2	C	8	0	0	0	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
3	C	3	0	0	0	0
4	A	18	24	24	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	18	24	24	0	0
4	C	12	16	16	0	0
5	A	8	12	12	0	0
5	B	12	18	17	1	0
5	C	12	18	18	0	0
6	A	977	0	0	4	7
6	B	908	0	0	7	4
6	C	738	0	0	10	4
All	All	16598	13426	13410	74	13

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 3.

All (74) 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:544[B]:ASP:OD1	6:B:1001:HOH:O	1.82	0.94
1:C:544[B]:ASP:OD1	6:C:1001:HOH:O	1.84	0.94
1:C:544[B]:ASP:OD2	6:C:1002:HOH:O	1.86	0.94
1:C:630[A]:GLU:O	6:C:1003:HOH:O	1.95	0.83
1:A:544[B]:ASP:OD1	6:A:1001:HOH:O	2.01	0.78
1:B:756:ASP:OD1	6:B:1002:HOH:O	2.04	0.75
1:B:629:ASP:OD2	6:B:1004:HOH:O	2.08	0.70
1:B:544[B]:ASP:OD2	6:B:1005:HOH:O	2.08	0.70
1:C:296:MET:HE2	1:C:298:SER:HB3	1.72	0.70
1:B:561[B]:GLU:OE2	6:B:1006:HOH:O	2.13	0.67
1:C:586:ASN:HB2	6:C:1525:HOH:O	1.95	0.66
1:C:352:TYR:OH	6:C:1005:HOH:O	2.10	0.66
1:C:298:SER:OG	6:C:1004:HOH:O	2.05	0.65
1:A:629:ASP:OD2	6:A:1002:HOH:O	2.14	0.64
1:C:629[B]:ASP:OD1	1:C:629[B]:ASP:N	2.31	0.60
1:C:629[B]:ASP:HB2	6:C:1168:HOH:O	2.03	0.58
1:A:272:ARG:NH2	1:A:292:ASN:OD1	2.31	0.58
1:B:586:ASN:HB2	6:B:1635:HOH:O	2.03	0.57
1:A:251:ILE:HG21	1:A:277:ILE:HD13	1.87	0.57
1:C:296:MET:CE	1:C:298:SER:HB3	2.38	0.52
1:B:714:LYS:NZ	6:B:1017:HOH:O	2.43	0.51
1:A:518:ARG:HE	1:A:551[B]:GLU:CD	2.19	0.50
1:C:392:ASN:O	1:C:393:VAL:HG22	2.11	0.50
1:A:251:ILE:CG2	1:A:277:ILE:HD13	2.42	0.49
1:C:456:CYS:O	1:C:477:PRO:HA	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:405:GLU:HA	1:B:449:VAL:O	2.14	0.48
1:B:456:CYS:O	1:B:477:PRO:HA	2.15	0.47
1:A:405[A]:GLU:HA	1:A:449:VAL:O	2.14	0.47
1:B:436[B]:ASP:OD1	5:B:916:EDO:O2	2.30	0.46
1:A:405[B]:GLU:HA	1:A:449:VAL:O	2.14	0.46
1:A:467[A]:ASN:HA	1:A:499:ASP:O	2.15	0.46
1:A:444:ARG:HA	1:A:466:LYS:O	2.15	0.46
1:A:518:ARG:NE	1:A:551[B]:GLU:OE2	2.48	0.45
1:B:466:LYS:HA	1:B:498:GLN:O	2.15	0.45
1:A:456:CYS:O	1:A:477:PRO:HA	2.16	0.45
1:A:519:MET:HB2	1:A:548:SER:HB3	1.98	0.45
1:C:519:MET:HB2	1:C:548:SER:HB3	1.99	0.45
1:A:670:SER:HA	6:A:1109:HOH:O	2.17	0.45
1:A:467[B]:ASN:HA	1:A:499:ASP:O	2.17	0.44
1:B:308[B]:ARG:HH12	1:B:356:TYR:HH	1.56	0.44
1:B:370:VAL:HA	1:B:397:HIS:CE1	2.52	0.44
1:A:618:MET:O	1:A:643:CYS:HA	2.18	0.44
1:B:382:HIS:HA	1:B:410:ALA:O	2.18	0.44
1:A:381:ILE:O	1:A:409:ILE:HA	2.18	0.44
1:C:244:VAL:HG23	1:C:245:THR:N	2.33	0.43
1:B:501:GLU:OE2	1:B:541:LYS:CE	2.66	0.43
1:C:620:TRP:O	1:C:645:GLN:HA	2.17	0.43
1:A:382:HIS:HA	1:A:410:ALA:O	2.19	0.43
1:B:497:CYS:O	1:B:535:PRO:HA	2.19	0.43
1:B:591:ARG:N	1:B:591:ARG:HD2	2.34	0.43
1:B:541:LYS:HA	1:B:567:SER:O	2.19	0.43
1:C:444:ARG:HA	1:C:466:LYS:O	2.19	0.43
1:B:618:MET:O	1:B:643:CYS:HA	2.19	0.42
1:C:633[A]:VAL:HG22	6:C:1100:HOH:O	2.19	0.42
1:C:370:VAL:HA	1:C:397:HIS:CE1	2.55	0.42
1:A:497:CYS:O	1:A:535:PRO:HA	2.20	0.42
1:B:519:MET:HB2	1:B:548:SER:HB3	2.00	0.42
1:B:398:TYR:CG	1:B:402:LEU:HB2	2.55	0.42
1:B:467:ASN:HA	1:B:499:ASP:O	2.19	0.42
1:C:405:GLU:HA	1:C:449:VAL:O	2.20	0.42
1:C:308:ARG:NH1	6:C:1027:HOH:O	2.52	0.41
1:B:351:SER:HA	1:B:377:SER:O	2.20	0.41
1:A:591:ARG:N	1:A:591:ARG:HD2	2.36	0.41
1:A:436[B]:ASP:OD2	6:A:1003:HOH:O	2.21	0.41
1:C:551:GLU:OE1	6:C:1006:HOH:O	2.22	0.41
1:A:351:SER:HA	1:A:377:SER:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:398:TYR:CG	1:A:402:LEU:HB2	2.56	0.41
1:A:620:TRP:O	1:A:645:GLN:HA	2.21	0.41
1:B:377:SER:HA	1:B:405:GLU:O	2.21	0.41
1:C:541:LYS:HA	1:C:567:SER:O	2.21	0.40
1:B:471:ARG:HA	1:B:503:ASP:O	2.22	0.40
1:B:305:GLU:HA	1:B:324:TYR:O	2.21	0.40
1:B:381:ILE:O	1:B:409:ILE:HA	2.21	0.40

All (13) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:1069:HOH:O	6:A:1607:HOH:O[3_655]	1.84	0.36
6:B:1488:HOH:O	6:B:1510:HOH:O[3_555]	1.95	0.25
6:C:1432:HOH:O	6:C:1563:HOH:O[2_655]	1.96	0.24
6:A:1501:HOH:O	6:A:1703:HOH:O[3_655]	2.00	0.20
6:A:1438:HOH:O	6:A:1684:HOH:O[3_655]	2.01	0.19
6:C:1560:HOH:O	6:C:1664:HOH:O[2_655]	2.03	0.17
6:A:1264:HOH:O	6:A:1746:HOH:O[2_545]	2.08	0.12
6:B:1649:HOH:O	6:B:1777:HOH:O[2_555]	2.09	0.11
6:C:1229:HOH:O	6:C:1519:HOH:O[3_665]	2.09	0.11
6:B:1749:HOH:O	6:B:1837:HOH:O[3_555]	2.13	0.07
6:A:1397:HOH:O	6:B:1571:HOH:O[2_656]	2.15	0.05
6:A:1241:HOH:O	6:A:1241:HOH:O[2_545]	2.19	0.01
6:A:1661:HOH:O	6:C:1574:HOH:O[2_655]	2.19	0.01

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	609/626 (97%)	584 (96%)	24 (4%)	1 (0%)	43 27

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	611/626 (98%)	585 (96%)	26 (4%)	0	100	100
1	C	610/626 (97%)	581 (95%)	29 (5%)	0	100	100
All	All	1830/1878 (97%)	1750 (96%)	79 (4%)	1 (0%)	48	32

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	597	GLY

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	499/509 (98%)	499 (100%)	0	100	100
1	B	501/509 (98%)	498 (99%)	3 (1%)	78	71
1	C	499/509 (98%)	499 (100%)	0	100	100
All	All	1499/1527 (98%)	1496 (100%)	3 (0%)	88	84

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	201	SER
1	B	786[A]	GLU
1	B	786[B]	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	236	GLN
1	A	445	ASN
1	A	568	ASN
1	A	587	ASN
1	A	726	GLN

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Mol	Chain	Res	Type
1	A	794	ASN
1	B	261	ASN
1	B	364	GLN
1	B	542	ASN
1	B	568	ASN
1	B	587	ASN
1	B	614	GLN
1	B	726	GLN
1	C	249	GLN
1	C	408	HIS
1	C	498	GLN
1	C	568	ASN
1	C	587	ASN
1	C	614	GLN
1	C	726	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](#)

Of 49 ligands modelled in this entry, 33 are monoatomic - leaving 16 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	914	-	3,3,3	0.51	0	2,2,2	0.30	0
4	GOL	A	913	-	5,5,5	1.23	1 (20%)	5,5,5	1.12	0
5	EDO	C	915	-	3,3,3	0.43	0	2,2,2	0.36	0
5	EDO	B	918	-	3,3,3	0.58	0	2,2,2	0.21	0
5	EDO	C	916	-	3,3,3	0.39	0	2,2,2	0.54	0
5	EDO	B	917	-	3,3,3	0.46	0	2,2,2	0.57	0
5	EDO	C	914	-	3,3,3	0.44	0	2,2,2	0.41	0
4	GOL	B	914	-	5,5,5	0.93	0	5,5,5	0.89	0
5	EDO	B	916	2	3,3,3	0.45	0	2,2,2	0.36	0
4	GOL	C	913	-	5,5,5	0.96	0	5,5,5	1.00	0
4	GOL	B	913	-	5,5,5	0.71	0	5,5,5	1.14	0
4	GOL	A	911	-	5,5,5	0.65	0	5,5,5	1.00	0
4	GOL	A	912	-	5,5,5	0.78	0	5,5,5	1.09	0
4	GOL	B	915	-	5,5,5	1.06	0	5,5,5	1.36	1 (20%)
5	EDO	A	915	-	3,3,3	0.30	0	2,2,2	0.49	0
4	GOL	C	912	-	5,5,5	1.12	0	5,5,5	1.00	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	914	-	-	0/1/1/1	-
4	GOL	A	913	-	-	0/4/4/4	-
5	EDO	C	915	-	-	0/1/1/1	-
5	EDO	B	918	-	-	1/1/1/1	-
5	EDO	C	916	-	-	0/1/1/1	-
5	EDO	B	917	-	-	1/1/1/1	-
5	EDO	C	914	-	-	0/1/1/1	-
4	GOL	B	914	-	-	0/4/4/4	-
5	EDO	B	916	2	-	0/1/1/1	-
4	GOL	C	913	-	-	2/4/4/4	-
4	GOL	B	913	-	-	0/4/4/4	-
4	GOL	A	911	-	-	2/4/4/4	-
4	GOL	A	912	-	-	2/4/4/4	-
4	GOL	B	915	-	-	0/4/4/4	-
5	EDO	A	915	-	-	1/1/1/1	-
4	GOL	C	912	-	-	0/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	913	GOL	C3-C2	2.20	1.60	1.51

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
4	B	915	GOL	C3-C2-C1	-2.13	103.99	111.80

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	911	GOL	C1-C2-C3-O3
4	A	912	GOL	C1-C2-C3-O3
4	C	913	GOL	O1-C1-C2-C3
4	C	913	GOL	O1-C1-C2-O2
5	A	915	EDO	O1-C1-C2-O2
4	A	911	GOL	O2-C2-C3-O3
5	B	917	EDO	O1-C1-C2-O2
4	A	912	GOL	O2-C2-C3-O3
5	B	918	EDO	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	916	EDO	1	0

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, 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	602/626 (96%)	-0.98	2 (0%)	90 92	8, 19, 35, 92	9 (1%)
1	B	602/626 (96%)	-0.81	2 (0%)	90 92	10, 24, 37, 77	10 (1%)
1	C	602/626 (96%)	-0.49	5 (0%)	82 86	10, 28, 55, 94	10 (1%)
All	All	1806/1878 (96%)	-0.76	9 (0%)	87 90	8, 23, 49, 94	29 (1%)

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	628[A]	GLY	5.4
1	A	201	SER	3.6
1	C	373	TYR	2.7
1	C	629[A]	ASP	2.5
1	B	802	ASN	2.4
1	A	802	ASN	2.3
1	C	201	SER	2.3
1	C	630[A]	GLU	2.1
1	B	201	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

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	EDO	B	917	4/4	0.79	0.23	56,67,67,69	0
5	EDO	C	914	4/4	0.81	0.20	63,75,76,77	0
4	GOL	B	913	6/6	0.84	0.13	52,62,65,66	0
5	EDO	A	914	4/4	0.86	0.13	44,53,55,56	0
5	EDO	B	918	4/4	0.88	0.13	36,43,51,51	0
4	GOL	A	911	6/6	0.89	0.12	45,54,56,56	0
5	EDO	A	915	4/4	0.89	0.12	47,56,57,59	0
5	EDO	B	916	4/4	0.89	0.14	52,62,64,65	0
5	EDO	C	915	4/4	0.91	0.12	36,43,49,52	0
4	GOL	C	912	6/6	0.92	0.10	38,45,48,51	0
4	GOL	C	913	6/6	0.92	0.11	39,47,53,54	0
4	GOL	B	914	6/6	0.92	0.10	34,42,46,50	0
2	SR	B	906	1/1	0.93	0.09	62,62,62,62	1
5	EDO	C	916	4/4	0.93	0.11	24,40,48,51	0
4	GOL	A	912	6/6	0.94	0.08	32,44,53,56	0
4	GOL	B	915	6/6	0.95	0.08	27,38,43,46	0
2	SR	A	907	1/1	0.97	0.06	65,65,65,65	1
2	SR	B	907	1/1	0.97	0.06	60,60,60,60	1
4	GOL	A	913	6/6	0.97	0.10	23,32,37,39	0
2	SR	B	909	1/1	0.97	0.07	64,64,64,64	1
2	SR	B	908	1/1	0.98	0.04	36,36,36,36	1
2	SR	A	906	1/1	0.99	0.03	30,30,30,30	1
2	SR	A	904	1/1	0.99	0.04	28,28,28,28	1
2	SR	A	905	1/1	0.99	0.02	27,27,27,27	1
2	SR	C	906	1/1	0.99	0.03	39,39,39,39	1
2	SR	C	907	1/1	0.99	0.05	44,44,44,44	1
2	SR	C	908	1/1	0.99	0.05	43,43,43,43	1
3	CL	B	911	1/1	0.99	0.05	39,39,39,39	0
3	CL	C	910	1/1	0.99	0.03	32,32,32,32	0
3	CL	B	912	1/1	1.00	0.02	23,23,23,23	0
3	CL	C	909	1/1	1.00	0.02	29,29,29,29	1
2	SR	A	902	1/1	1.00	0.03	18,18,18,18	1
3	CL	C	911	1/1	1.00	0.02	28,28,28,28	0
2	SR	A	903	1/1	1.00	0.03	26,26,26,26	1
2	SR	A	901	1/1	1.00	0.01	15,15,15,15	1
2	SR	B	901	1/1	1.00	0.04	17,17,17,17	1
2	SR	C	901	1/1	1.00	0.07	22,22,22,22	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	SR	C	902	1/1	1.00	0.04	23,23,23,23	1
2	SR	C	903	1/1	1.00	0.03	34,34,34,34	1
2	SR	C	904	1/1	1.00	0.02	27,27,27,27	1
2	SR	C	905	1/1	1.00	0.05	36,36,36,36	1
2	SR	B	902	1/1	1.00	0.04	26,26,26,26	1
2	SR	B	903	1/1	1.00	0.03	29,29,29,29	1
2	SR	B	904	1/1	1.00	0.03	40,40,40,40	1
3	CL	A	908	1/1	1.00	0.02	17,17,17,17	0
3	CL	A	909	1/1	1.00	0.01	25,25,25,25	1
3	CL	A	910	1/1	1.00	0.02	31,31,31,31	0
3	CL	B	910	1/1	1.00	0.01	26,26,26,26	1
2	SR	B	905	1/1	1.00	0.03	27,27,27,27	1

6.5 Other polymers [i](#)

There are no such residues in this entry.