



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:03 AM UTC

PDB ID : 3EE7 / pdb_00003ee7
Title : Crystal Structure of SARS-CoV nsp9 G104E
Authors : Miknis, Z.J.; Donaldson, E.F.; Umland, T.C.; Rimmer, R.; Baric, R.S.;
Schultz, L.W.
Deposited on : 2008-09-04
Resolution : 2.60 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

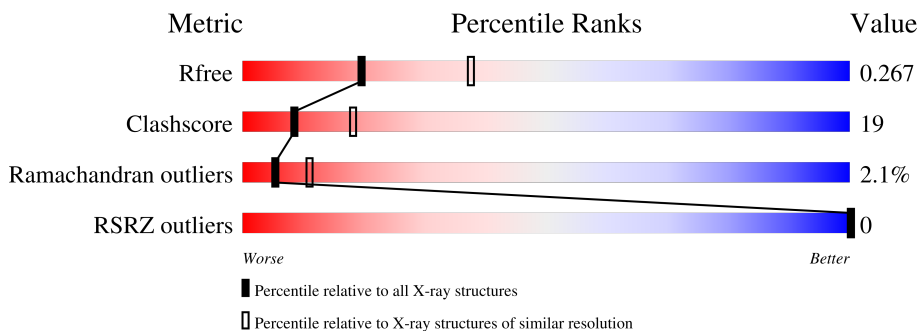
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	121	
1	B	121	
1	C	121	
1	D	121	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3710 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 Replicase polypeptide 1a.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	106	825	524	143	153	5	0	0	0
1	B	115	899	567	161	166	5	0	0	0
1	C	110	861	545	150	161	5	0	0	0
1	D	112	873	553	152	163	5	0	0	0

There are 36 discrepancies between the modelled and reference sequences:

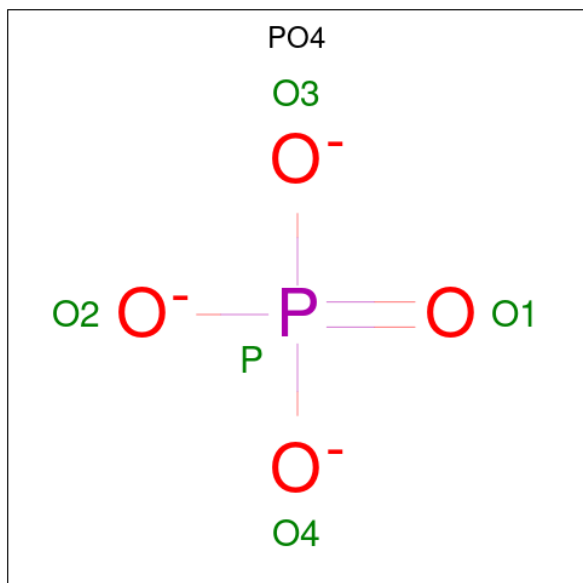
Chain	Residue	Modelled	Actual	Comment	Reference
A	104	GLU	GLY	engineered mutation	UNP P0C6U8
A	114	LEU	-	expression tag	UNP P0C6U8
A	115	GLU	-	expression tag	UNP P0C6U8
A	116	HIS	-	expression tag	UNP P0C6U8
A	117	HIS	-	expression tag	UNP P0C6U8
A	118	HIS	-	expression tag	UNP P0C6U8
A	119	HIS	-	expression tag	UNP P0C6U8
A	120	HIS	-	expression tag	UNP P0C6U8
A	121	HIS	-	expression tag	UNP P0C6U8
B	104	GLU	GLY	engineered mutation	UNP P0C6U8
B	114	LEU	-	expression tag	UNP P0C6U8
B	115	GLU	-	expression tag	UNP P0C6U8
B	116	HIS	-	expression tag	UNP P0C6U8
B	117	HIS	-	expression tag	UNP P0C6U8
B	118	HIS	-	expression tag	UNP P0C6U8
B	119	HIS	-	expression tag	UNP P0C6U8
B	120	HIS	-	expression tag	UNP P0C6U8
B	121	HIS	-	expression tag	UNP P0C6U8
C	104	GLU	GLY	engineered mutation	UNP P0C6U8
C	114	LEU	-	expression tag	UNP P0C6U8
C	115	GLU	-	expression tag	UNP P0C6U8

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Chain	Residue	Modelled	Actual	Comment	Reference
C	116	HIS	-	expression tag	UNP P0C6U8
C	117	HIS	-	expression tag	UNP P0C6U8
C	118	HIS	-	expression tag	UNP P0C6U8
C	119	HIS	-	expression tag	UNP P0C6U8
C	120	HIS	-	expression tag	UNP P0C6U8
C	121	HIS	-	expression tag	UNP P0C6U8
D	104	GLU	GLY	engineered mutation	UNP P0C6U8
D	114	LEU	-	expression tag	UNP P0C6U8
D	115	GLU	-	expression tag	UNP P0C6U8
D	116	HIS	-	expression tag	UNP P0C6U8
D	117	HIS	-	expression tag	UNP P0C6U8
D	118	HIS	-	expression tag	UNP P0C6U8
D	119	HIS	-	expression tag	UNP P0C6U8
D	120	HIS	-	expression tag	UNP P0C6U8
D	121	HIS	-	expression tag	UNP P0C6U8

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



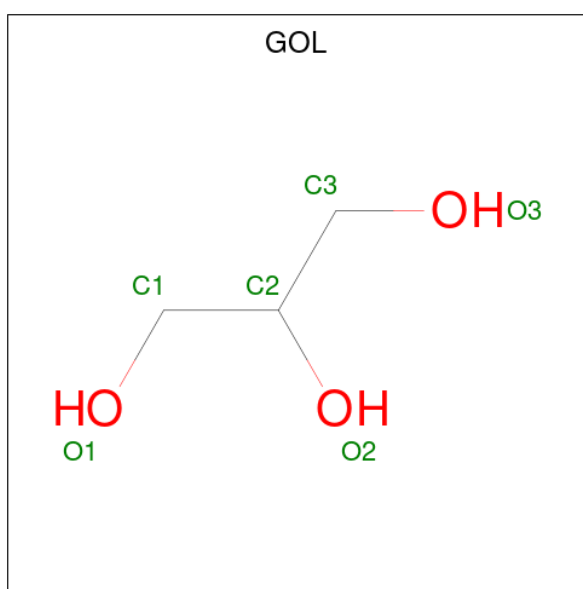
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O P 5 4 1	0	0
2	A	1	Total O P 5 4 1	0	0
2	A	1	Total O P 5 4 1	0	0
2	B	1	Total O P 5 4 1	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	1	Total C O 6 3 3	0	0
3	C	1	Total C O 6 3 3	0	0
3	C	1	Total C O 6 3 3	0	0
3	C	1	Total C O 6 3 3	0	0
3	D	1	Total C O 6 3 3	0	0
3	D	1	Total C O 6 3 3	0	0
3	D	1	Total C O 6 3 3	0	0
3	D	1	Total C O 6 3 3	0	0
3	D	1	Total C O 6 3 3	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	27	Total O 27 27	0	0
4	B	25	Total O 25 25	0	0
4	C	35	Total O 35 35	0	0
4	D	29	Total O 29 29	0	0

V110	HIS
R111	HIS
L112	HIS
Q113	HIS
H116	HIS
	HIS
	HIS
	HIS
	HIS

4 Data and refinement statistics i

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	91.84Å 91.84Å 84.22Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	35.96 – 2.60 35.96 – 2.60	Depositor EDS
% Data completeness (in resolution range)	98.8 (35.96-2.60) 98.8 (35.96-2.60)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.78 (at 2.61Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.216 , 0.268 0.215 , 0.267	Depositor DCC
R_{free} test set	2390 reflections (9.90%)	wwPDB-VP
Wilson B-factor (Å ²)	61.9	Xtrriage
Anisotropy	0.128	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 53.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.024 for -h,-k,l 0.479 for h,-h-k,-l 0.023 for -k,-h,-l	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	3710	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.21% 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: GOL, PO4

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	0.41	0/840	0.87	0/1138
1	B	0.44	0/920	0.93	2/1248 (0.2%)
1	C	0.48	0/878	1.04	4/1190 (0.3%)
1	D	0.41	0/890	0.87	0/1206
All	All	0.43	0/3528	0.93	6/4782 (0.1%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	34	ASN	N-CA-C	-8.22	100.36	110.88
1	B	70	GLU	N-CA-C	-6.36	102.82	110.13
1	B	54	ALA	N-CA-C	-6.18	99.64	109.59
1	C	28	ALA	N-CA-C	5.92	116.91	108.74
1	C	70	GLU	N-CA-C	-5.27	103.49	110.40
1	C	18	THR	N-CA-C	-5.06	106.62	112.89

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	825	0	830	39	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	899	0	889	35	0
1	C	861	0	861	29	0
1	D	873	0	875	36	0
2	A	15	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	15	0	0	0	0
3	A	30	0	40	5	0
3	B	12	0	16	2	0
3	C	24	0	32	1	0
3	D	30	0	40	6	0
4	A	27	0	0	1	0
4	B	25	0	0	2	0
4	C	35	0	0	0	0
4	D	29	0	0	1	0
All	All	3710	0	3583	136	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 19.

All (136) 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:D:41:VAL:HG12	1:D:91:ILE:HD11	1.37	1.03
1:B:94:LEU:HD12	1:B:99:ARG:HG3	1.46	0.97
1:D:41:VAL:O	1:D:91:ILE:HD12	1.64	0.97
1:D:41:VAL:O	1:D:91:ILE:CD1	2.22	0.86
1:A:75:PHE:CE1	1:A:77:THR:CG2	2.61	0.84
1:A:75:PHE:HE1	1:A:77:THR:CG2	1.92	0.82
1:C:79:THR:HG22	1:C:81:LYS:H	1.45	0.82
1:A:75:PHE:CE1	1:A:77:THR:HG23	2.18	0.78
1:A:57:PRO:HA	1:A:64:THR:HG22	1.66	0.74
1:B:15:ALA:HA	1:B:25:ASP:O	1.87	0.74
1:D:41:VAL:CG1	1:D:91:ILE:HD11	2.15	0.73
1:D:111:ARG:C	1:D:112:LEU:HD22	2.12	0.73
1:C:46:SER:HA	3:C:123:GOL:H32	1.72	0.70
1:D:41:VAL:C	1:D:91:ILE:HD12	2.15	0.70
1:A:41:VAL:H	3:A:127:GOL:H12	1.56	0.69
1:D:78:ASP:HB2	1:D:112:LEU:HD23	1.74	0.69
1:C:79:THR:HG23	1:C:80:PRO:HD2	1.73	0.69
1:B:79:THR:HB	1:B:80:PRO:HD2	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:18:THR:HG22	1:A:50:ASP:O	1.93	0.68
1:A:5:SER:HB2	1:A:6:PRO:HD2	1.76	0.67
1:B:7:VAL:HG23	1:B:101:MET:HE1	1.76	0.66
1:D:41:VAL:C	1:D:91:ILE:CD1	2.70	0.65
3:A:129:GOL:H2	1:B:95:ASN:HD22	1.63	0.64
1:C:79:THR:HG22	1:C:81:LYS:N	2.12	0.64
1:A:75:PHE:HE1	1:A:77:THR:HG21	1.63	0.64
1:C:12:MET:HE2	1:C:56:PHE:HE2	1.63	0.62
1:A:110:VAL:HG12	1:A:111:ARG:N	2.13	0.62
1:A:44:LEU:HD11	1:A:54:ALA:HB2	1.82	0.62
1:B:5:SER:N	1:B:6:PRO:CD	2.63	0.61
1:C:79:THR:HG23	1:C:80:PRO:CD	2.32	0.59
1:A:85:VAL:O	1:A:86:LYS:HG3	2.04	0.58
1:C:12:MET:HE2	1:C:56:PHE:CE2	2.39	0.58
1:A:44:LEU:HD12	1:A:69:LEU:HD11	1.85	0.57
1:C:15:ALA:HA	1:C:25:ASP:O	2.04	0.57
1:C:60:ASP:O	1:C:61:GLY:C	2.47	0.57
1:D:44:LEU:HD11	1:D:54:ALA:HB2	1.86	0.57
1:D:45:LEU:HD11	1:D:75:PHE:CE2	2.40	0.56
1:D:22:ALA:O	1:D:24:THR:HG23	2.06	0.56
1:D:18:THR:HG22	1:D:50:ASP:O	2.06	0.56
1:A:51:LEU:HB2	1:A:89:TYR:CZ	2.41	0.56
1:A:75:PHE:CE1	1:A:77:THR:HG21	2.40	0.56
1:A:59:SER:HB3	4:A:151:HOH:O	2.06	0.55
1:B:96:ASN:HA	1:B:99:ARG:HD2	1.87	0.55
1:A:11:GLN:HG2	1:A:29:LEU:HD11	1.88	0.55
1:D:106:LEU:HA	1:D:109:THR:HG22	1.88	0.54
1:A:96:ASN:HA	1:A:99:ARG:HD2	1.89	0.54
1:A:67:THR:HG21	1:A:91:ILE:HD12	1.89	0.54
1:B:25:ASP:O	1:B:27:ASN:N	2.40	0.54
1:A:92:LYS:HD3	1:C:62:THR:HA	1.90	0.54
1:B:49:GLN:HB3	1:B:87:TYR:CZ	2.44	0.53
1:D:96:ASN:HA	1:D:99:ARG:HD2	1.89	0.53
1:D:59:SER:HB2	3:D:125:GOL:H2	1.91	0.53
1:B:84:LYS:HZ3	3:B:123:GOL:H11	1.73	0.53
1:C:96:ASN:HA	1:C:99:ARG:HD2	1.89	0.53
1:D:106:LEU:HA	1:D:109:THR:CG2	2.38	0.53
1:A:95:ASN:HD22	3:A:125:GOL:H32	1.75	0.52
1:C:7:VAL:HG12	1:C:101:MET:HE1	1.91	0.52
1:A:80:PRO:HG3	1:A:111:ARG:NH1	2.25	0.52
1:B:35:SER:O	1:B:36:LYS:HB2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:55:ARG:HG2	1:C:55:ARG:HH11	1.75	0.51
1:C:79:THR:HB	1:C:82:GLY:O	2.10	0.51
1:D:72:PRO:HB3	1:D:89:TYR:CE2	2.46	0.51
1:C:72:PRO:HB3	1:C:89:TYR:CE2	2.45	0.51
1:A:68:GLU:OE2	1:A:92:LYS:HD2	2.11	0.51
1:A:104:GLU:HG2	1:B:101:MET:HE2	1.94	0.50
1:D:38:GLY:HA2	3:D:125:GOL:H32	1.92	0.50
1:C:18:THR:HG22	1:C:50:ASP:O	2.12	0.50
1:B:5:SER:O	1:B:7:VAL:N	2.45	0.50
1:C:49:GLN:HB3	1:C:87:TYR:CZ	2.47	0.50
1:B:110:VAL:O	1:B:110:VAL:HG23	2.12	0.50
1:A:67:THR:CG2	1:A:91:ILE:HD12	2.42	0.49
1:B:113:GLN:OE1	1:B:117:HIS:HB3	2.12	0.49
1:A:41:VAL:HG23	3:A:127:GOL:H32	1.93	0.49
1:C:60:ASP:O	1:C:62:THR:HG23	2.13	0.49
1:A:110:VAL:CG1	1:A:111:ARG:N	2.76	0.48
1:D:49:GLN:H	3:D:127:GOL:H12	1.78	0.48
1:B:109:THR:HG23	1:B:119:HIS:NE2	2.29	0.48
1:C:41:VAL:O	1:C:91:ILE:HD13	2.14	0.48
1:B:39:ARG:HH11	1:B:39:ARG:HG3	1.78	0.48
1:C:5:SER:N	1:C:6:PRO:CD	2.77	0.48
1:B:10:ARG:NH1	4:B:134:HOH:O	2.46	0.47
1:A:45:LEU:HD23	1:A:46:SER:N	2.29	0.47
1:A:72:PRO:HB3	1:A:89:TYR:CE2	2.50	0.47
1:B:94:LEU:CD1	1:B:99:ARG:HG3	2.32	0.47
1:A:41:VAL:N	3:A:127:GOL:H12	2.28	0.47
1:B:94:LEU:HD13	1:B:95:ASN:N	2.29	0.47
1:D:106:LEU:O	1:D:109:THR:HG22	2.15	0.47
1:B:94:LEU:HD11	1:B:98:ASN:HB2	1.97	0.46
1:D:30:ALA:HB2	1:D:44:LEU:CD2	2.45	0.46
1:D:111:ARG:O	1:D:112:LEU:HD22	2.15	0.46
1:C:33:ASN:HB3	1:C:35:SER:OG	2.16	0.46
1:D:45:LEU:HD11	1:D:75:PHE:CZ	2.51	0.46
1:C:111:ARG:NH2	1:C:115:GLU:O	2.48	0.45
1:A:11:GLN:HE21	1:A:31:TYR:HD2	1.62	0.45
1:D:49:GLN:HA	1:D:89:TYR:OH	2.16	0.45
1:B:24:THR:O	1:B:25:ASP:HB3	2.17	0.45
1:D:106:LEU:CA	1:D:109:THR:HG22	2.47	0.45
1:A:30:ALA:HB2	1:A:44:LEU:CD2	2.47	0.45
1:A:11:GLN:CG	1:A:29:LEU:HD11	2.47	0.45
1:D:55:ARG:HG3	1:D:66:TYR:CZ	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:6:PRO:C	1:B:8:ALA:H	2.25	0.44
1:D:57:PRO:HA	1:D:64:THR:HA	1.99	0.44
1:A:44:LEU:HD11	1:A:54:ALA:CB	2.47	0.44
1:C:42:LEU:HD23	1:C:98:ASN:HB3	1.98	0.44
1:B:94:LEU:CD1	1:B:98:ASN:HB2	2.47	0.44
1:A:110:VAL:HG12	1:A:111:ARG:H	1.82	0.44
1:B:94:LEU:HD13	1:B:95:ASN:O	2.18	0.44
1:B:10:ARG:NH2	4:B:126:HOH:O	2.49	0.43
1:D:45:LEU:HD11	1:D:75:PHE:HE2	1.82	0.43
1:A:44:LEU:HD12	1:A:69:LEU:CD1	2.49	0.43
1:B:45:LEU:HD22	1:B:106:LEU:HD11	2.00	0.43
1:B:72:PRO:HB3	1:B:89:TYR:CE2	2.54	0.42
1:A:58:LYS:H	1:A:64:THR:HA	1.83	0.42
1:C:55:ARG:HG2	1:C:55:ARG:NH1	2.34	0.42
1:D:4:LEU:N	4:D:157:HOH:O	2.52	0.42
1:B:33:ASN:OD1	1:B:33:ASN:C	2.61	0.42
1:C:5:SER:N	1:C:6:PRO:HD3	2.34	0.42
1:C:20:GLN:HG2	1:C:66:TYR:CD2	2.54	0.42
1:C:113:GLN:HB3	1:D:113:GLN:NE2	2.35	0.42
1:D:42:LEU:N	1:D:42:LEU:HD12	2.34	0.42
1:B:84:LYS:NZ	3:B:123:GOL:H31	2.34	0.42
1:C:96:ASN:HD22	3:D:128:GOL:C1	2.33	0.42
1:D:95:ASN:HB2	3:D:128:GOL:O3	2.20	0.42
1:A:55:ARG:HB3	1:A:66:TYR:CE2	2.55	0.41
1:D:51:LEU:HB2	1:D:89:TYR:CZ	2.55	0.41
1:C:96:ASN:HD22	3:D:128:GOL:H11	1.84	0.41
1:B:19:THR:H	1:B:22:ALA:HB3	1.84	0.41
1:B:84:LYS:HB2	1:B:84:LYS:HE3	1.88	0.41
1:A:94:LEU:HD23	1:A:99:ARG:HG3	2.01	0.41
1:D:11:GLN:HB3	1:D:29:LEU:HD11	2.02	0.41
1:A:33:ASN:OD1	1:A:33:ASN:C	2.64	0.40
1:B:36:LYS:O	1:B:38:GLY:N	2.54	0.40
1:B:75:PHE:CZ	1:B:86:LYS:HB2	2.56	0.40
1:D:94:LEU:HD23	1:D:99:ARG:HG3	2.04	0.40
1:B:111:ARG:HH12	1:B:117:HIS:H	1.69	0.40
1:D:45:LEU:CD1	1:D:75:PHE:HE2	2.34	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	100/121 (83%)	90 (90%)	9 (9%)	1 (1%)	12	28
1	B	113/121 (93%)	98 (87%)	9 (8%)	6 (5%)	1	1
1	C	106/121 (88%)	99 (93%)	7 (7%)	0	100	100
1	D	108/121 (89%)	98 (91%)	8 (7%)	2 (2%)	6	13
All	All	427/484 (88%)	385 (90%)	33 (8%)	9 (2%)	5	11

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	58	LYS
1	B	26	ASP
1	B	25	ASP
1	B	116	HIS
1	D	23	CYS
1	B	37	GLY
1	B	118	HIS
1	B	6	PRO
1	D	110	VAL

5.3.2 Protein sidechains [i](#)

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

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](#)

24 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
3	GOL	C	123	-	5,5,5	0.48	0	5,5,5	0.36	0
3	GOL	A	126	-	5,5,5	0.29	0	5,5,5	0.34	0
3	GOL	A	129	-	5,5,5	0.28	0	5,5,5	0.30	0
3	GOL	D	125	-	5,5,5	0.38	0	5,5,5	0.35	0
3	GOL	D	128	-	5,5,5	0.28	0	5,5,5	0.39	0
3	GOL	D	129	-	5,5,5	0.29	0	5,5,5	0.32	0
3	GOL	A	125	-	5,5,5	0.42	0	5,5,5	0.30	0
3	GOL	C	124	-	5,5,5	0.43	0	5,5,5	0.34	0
2	PO4	D	123	-	4,4,4	1.58	0	6,6,6	0.47	0
3	GOL	B	123	-	5,5,5	0.19	0	5,5,5	0.29	0
3	GOL	C	126	-	5,5,5	0.33	0	5,5,5	0.28	0
3	GOL	D	127	-	5,5,5	0.15	0	5,5,5	0.33	0
2	PO4	A	122	-	4,4,4	1.69	0	6,6,6	0.47	0
2	PO4	C	122	-	4,4,4	1.66	0	6,6,6	0.46	0
3	GOL	A	128	-	5,5,5	0.21	0	5,5,5	0.40	0
3	GOL	C	125	-	5,5,5	0.33	0	5,5,5	0.27	0
2	PO4	A	124	-	4,4,4	1.66	0	6,6,6	0.46	0
3	GOL	A	127	-	5,5,5	0.42	0	5,5,5	0.32	0
2	PO4	B	122	-	4,4,4	1.84	2 (50%)	6,6,6	0.49	0
3	GOL	D	126	-	5,5,5	0.42	0	5,5,5	0.31	0
2	PO4	A	123	-	4,4,4	1.72	0	6,6,6	0.45	0
2	PO4	D	124	-	4,4,4	1.66	1 (25%)	6,6,6	0.45	0
2	PO4	D	122	-	4,4,4	1.78	1 (25%)	6,6,6	0.47	0
3	GOL	B	124	-	5,5,5	0.23	0	5,5,5	0.34	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
3	GOL	C	123	-	-	0/4/4/4	-
3	GOL	B	123	-	-	0/4/4/4	-
3	GOL	A	127	-	-	0/4/4/4	-
3	GOL	D	126	-	-	0/4/4/4	-
3	GOL	C	124	-	-	0/4/4/4	-
3	GOL	A	129	-	-	0/4/4/4	-
3	GOL	C	125	-	-	0/4/4/4	-
3	GOL	D	125	-	-	0/4/4/4	-
3	GOL	D	128	-	-	0/4/4/4	-
3	GOL	C	126	-	-	0/4/4/4	-
3	GOL	D	129	-	-	0/4/4/4	-
3	GOL	D	127	-	-	0/4/4/4	-
3	GOL	A	125	-	-	0/4/4/4	-
3	GOL	B	124	-	-	0/4/4/4	-
3	GOL	A	128	-	-	0/4/4/4	-
3	GOL	A	126	-	-	0/4/4/4	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	122	PO4	P-O2	-2.16	1.48	1.54
2	D	122	PO4	P-O2	-2.09	1.48	1.54
2	B	122	PO4	P-O4	-2.08	1.48	1.54
2	D	124	PO4	P-O2	-2.07	1.48	1.54

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	123	GOL	1	0
3	A	129	GOL	1	0
3	D	125	GOL	2	0
3	D	128	GOL	3	0
3	A	125	GOL	1	0
3	B	123	GOL	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	127	GOL	1	0
3	A	127	GOL	3	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	106/121 (87%)	-1.22	0 100 100	35, 58, 89, 100	0
1	B	115/121 (95%)	-1.25	0 100 100	37, 54, 100, 100	0
1	C	110/121 (90%)	-1.24	0 100 100	36, 54, 96, 100	0
1	D	112/121 (92%)	-1.25	0 100 100	35, 59, 92, 100	0
All	All	443/484 (91%)	-1.24	0 100 100	35, 57, 97, 100	0

There are no RSRZ outliers to report.

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	GOL	A	129	6/6	0.96	0.10	78,78,78,78	6
3	GOL	C	126	6/6	0.96	0.07	92,92,92,92	6
3	GOL	B	124	6/6	0.97	0.08	85,85,85,85	0
3	GOL	C	124	6/6	0.97	0.07	99,99,99,99	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	PO4	C	122	5/5	0.97	0.07	99,99,99,99	5
3	GOL	D	126	6/6	0.97	0.08	70,70,70,70	0
3	GOL	A	125	6/6	0.98	0.06	72,72,72,72	6
3	GOL	C	123	6/6	0.98	0.06	86,86,86,86	0
3	GOL	A	127	6/6	0.98	0.09	86,86,86,86	0
3	GOL	C	125	6/6	0.98	0.08	75,75,75,75	0
2	PO4	A	124	5/5	0.98	0.04	99,99,99,99	0
3	GOL	D	125	6/6	0.98	0.08	89,89,89,89	0
3	GOL	B	123	6/6	0.98	0.05	80,83,88,88	0
2	PO4	D	124	5/5	0.99	0.04	99,99,99,99	0
2	PO4	A	122	5/5	0.99	0.06	62,72,74,74	0
3	GOL	A	126	6/6	0.99	0.06	76,76,76,76	0
2	PO4	B	122	5/5	0.99	0.03	58,62,66,69	0
3	GOL	A	128	6/6	0.99	0.08	85,85,85,85	0
2	PO4	A	123	5/5	0.99	0.05	97,97,97,97	5
2	PO4	D	123	5/5	0.99	0.06	68,73,76,78	0
3	GOL	D	127	6/6	0.99	0.04	95,95,95,95	0
3	GOL	D	128	6/6	0.99	0.06	83,83,83,83	0
3	GOL	D	129	6/6	0.99	0.07	80,80,80,80	6
2	PO4	D	122	5/5	1.00	0.03	59,61,65,66	0

6.5 Other polymers [i](#)

There are no such residues in this entry.