



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 12:56 AM UTC

PDB ID : 7RRG / pdb_00007rrg
Title : Crystal structure of human 0606T1-2 TCR bound to HLA-A*03:01 in complex with a mutant PIK3CA peptide
Authors : Ma, J.; Baker, B.M.
Deposited on : 2021-08-09
Resolution : 2.12 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

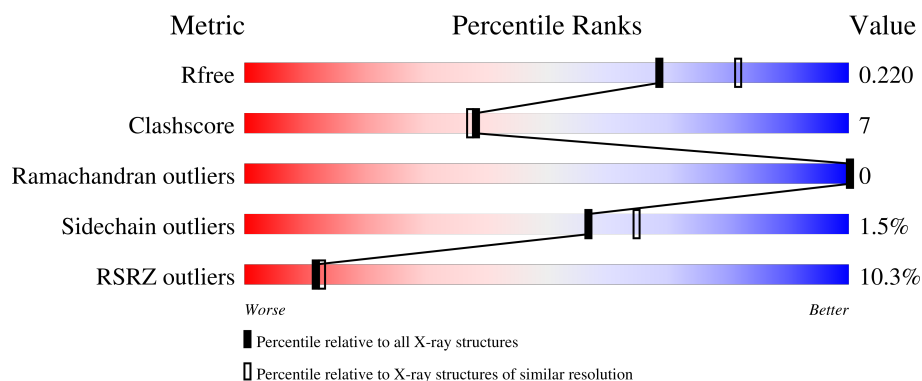
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.12 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	8290 (2.14-2.10)
Clashscore	190562	8817 (2.14-2.10)
Ramachandran outliers	187476	8738 (2.14-2.10)
Sidechain outliers	187428	8739 (2.14-2.10)
RSRZ outliers	180081	8294 (2.14-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 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	274	3% 89% 10% .
2	B	100	93% 7%
3	D	207	17% 78% 11% 11%
4	E	245	16% 71% 24% ..
5	C	9	78% 22%

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	GOL	A	303	-	-	X	-
6	GOL	B	103	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6912 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 HLA class I histocompatibility antigen, A alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	272	Total	C	N	O	S	0	1	0
			2208	1374	399	425	10			

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	100	Total	C	N	O	S	0	0	0
			837	533	141	159	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	initiating methionine	UNP P61769

- Molecule 3 is a protein called T cell receptor, alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	185	Total	C	N	O	S	0	1	0
			1416	893	234	281	8			

- Molecule 4 is a protein called T cell receptor, beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	237	Total	C	N	O	S	0	0	0
			1890	1203	323	359	5			

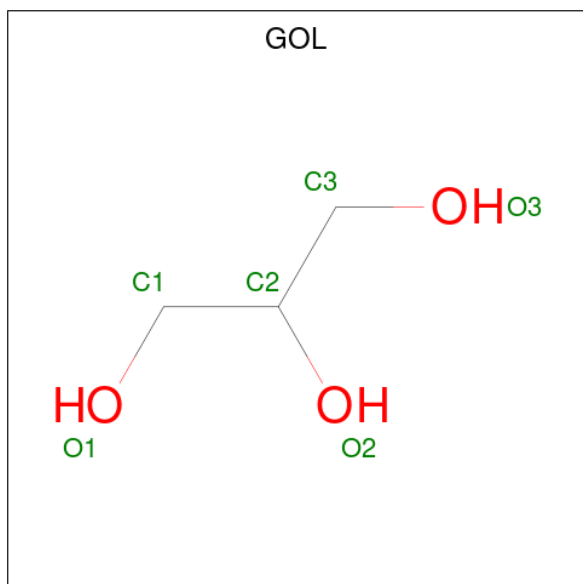
- Molecule 5 is a protein called Mutant PIK3CA peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	C	9	Total	C	N	O	0	0	0
			69	44	13	12			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	2	LEU	HIS	engineered mutation	UNP P42336

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

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

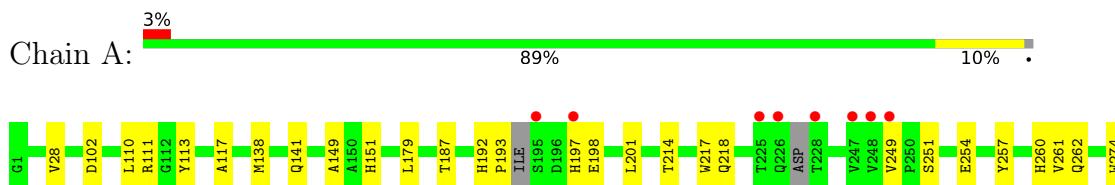
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	182	Total	O	0	0
			182	182		
7	B	80	Total	O	0	0
			80	80		
7	D	83	Total	O	0	0
			83	83		
7	E	61	Total	O	0	0
			61	61		
7	C	8	Total	O	0	0
			8	8		

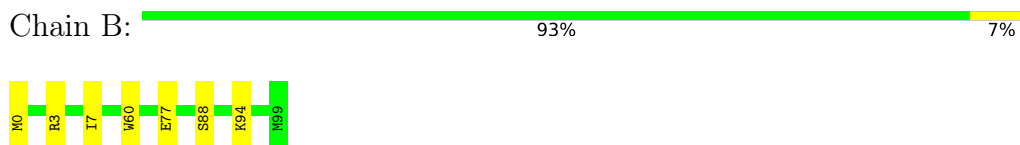
3 Residue-property plots [i](#)

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.

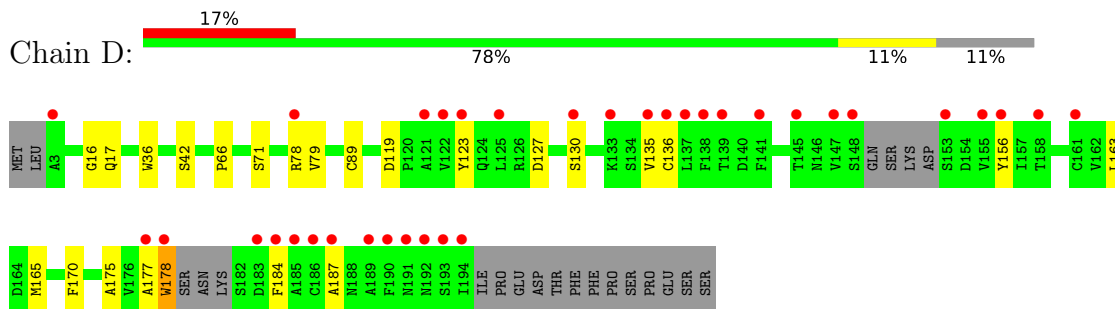
- Molecule 1: HLA class I histocompatibility antigen, A alpha chain



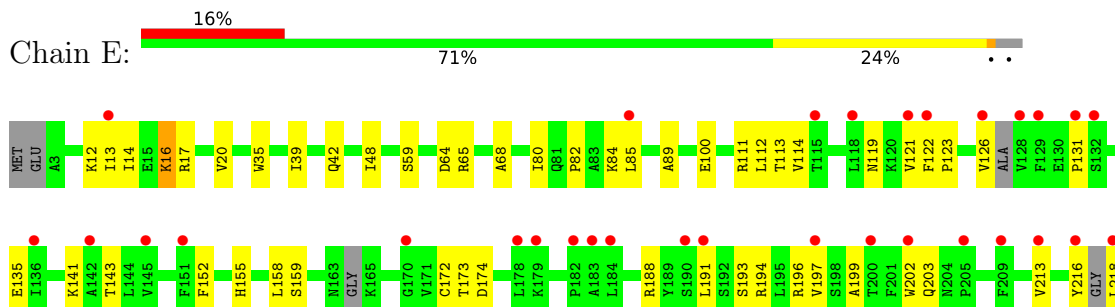
- Molecule 2: Beta-2-microglobulin

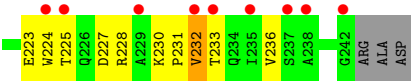


- Molecule 3: T cell receptor, alpha chain

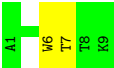
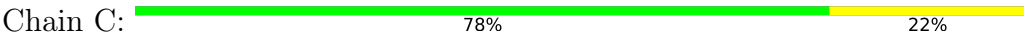


- Molecule 4: T cell receptor, beta chain





● Molecule 5: Mutant PIK3CA peptide



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	227.27Å 46.25Å 120.26Å 90.00° 118.67° 90.00°	Depositor
Resolution (Å)	49.85 – 2.12 49.85 – 2.12	Depositor EDS
% Data completeness (in resolution range)	95.0 (49.85-2.12) 94.5 (49.85-2.12)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.56 (at 2.12Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.193 , 0.221 0.192 , 0.220	Depositor DCC
R_{free} test set	6144 reflections (9.76%)	wwPDB-VP
Wilson B-factor (Å ²)	29.1	Xtriage
Anisotropy	0.537	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 55.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6912	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.59% 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

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	0.16	0/2265	0.32	0/3070
2	B	0.12	0/860	0.30	0/1162
3	D	0.15	0/1445	0.38	0/1964
4	E	0.14	0/1939	0.36	0/2639
5	C	0.20	0/71	0.34	0/94
All	All	0.15	0/6580	0.34	0/8929

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	2208	0	2056	18	0
2	B	837	0	803	9	0
3	D	1416	0	1326	17	0
4	E	1890	0	1811	46	0
5	C	69	0	68	2	0
6	A	24	0	32	4	0
6	B	36	0	48	7	0
6	C	6	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	D	12	0	16	0	0
7	A	182	0	0	0	0
7	B	80	0	0	0	0
7	C	8	0	0	0	0
7	D	83	0	0	0	0
7	E	61	0	0	0	0
All	All	6912	0	6168	87	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 7.

All (87) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:135:VAL:HG12	3:D:178:TRP:HB3	1.56	0.86
2:B:94:LYS:HB3	6:B:103:GOL:H11	1.68	0.74
4:E:16:LYS:HE3	4:E:85:LEU:HD23	1.74	0.70
3:D:136:CYS:HB3	3:D:177:ALA:HB3	1.73	0.69
4:E:17:ARG:HA	4:E:82:PRO:HB2	1.73	0.69
4:E:119:ASN:HA	4:E:224:TRP:HZ3	1.57	0.68
4:E:158:LEU:HD13	4:E:213:VAL:HG22	1.79	0.65
1:A:201:LEU:HD12	1:A:249:VAL:HG11	1.80	0.63
2:B:77:GLU:HA	6:B:102:GOL:H32	1.80	0.63
2:B:94:LYS:HE3	6:B:103:GOL:H32	1.79	0.63
3:D:165:MET:HE3	3:D:170:PHE:CD2	2.33	0.62
3:D:163:LEU:HB3	4:E:172:CYS:HB2	1.80	0.61
4:E:158:LEU:HD12	4:E:159:SER:H	1.66	0.61
4:E:121:VAL:HG23	4:E:231:PRO:HG2	1.81	0.60
3:D:184:PHE:CZ	3:D:187:ALA:HA	2.35	0.60
2:B:77:GLU:HG2	6:B:102:GOL:H12	1.84	0.59
5:C:6:TRP:CG	5:C:7:THR:H	2.22	0.58
3:D:16:GLY:HA2	3:D:78:ARG:HG3	1.86	0.58
4:E:39:ILE:HG22	4:E:89:ALA:HB2	1.85	0.57
4:E:113:THR:HG1	4:E:155:HIS:HE2	1.49	0.57
3:D:165:MET:HE3	3:D:170:PHE:HD2	1.72	0.55
4:E:199:ALA:O	4:E:203:GLN:HG2	2.06	0.55
3:D:165:MET:HE1	4:E:141:LYS:HD3	1.89	0.54
1:A:151:HIS:H	6:A:303:GOL:H12	1.72	0.54
4:E:227:ASP:OD1	4:E:228:ARG:N	2.37	0.53
4:E:39:ILE:HD11	4:E:42:GLN:HE21	1.74	0.53
1:A:214:THR:HB	1:A:262:GLN:HB2	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:173:THR:HG23	4:E:193:SER:HB2	1.90	0.52
6:A:303:GOL:O1	6:A:303:GOL:O3	2.22	0.51
3:D:156:TYR:O	3:D:177:ALA:HA	2.11	0.51
4:E:12:LYS:HB3	4:E:112:LEU:HD12	1.93	0.51
4:E:111:ARG:HH11	4:E:111:ARG:HG2	1.76	0.51
4:E:131:PRO:HD2	4:E:202:TRP:CZ2	2.46	0.51
4:E:224:TRP:O	4:E:225:THR:OG1	2.25	0.50
3:D:165:MET:CE	4:E:196:ARG:HG2	2.41	0.50
1:A:187:THR:HG21	1:A:261:VAL:HG21	1.94	0.50
1:A:138:MET:HA	1:A:141:GLN:HG2	1.94	0.49
1:A:151:HIS:ND1	6:A:303:GOL:H12	2.27	0.49
4:E:48:ILE:HD13	4:E:68:ALA:HB3	1.93	0.49
4:E:100:GLU:H	4:E:100:GLU:CD	2.21	0.48
4:E:158:LEU:HD12	4:E:159:SER:N	2.28	0.48
4:E:84:LYS:HE2	4:E:84:LYS:HB3	1.76	0.48
2:B:7:ILE:H	6:B:106:GOL:H2	1.79	0.48
3:D:36:TRP:CZ2	3:D:89:CYS:HB2	2.49	0.48
1:A:149:ALA:O	6:A:303:GOL:H11	2.15	0.47
1:A:28:VAL:HG11	1:A:179:LEU:HD13	1.97	0.47
2:B:0:MET:HE3	2:B:3:ARG:HA	1.97	0.46
4:E:174:ASP:HB2	4:E:191:LEU:HD12	1.98	0.46
3:D:175:ALA:HA	4:E:194:ARG:HH21	1.81	0.46
1:A:197:HIS:HA	1:A:251:SER:HB3	1.98	0.45
1:A:218:GLN:HG3	1:A:260:HIS:ND1	2.32	0.45
4:E:84:LYS:O	4:E:114:VAL:HG11	2.15	0.45
4:E:216:TYR:HA	4:E:233:THR:HB	1.98	0.45
4:E:39:ILE:HG13	4:E:42:GLN:HG3	1.98	0.45
4:E:121:VAL:HG12	4:E:152:PHE:CD2	2.52	0.45
4:E:121:VAL:O	4:E:231:PRO:HG3	2.16	0.45
3:D:127:ASP:HB3	3:D:130:SER:O	2.18	0.44
4:E:12:LYS:HG2	4:E:20:VAL:HG21	2.00	0.44
4:E:141:LYS:CB	4:E:196:ARG:HD2	2.48	0.44
4:E:224:TRP:HD1	4:E:225:THR:N	2.16	0.44
2:B:77:GLU:HG2	6:B:103:GOL:H31	1.99	0.44
3:D:66:PRO:HD2	3:D:71:SER:O	2.17	0.43
4:E:121:VAL:HA	4:E:152:PHE:HD2	1.82	0.43
3:D:184:PHE:H	3:D:184:PHE:HD1	1.65	0.43
4:E:143:THR:HA	4:E:196:ARG:HA	1.99	0.43
4:E:126:VAL:HG22	4:E:236:VAL:HG12	2.00	0.43
4:E:230:LYS:O	4:E:232:VAL:N	2.51	0.43
1:A:249:VAL:HG12	1:A:257:TYR:CE2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:217:TRP:C	1:A:218:GLN:HG2	2.45	0.42
4:E:111:ARG:HG2	4:E:111:ARG:NH1	2.35	0.42
4:E:223:GLU:HA	4:E:230:LYS:NZ	2.35	0.42
3:D:17:GLN:O	3:D:79:VAL:HG22	2.20	0.41
4:E:122:PHE:HB3	4:E:188:ARG:HH21	1.85	0.41
5:C:6:TRP:CG	5:C:7:THR:N	2.88	0.41
1:A:254:GLU:HB3	1:A:274:TRP:HD1	1.84	0.41
2:B:94:LYS:HG2	6:B:103:GOL:H32	2.02	0.41
4:E:121:VAL:HG23	4:E:231:PRO:CG	2.49	0.41
4:E:123:PRO:HD3	4:E:231:PRO:HB3	2.03	0.41
1:A:110:LEU:HB3	1:A:111:ARG:HH11	1.85	0.41
4:E:13:ILE:HG23	4:E:218:LEU:HD23	2.02	0.41
1:A:198:GLU:HA	1:A:249:VAL:O	2.21	0.41
3:D:123:TYR:CE2	4:E:135:GLU:HA	2.57	0.40
1:A:102:ASP:OD2	1:A:113:TYR:OH	2.31	0.40
1:A:117:ALA:HB2	2:B:60:TRP:CE2	2.56	0.40
4:E:35:TRP:HB2	4:E:48:ILE:HG22	2.03	0.40
4:E:64:ASP:OD1	4:E:65:ARG:N	2.55	0.40
1:A:192:HIS:HA	1:A:193:PRO:HD2	1.87	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	267/274 (97%)	265 (99%)	2 (1%)	0	100	100
2	B	98/100 (98%)	98 (100%)	0	0	100	100
3	D	180/207 (87%)	170 (94%)	10 (6%)	0	100	100
4	E	229/245 (94%)	215 (94%)	14 (6%)	0	100	100
5	C	7/9 (78%)	6 (86%)	1 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	781/835 (94%)	754 (96%)	27 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	227/231 (98%)	227 (100%)	0	100	100
2	B	95/95 (100%)	94 (99%)	1 (1%)	65	74
3	D	154/184 (84%)	151 (98%)	3 (2%)	50	57
4	E	207/213 (97%)	201 (97%)	6 (3%)	37	41
5	C	6/6 (100%)	6 (100%)	0	100	100
All	All	689/729 (94%)	679 (98%)	10 (2%)	57	65

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	88	SER
3	D	42	SER
3	D	119	ASP
3	D	178	TRP
4	E	14	ILE
4	E	16	LYS
4	E	59	SER
4	E	80	ILE
4	E	197	VAL
4	E	232	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	GLN

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Mol	Chain	Res	Type
1	A	62	GLN
1	A	70	GLN
2	B	13	HIS
4	E	42	GLN
4	E	181	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](#)

13 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	$\# Z > 2$
6	GOL	A	304	-	5,5,5	0.91	0	5,5,5	1.07	0
6	GOL	B	105	-	5,5,5	0.93	0	5,5,5	1.05	0
6	GOL	B	106	-	5,5,5	0.95	0	5,5,5	1.02	0
6	GOL	A	302	-	5,5,5	1.03	0	5,5,5	0.91	0
6	GOL	B	102	-	5,5,5	0.97	0	5,5,5	1.00	0
6	GOL	D	302	-	5,5,5	0.92	0	5,5,5	1.03	0
6	GOL	B	103	-	5,5,5	0.94	0	5,5,5	0.96	0
6	GOL	B	104	-	5,5,5	0.93	0	5,5,5	1.10	0
6	GOL	A	303	-	5,5,5	0.87	0	5,5,5	1.05	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	GOL	B	101	-	5,5,5	0.95	0	5,5,5	1.08	0
6	GOL	A	301	-	5,5,5	0.87	0	5,5,5	1.09	0
6	GOL	D	301	-	5,5,5	0.93	0	5,5,5	0.95	0
6	GOL	C	101	-	5,5,5	0.98	0	5,5,5	1.02	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
6	GOL	A	304	-	-	2/4/4/4	-
6	GOL	B	105	-	-	0/4/4/4	-
6	GOL	B	106	-	-	2/4/4/4	-
6	GOL	A	302	-	-	4/4/4/4	-
6	GOL	B	102	-	-	2/4/4/4	-
6	GOL	D	302	-	-	2/4/4/4	-
6	GOL	B	103	-	-	2/4/4/4	-
6	GOL	B	104	-	-	0/4/4/4	-
6	GOL	A	303	-	-	0/4/4/4	-
6	GOL	B	101	-	-	4/4/4/4	-
6	GOL	A	301	-	-	0/4/4/4	-
6	GOL	D	301	-	-	0/4/4/4	-
6	GOL	C	101	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	302	GOL	C1-C2-C3-O3
6	A	304	GOL	C1-C2-C3-O3
6	A	304	GOL	O2-C2-C3-O3
6	B	102	GOL	O2-C2-C3-O3
6	A	302	GOL	O1-C1-C2-O2
6	C	101	GOL	O1-C1-C2-O2
6	A	302	GOL	O1-C1-C2-C3
6	B	101	GOL	O1-C1-C2-C3

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Mol	Chain	Res	Type	Atoms
6	B	101	GOL	C1-C2-C3-O3
6	B	102	GOL	C1-C2-C3-O3
6	B	103	GOL	C1-C2-C3-O3
6	B	106	GOL	O1-C1-C2-C3
6	C	101	GOL	O1-C1-C2-C3
6	A	302	GOL	O2-C2-C3-O3
6	B	106	GOL	O1-C1-C2-O2
6	B	101	GOL	O2-C2-C3-O3
6	B	101	GOL	O1-C1-C2-O2
6	B	103	GOL	O2-C2-C3-O3
6	D	302	GOL	C1-C2-C3-O3
6	D	302	GOL	O1-C1-C2-O2

There are no ring outliers.

4 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	106	GOL	1	0
6	B	102	GOL	2	0
6	B	103	GOL	4	0
6	A	303	GOL	4	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 ⓘ

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	272/274 (99%)	0.01	8 (2%) 53 56	12, 35, 102, 118	1 (0%)
2	B	100/100 (100%)	-0.24	0 100 100	18, 33, 59, 65	0
3	D	185/207 (89%)	0.87	35 (18%) 3 3	18, 46, 131, 145	1 (0%)
4	E	237/245 (96%)	1.03	40 (16%) 4 4	20, 81, 121, 152	0
5	C	9/9 (100%)	-0.82	0 100 100	19, 20, 22, 25	0
All	All	803/835 (96%)	0.47	83 (10%) 12 13	12, 46, 117, 152	2 (0%)

All (83) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	D	136	CYS	9.0
3	D	194	ILE	6.7
3	D	185	ALA	6.3
3	D	186	CYS	6.1
4	E	218	LEU	5.5
3	D	122	VAL	5.1
4	E	191	LEU	5.0
3	D	190	PHE	4.8
3	D	177	ALA	4.4
3	D	189	ALA	4.1
3	D	192	ASN	4.0
3	D	191	ASN	3.9
4	E	237	SER	3.8
3	D	184	PHE	3.7
4	E	233	THR	3.7
3	D	135	VAL	3.7
4	E	128	VAL	3.6
3	D	187	ALA	3.5
4	E	145	VAL	3.4
4	E	190	SER	3.4

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Mol	Chain	Res	Type	RSRZ
4	E	242	GLY	3.4
3	D	145	THR	3.3
1	A	249	VAL	3.3
4	E	205	PRO	3.2
3	D	178	TRP	3.2
4	E	13	ILE	3.2
3	D	153	SER	3.2
4	E	126	VAL	3.1
1	A	248	VAL	3.0
4	E	121	VAL	3.0
4	E	213	VAL	3.0
4	E	216	TYR	3.0
4	E	129	PHE	3.0
3	D	138	PHE	2.9
3	D	155	VAL	2.7
4	E	229	ALA	2.7
1	A	226	GLN	2.7
4	E	224	TRP	2.7
4	E	232	VAL	2.6
4	E	202	TRP	2.6
4	E	235	ILE	2.6
4	E	178	LEU	2.6
4	E	85	LEU	2.5
3	D	137	LEU	2.5
4	E	179	LYS	2.5
3	D	161	CYS	2.4
4	E	115	THR	2.4
3	D	147	VAL	2.4
3	D	148	SER	2.4
4	E	225	THR	2.4
4	E	131	PRO	2.3
4	E	197	VAL	2.3
3	D	139	THR	2.3
3	D	193	SER	2.3
4	E	132	SER	2.3
3	D	141	PHE	2.3
4	E	182	PRO	2.3
3	D	156	TYR	2.3
3	D	130	SER	2.2
3	D	121	ALA	2.2
4	E	122	PHE	2.2
4	E	136	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
4	E	118	LEU	2.2
3	D	123	TYR	2.2
3	D	183	ASP	2.2
3	D	158	THR	2.2
1	A	197	HIS	2.1
3	D	133	LYS	2.1
4	E	200	THR	2.1
4	E	151	PHE	2.1
1	A	247	VAL	2.1
4	E	142	ALA	2.1
4	E	184	LEU	2.1
1	A	225	THR	2.1
4	E	183	ALA	2.1
1	A	195	SER	2.1
3	D	125	LEU	2.1
3	D	78	ARG	2.1
4	E	170	GLY	2.1
4	E	209	PHE	2.1
3	D	3	ALA	2.1
4	E	238	ALA	2.0
1	A	228	THR	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($\text{\AA}^2$)	Q<0.9
6	GOL	B	103	6/6	0.65	0.16	60,69,73,74	0
6	GOL	A	304	6/6	0.73	0.16	53,66,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	GOL	B	101	6/6	0.74	0.16	44,50,66,68	0
6	GOL	A	303	6/6	0.75	0.14	36,48,52,57	0
6	GOL	B	102	6/6	0.78	0.14	39,60,63,74	0
6	GOL	B	105	6/6	0.78	0.17	56,61,66,69	0
6	GOL	B	106	6/6	0.79	0.12	43,50,61,65	0
6	GOL	A	302	6/6	0.80	0.15	53,57,61,63	0
6	GOL	D	302	6/6	0.82	0.13	42,49,59,61	0
6	GOL	C	101	6/6	0.84	0.20	37,44,46,50	0
6	GOL	B	104	6/6	0.88	0.12	34,38,42,44	0
6	GOL	D	301	6/6	0.89	0.13	26,34,38,39	0
6	GOL	A	301	6/6	0.91	0.11	34,40,48,49	0

6.5 Other polymers [i](#)

There are no such residues in this entry.