WORLDWIDE
wwPDB
PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report (i)

Dec 2, 2023 – 10:15 pm GMT

PDB ID	:	1OK3
Title	:	Decay accelerating factor (cd55): the structure of an intact human complement regulator.
Authors	:	Lukacik, P.; Roversi, P.; White, J.; Esser, D.; Smith, G.P.; Billington, J.; Williams, P.A.; Rudd, P.M.; Wormald, M.R.; Crispin, M.D.M.; Radcliffe, C.M.; Dwek, R.A.; Evans, D.J.; Morgan, B.P.; Smith, R.A.G.; Lea, S.M.
Deposited on	:	2003-07-16
Resolution	:	2.20 Å(reported)

The following versions of software and data (see references (i)) were used in the production of this report:

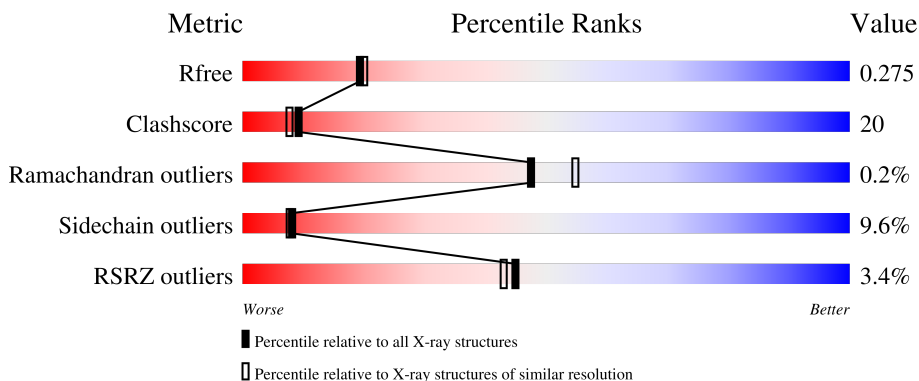|		
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.20 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	Percentile Ranks	Value
Rfree		0.275
Clashscore		20
Ramachandran outliers		0.2%
Sidechain outliers		9.6%
RSRZ outliers		3.4%

Worse *Better*

▌ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 <=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	254	4% / 70% / 27% / •
1	B	254	3% / 58% / 37% / •

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
2	ACT	A	300	-	-	X	-
2	ACT	A	301	-	-	X	-
2	ACT	B	300	-	-	X	-
2	ACT	B	301	-	-	X	-
4	GOL	A	1256	-	X	-	-
4	GOL	A	1257	-	X	-	-
4	GOL	A	1258	-	X	-	-
4	GOL	A	1259	-	X	-	-
4	GOL	B	1256	-	X	-	-
4	GOL	B	1257	-	X	-	-
4	GOL	B	1258	-	X	-	-
4	GOL	B	1259	-	X	-	-
4	GOL	B	1260	-	X	-	-

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 4271 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.
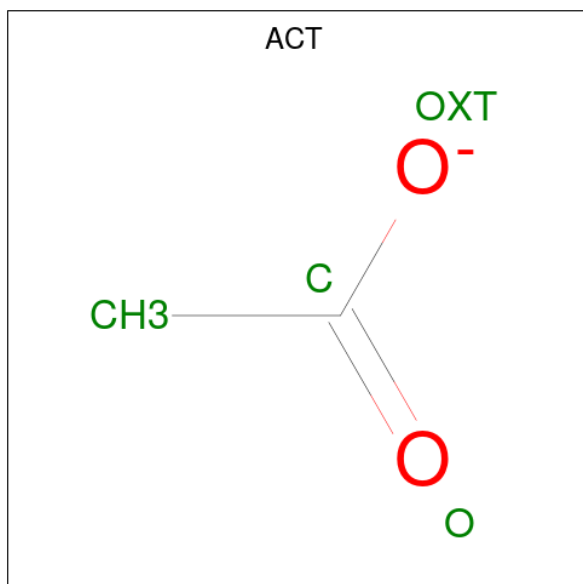
- Molecule 1 is a protein called COMPLEMENT DECAY-ACCELERATING FACTOR.

Mol	Chain	Residues	Atoms							ZeroOcc	AltConf	Trace
1	A	254	Total	C	N	O	S	Se		0	0	0
			1969	1234	330	386	17	2				
1	B	253	Total	C	N	O	S	Se		0	0	0
			1961	1229	329	385	17	1				

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	48	ILE	THR	SEE REMARK 999	UNP P08174
B	48	ILE	THR	SEE REMARK 999	UNP P08174

- Molecule 2 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).
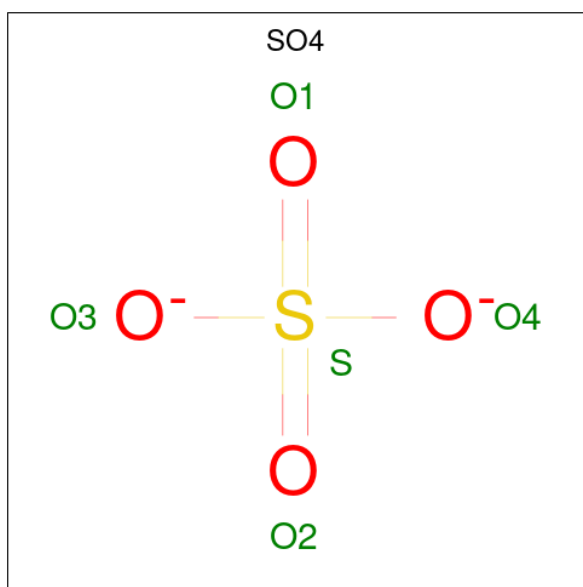

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		

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

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 5	O 4	S 1	0	0
3	B	1	Total 5	O 4	S 1	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).

GOL

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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	126	Total 126	O 126	0	0
5	B	135	Total 135	O 135	0	0

3 Residue-property plots ⓘ

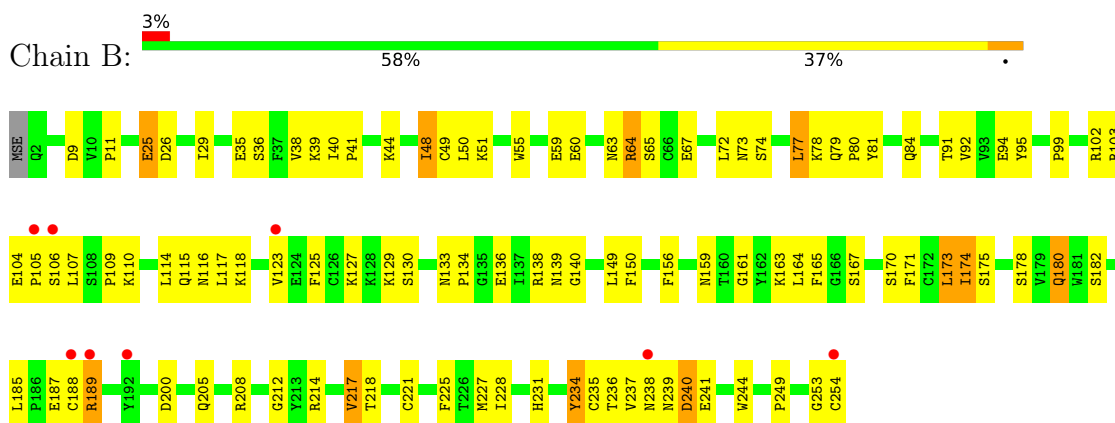These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: COMPLEMENT DECAY-ACCELERATING FACTOR

Chain A:

- Molecule 1: COMPLEMENT DECAY-ACCELERATING FACTOR

Chain B:

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	46.67Å 55.08Å 61.65Å 86.47° 84.37° 64.91°	Depositor
Resolution (Å)	25.00 – 2.20 24.94 – 2.19	Depositor EDS
% Data completeness (in resolution range)	93.5 (25.00-2.20) 93.0 (24.94-2.19)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.37 (at 2.19Å)	Xtriage
Refinement program	TNT 5F	Depositor
R, R_{free}	0.211 , (Not available) 0.223 , 0.275	Depositor DCC
R_{free} test set	1342 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å^2)	27.9	Xtriage
Anisotropy	0.631	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 55.0	EDS
L-test for twinning[2]	$< |L| > = 0.48, < L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.023 for -h,-h+k,-l	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	4271	wwPDB-VP
Average B, all atoms (Å^2)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.65% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, ACT, 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	0.36	0/2021	0.55	0/2746
1	B	0.36	0/2013	0.53	0/2736
All	All	0.36	0/4034	0.54	0/5482

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	63	ASN	Mainchain,Peptide

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	1969	0	1867	63	1
1	B	1961	0	1855	92	1
2	A	8	0	6	8	0
2	B	8	0	6	10	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	24	0	16	5	0
4	B	30	0	20	2	0
5	A	126	0	0	7	0
5	B	135	0	0	10	0
All	All	4271	0	3770	155	1

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 20.

All (155) 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:116:ASN:HB2	1:B:118:LYS:HE3	1.35	1.09
1:A:116:ASN:HB2	1:A:118:LYS:HE3	1.35	1.08
1:A:165:PHE:HD2	1:A:189:ARG:HG3	1.15	1.06
1:B:26:ASP:HA	1:B:48:ILE:HD11	1.45	0.99
1:B:171:PHE:CD1	1:B:173:LEU:HD13	2.02	0.94
1:A:165:PHE:CD2	1:A:189:ARG:HG3	2.02	0.93
1:B:99:PRO:HB2	1:B:174:ILE:HD12	1.55	0.87
1:B:171:PHE:HD1	1:B:173:LEU:HD13	1.38	0.85
1:B:150:PHE:CE2	1:B:174:ILE:HG22	2.16	0.80
1:A:38:VAL:N	1:A:63:ASN:O	2.14	0.80
1:B:116:ASN:CB	1:B:118:LYS:HE3	2.12	0.79
1:B:73:ASN:H	2:B:301:ACT:CH3	1.96	0.79
1:A:116:ASN:CB	1:A:118:LYS:HE3	2.12	0.78
1:A:209:ASP:HB2	2:A:301:ACT:H1	1.66	0.77
1:B:227:MSE:O	1:B:228:ILE:HD13	1.84	0.77
1:A:209:ASP:H	2:A:301:ACT:H1	1.49	0.75
1:A:163:LYS:HE2	1:A:165:PHE:CZ	2.22	0.74
1:B:163:LYS:HE2	1:B:165:PHE:CZ	2.22	0.74
1:A:209:ASP:CB	2:A:301:ACT:H1	2.17	0.74
1:A:209:ASP:H	2:A:301:ACT:CH3	2.00	0.73
4:A:1256:GOL:H12	5:A:2099:HOH:O	1.89	0.72
1:B:159:ASN:ND2	5:B:2084:HOH:O	2.23	0.71
1:B:81:TYR:HA	1:B:84:GLN:NE2	2.05	0.70
1:A:81:TYR:HA	1:A:84:GLN:NE2	2.05	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:79:GLN:HE22	1:A:83:THR:HG23	1.56	0.70
1:B:104:GLU:OE2	1:B:105:PRO:HD2	1.90	0.70
1:B:73:ASN:ND2	2:B:301:ACT:H3	2.07	0.70
1:A:79:GLN:HG3	1:A:80:PRO:HA	1.74	0.69
5:A:2070:HOH:O	1:B:231:HIS:HD2	1.77	0.68
1:A:1:MSE:HE3	5:A:2001:HOH:O	1.92	0.68
1:B:73:ASN:HD22	2:B:301:ACT:H3	1.59	0.68
1:B:138:ARG:O	1:B:188:CYS:HB2	1.94	0.68
1:B:26:ASP:CA	1:B:48:ILE:HD11	2.23	0.67
1:B:200:ASP:HB2	4:B:1257:GOL:H11	1.76	0.66
1:B:99:PRO:HB2	1:B:174:ILE:CD1	2.26	0.66
1:A:25:GLU:OE1	1:A:51:LYS:HD3	1.96	0.66
1:B:51:LYS:NZ	5:B:2036:HOH:O	2.27	0.66
1:B:35:GLU:O	1:B:36:SER:HB2	1.94	0.66
1:A:69:PRO:HG2	1:A:77:LEU:HD21	1.78	0.63
1:A:122:ALA:HB2	5:A:2013:HOH:O	1.99	0.63
1:A:77:LEU:HD13	1:A:95:TYR:CZ	2.34	0.62
1:B:74:SER:N	2:B:301:ACT:O	2.33	0.61
1:B:187:GLU:HG2	1:B:189:ARG:HG2	1.82	0.61
1:B:73:ASN:H	2:B:301:ACT:H2	1.65	0.60
1:A:116:ASN:HB2	1:A:118:LYS:CE	2.23	0.59
1:B:72:LEU:HA	2:B:301:ACT:H2	1.83	0.59
1:A:115:GLN:N	5:A:2056:HOH:O	2.28	0.59
1:B:150:PHE:HE2	1:B:174:ILE:HG22	1.67	0.59
1:B:221:CYS:SG	1:B:227:MSE:HE3	2.43	0.59
1:A:20:ARG:HD2	1:A:22:SER:O	2.02	0.58
1:A:156:PHE:HZ	2:A:300:ACT:H2	1.67	0.58
1:A:253:GLY:HA3	1:A:254:CYS:C	2.24	0.58
1:A:159:ASN:HA	4:A:1259:GOL:H11	1.86	0.58
1:B:171:PHE:CE1	1:B:173:LEU:HD13	2.38	0.58
1:B:173:LEU:HD22	1:B:182:SER:HB3	1.85	0.57
1:A:156:PHE:CZ	2:A:300:ACT:H2	2.40	0.57
1:A:1:MSE:O	1:A:3:ASP:N	2.38	0.56
1:B:116:ASN:HB2	1:B:118:LYS:CE	2.23	0.55
1:A:77:LEU:HD13	1:A:95:TYR:CE2	2.43	0.54
1:A:238:ASN:HA	4:A:1258:GOL:H11	1.90	0.54
1:A:34:GLU:O	1:A:37:PHE:HB2	2.06	0.54
1:B:227:MSE:C	1:B:228:ILE:HD13	2.28	0.54
1:B:227:MSE:HG3	1:B:249:PRO:HB2	1.90	0.53
1:B:25:GLU:OE1	1:B:51:LYS:HG2	2.09	0.53
1:B:174:ILE:HG23	5:B:2090:HOH:O	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:81:TYR:HA	1:A:84:GLN:HE21	1.73	0.52
1:B:156:PHE:HZ	2:B:300:ACT:H2	1.72	0.52
1:A:25:GLU:O	1:A:26:ASP:HB2	2.10	0.52
1:A:209:ASP:C	1:A:210:HIS:HD2	2.14	0.52
1:B:25:GLU:O	1:B:26:ASP:HB2	2.10	0.51
1:A:79:GLN:HE22	1:A:83:THR:CG2	2.20	0.51
1:B:79:GLN:OE1	1:B:80:PRO:HA	2.10	0.51
1:B:175:SER:HB2	1:B:180:GLN:CG	2.41	0.51
1:B:77:LEU:HG	1:B:81:TYR:HB2	1.92	0.51
1:B:239:ASN:OD1	1:B:240:ASP:OD1	2.29	0.51
1:B:81:TYR:HA	1:B:84:GLN:HE21	1.73	0.50
1:A:209:ASP:N	2:A:301:ACT:H1	2.24	0.50
1:A:1:MSE:C	1:A:3:ASP:H	2.15	0.50
1:B:78:LYS:HE2	1:B:94:GLU:HG2	1.93	0.50
1:B:212:GLY:O	1:B:235:CYS:HB3	2.12	0.49
1:B:59:GLU:HB3	5:B:2035:HOH:O	2.12	0.49
1:A:29:ILE:HD12	1:A:55:TRP:CH2	2.47	0.49
1:B:133:ASN:OD1	1:B:134:PRO:HD2	2.13	0.49
1:B:29:ILE:HD12	1:B:55:TRP:CH2	2.47	0.49
1:B:48:ILE:HG13	1:B:49:CYS:N	2.27	0.49
1:B:178:SER:HB3	5:B:2069:HOH:O	2.13	0.48
1:B:38:VAL:HG23	1:B:65:SER:HB3	1.96	0.48
1:A:163:LYS:N	1:A:189:ARG:O	2.35	0.48
1:A:130:SER:HB2	5:A:2052:HOH:O	2.13	0.48
1:A:116:ASN:O	1:A:117:LEU:HB2	2.14	0.48
1:A:209:ASP:O	1:A:210:HIS:HD2	1.97	0.47
1:A:165:PHE:N	1:A:187:GLU:O	2.38	0.47
1:B:156:PHE:CZ	2:B:300:ACT:H2	2.48	0.47
1:B:116:ASN:O	1:B:117:LEU:HB2	2.14	0.47
1:B:175:SER:HB2	1:B:180:GLN:HG3	1.97	0.47
1:B:171:PHE:CE1	1:B:173:LEU:CD1	2.98	0.47
1:B:140:GLY:HA3	1:B:188:CYS:SG	2.55	0.47
1:A:228:ILE:HB	1:A:250:GLU:HG2	1.96	0.46
1:B:9:ASP:O	4:B:1258:GOL:H12	2.16	0.46
1:B:163:LYS:HA	1:B:240:ASP:OD2	2.16	0.46
1:B:234:TYR:CZ	1:B:236:THR:HG22	2.50	0.46
1:B:238:ASN:N	1:B:241:GLU:O	2.49	0.45
1:B:103:ARG:NH1	1:B:107:LEU:O	2.39	0.44
1:A:37:PHE:HA	1:A:63:ASN:O	2.17	0.44
1:B:205:GLN:NE2	1:B:218:THR:HG22	2.33	0.44
1:A:103:ARG:NH2	1:A:107:LEU:O	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:214:ARG:HA	1:B:234:TYR:CD2	2.52	0.44
4:A:1258:GOL:H12	1:B:214:ARG:NH1	2.34	0.43
1:A:52:GLY:O	1:A:53:SER:HB3	2.19	0.43
1:B:73:ASN:H	2:B:301:ACT:C	2.31	0.43
1:B:123:VAL:HG22	5:B:2063:HOH:O	2.18	0.43
1:A:79:GLN:CG	1:A:80:PRO:HA	2.44	0.43
1:A:69:PRO:O	5:A:2028:HOH:O	2.22	0.43
1:B:239:ASN:HA	1:B:240:ASP:HA	1.57	0.43
1:B:39:LYS:HE2	5:B:2031:HOH:O	2.19	0.42
1:B:170:SER:CB	2:B:300:ACT:H1	2.50	0.42
1:B:40:ILE:HA	1:B:41:PRO:HD3	1.95	0.42
1:A:109:PRO:HA	1:A:125:PHE:CG	2.55	0.42
1:A:143:ASP:HB3	1:A:155:SER:OG	2.20	0.42
1:A:178:SER:HB2	1:A:179:VAL:H	1.69	0.42
1:B:77:LEU:HD13	1:B:95:TYR:CZ	2.54	0.42
1:B:109:PRO:HA	1:B:125:PHE:CG	2.55	0.42
1:B:99:PRO:O	5:B:2060:HOH:O	2.20	0.42
1:B:175:SER:CB	1:B:180:GLN:HG2	2.49	0.42
1:B:175:SER:CB	1:B:180:GLN:CG	2.98	0.42
1:B:130:SER:HB2	1:B:149:LEU:HD23	2.01	0.42
1:B:138:ARG:O	1:B:139:ASN:HB2	2.19	0.42
1:A:73:ASN:O	1:A:98:ARG:HD2	2.19	0.41
1:A:218:THR:OG1	1:B:136:GLU:OE2	2.38	0.41
1:A:164:LEU:C	1:A:164:LEU:HD23	2.40	0.41
1:A:209:ASP:C	1:A:210:HIS:CD2	2.93	0.41
1:B:11:PRO:HD2	1:B:60:GLU:HG2	2.02	0.41
1:B:187:GLU:CG	1:B:189:ARG:HG2	2.50	0.41
1:B:91:THR:HA	5:B:2056:HOH:O	2.21	0.41
1:B:64:ARG:H	1:B:64:ARG:HG2	1.66	0.41
1:B:187:GLU:HG2	1:B:189:ARG:CG	2.48	0.41
1:A:11:PRO:HD2	1:A:60:GLU:HG2	2.02	0.41
1:A:116:ASN:CG	1:A:118:LYS:HE3	2.41	0.41
1:A:140:GLY:HA3	1:A:188:CYS:SG	2.61	0.41
1:B:102:ARG:NH2	1:B:129:LYS:HG2	2.35	0.41
1:B:116:ASN:CG	1:B:118:LYS:HE3	2.41	0.41
1:B:161:GLY:HA2	1:B:237:VAL:HG21	2.02	0.41
1:B:175:SER:HB3	1:B:180:GLN:HG2	2.02	0.41
1:A:214:ARG:HD3	1:A:214:ARG:HA	1.79	0.40
1:B:102:ARG:O	1:B:127:LYS:N	2.50	0.40
1:B:217:VAL:CG1	1:B:244:TRP:CZ3	3.04	0.40
1:A:239:ASN:H	4:A:1258:GOL:C3	2.34	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:253:GLY:CA	1:A:254:CYS:C	2.88	0.40
1:A:156:PHE:HZ	2:A:300:ACT:CH3	2.33	0.40
1:A:217:VAL:CG1	1:A:244:TRP:CZ3	3.04	0.40
1:A:101:TYR:HA	1:A:127:LYS:O	2.21	0.40
1:B:39:LYS:CE	5:B:2031:HOH:O	2.70	0.40
1:B:44:LYS:HB2	1:B:44:LYS:HE2	1.63	0.40
1:B:164:LEU:HD23	1:B:164:LEU:C	2.40	0.40
1:B:225:PHE:CD2	1:B:253:GLY:HA2	2.56	0.40

All (1) 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)
1:A:52:GLY:O	1:B:110:LYS:NZ[1_386]	2.10	0.10

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	252/254 (99%)	239 (95%)	12 (5%)	1 (0%)	34	37
1	B	251/254 (99%)	240 (96%)	11 (4%)	0	100	100
All	All	503/508 (99%)	479 (95%)	23 (5%)	1 (0%)	47	55

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	GLN

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	225/223 (101%)	204 (91%)	21 (9%)	9	8
1	B	224/223 (100%)	202 (90%)	22 (10%)	8	7
All	All	449/446 (101%)	406 (90%)	43 (10%)	8	8

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	GLN
1	A	25	GLU
1	A	50	LEU
1	A	63	ASN
1	A	65	SER
1	A	71	ARG
1	A	77	LEU
1	A	92	VAL
1	A	114	LEU
1	A	115	GLN
1	A	127	LYS
1	A	136	GLU
1	A	138	ARG
1	A	167	SER
1	A	173	LEU
1	A	174	ILE
1	A	185	LEU
1	A	189	ARG
1	A	208	ARG
1	A	217	VAL
1	A	250	GLU
1	B	25	GLU
1	B	48	ILE
1	B	50	LEU
1	B	63	ASN
1	B	64	ARG
1	B	67	GLU

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Mol	Chain	Res	Type
1	B	77	LEU
1	B	92	VAL
1	B	106	SER
1	B	114	LEU
1	B	115	GLN
1	B	167	SER
1	B	173	LEU
1	B	174	ILE
1	B	180	GLN
1	B	185	LEU
1	B	189	ARG
1	B	208	ARG
1	B	217	VAL
1	B	234	TYR
1	B	240	ASP
1	B	254	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	GLN
1	A	79	GLN
1	A	84	GLN
1	A	139	ASN
1	A	159	ASN
1	A	180	GLN
1	A	198	GLN
1	A	222	ASN
1	B	54	GLN
1	B	63	ASN
1	B	84	GLN
1	B	210	HIS
1	B	231	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

15 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#|Z| > 2$	Counts	RMSZ	$\#|Z| > 2$
4	GOL	A	1257	-	5,5,5	4.52	5 (100%)	5,5,5	5.73	3 (60%)
3	SO4	B	1255	-	4,4,4	0.43	0	6,6,6	0.77	0
2	ACT	A	301	-	3,3,3	1.27	1 (33%)	3,3,3	0.79	0
2	ACT	A	300	-	3,3,3	1.25	1 (33%)	3,3,3	0.70	0
4	GOL	B	1259	-	5,5,5	4.51	5 (100%)	5,5,5	5.72	3 (60%)
4	GOL	A	1258	-	5,5,5	4.56	5 (100%)	5,5,5	5.67	3 (60%)
4	GOL	A	1259	-	5,5,5	4.47	5 (100%)	5,5,5	5.71	3 (60%)
3	SO4	A	1255	-	4,4,4	0.41	0	6,6,6	0.79	0
4	GOL	B	1256	-	5,5,5	4.45	5 (100%)	5,5,5	5.72	3 (60%)
4	GOL	B	1260	-	5,5,5	4.48	5 (100%)	5,5,5	5.70	3 (60%)
4	GOL	A	1256	-	5,5,5	4.52	5 (100%)	5,5,5	5.71	3 (60%)
4	GOL	B	1257	-	5,5,5	4.52	5 (100%)	5,5,5	5.72	3 (60%)
2	ACT	B	301	-	3,3,3	1.30	1 (33%)	3,3,3	0.80	0
4	GOL	B	1258	-	5,5,5	4.51	5 (100%)	5,5,5	5.73	3 (60%)
2	ACT	B	300	-	3,3,3	1.14	0	3,3,3	0.75	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
4	GOL	A	1257	-	-	2/4/4/4	-
4	GOL	B	1259	-	-	2/4/4/4	-
4	GOL	B	1256	-	-	3/4/4/4	-
4	GOL	A	1258	-	-	2/4/4/4	-
4	GOL	A	1259	-	-	2/4/4/4	-
4	GOL	B	1260	-	-	3/4/4/4	-
4	GOL	A	1256	-	-	2/4/4/4	-
4	GOL	B	1257	-	-	3/4/4/4	-
4	GOL	B	1258	-	-	3/4/4/4	-

All (48) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1256	GOL	C3-C2	-7.45	1.21	1.51
4	B	1257	GOL	C3-C2	-7.44	1.21	1.51
4	A	1257	GOL	C3-C2	-7.43	1.21	1.51
4	A	1258	GOL	C3-C2	-7.38	1.21	1.51
4	B	1260	GOL	C3-C2	-7.35	1.21	1.51
4	B	1259	GOL	C3-C2	-7.32	1.21	1.51
4	B	1258	GOL	C3-C2	-7.32	1.21	1.51
4	B	1256	GOL	C3-C2	-7.31	1.21	1.51
4	A	1259	GOL	C3-C2	-7.29	1.21	1.51
4	A	1258	GOL	O1-C1	4.63	1.61	1.42
4	A	1256	GOL	O1-C1	4.59	1.61	1.42
4	B	1259	GOL	O1-C1	4.58	1.61	1.42
4	B	1256	GOL	O1-C1	4.54	1.61	1.42
4	B	1260	GOL	O1-C1	4.54	1.61	1.42
4	B	1258	GOL	O1-C1	4.53	1.61	1.42
4	B	1257	GOL	O1-C1	4.51	1.61	1.42
4	A	1257	GOL	O1-C1	4.48	1.61	1.42
4	A	1259	GOL	O1-C1	4.45	1.61	1.42
4	B	1258	GOL	O3-C3	3.50	1.57	1.42
4	A	1258	GOL	O3-C3	3.45	1.57	1.42
4	A	1259	GOL	O3-C3	3.43	1.56	1.42
4	B	1259	GOL	O3-C3	3.42	1.56	1.42
4	A	1257	GOL	O3-C3	3.40	1.56	1.42
4	A	1256	GOL	O3-C3	3.38	1.56	1.42
4	B	1256	GOL	O3-C3	3.37	1.56	1.42
4	B	1257	GOL	O3-C3	3.35	1.56	1.42
4	B	1260	GOL	O3-C3	3.27	1.56	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1258	GOL	O2-C2	-2.96	1.34	1.43
4	B	1259	GOL	O2-C2	-2.85	1.34	1.43
4	A	1259	GOL	C1-C2	-2.82	1.40	1.51
4	B	1258	GOL	C1-C2	-2.81	1.40	1.51
4	A	1257	GOL	O2-C2	-2.79	1.35	1.43
4	A	1257	GOL	C1-C2	-2.78	1.40	1.51
4	B	1257	GOL	O2-C2	-2.78	1.35	1.43
4	B	1258	GOL	O2-C2	-2.77	1.35	1.43
4	B	1257	GOL	C1-C2	-2.76	1.40	1.51
4	B	1260	GOL	O2-C2	-2.74	1.35	1.43
4	B	1259	GOL	C1-C2	-2.74	1.40	1.51
4	A	1258	GOL	C1-C2	-2.73	1.40	1.51
4	B	1260	GOL	C1-C2	-2.73	1.40	1.51
4	A	1256	GOL	O2-C2	-2.73	1.35	1.43
4	B	1256	GOL	C1-C2	-2.71	1.40	1.51
4	A	1259	GOL	O2-C2	-2.70	1.35	1.43
4	A	1256	GOL	C1-C2	-2.56	1.41	1.51
4	B	1256	GOL	O2-C2	-2.52	1.35	1.43
2	B	301	ACT	O-C	2.16	1.32	1.22
2	A	301	ACT	O-C	2.14	1.32	1.22
2	A	300	ACT	O-C	2.05	1.31	1.22

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	1257	GOL	O3-C3-C2	10.53	160.68	110.20
4	B	1259	GOL	O3-C3-C2	10.49	160.50	110.20
4	B	1256	GOL	O3-C3-C2	10.49	160.49	110.20
4	B	1258	GOL	O3-C3-C2	10.45	160.30	110.20
4	A	1259	GOL	O3-C3-C2	10.45	160.29	110.20
4	B	1260	GOL	O3-C3-C2	10.44	160.26	110.20
4	B	1257	GOL	O3-C3-C2	10.43	160.22	110.20
4	A	1256	GOL	O3-C3-C2	10.41	160.10	110.20
4	A	1258	GOL	O3-C3-C2	10.35	159.81	110.20
4	B	1258	GOL	O2-C2-C3	6.62	138.29	109.12
4	B	1257	GOL	O2-C2-C3	6.59	138.17	109.12
4	A	1256	GOL	O2-C2-C3	6.55	137.98	109.12
4	A	1259	GOL	O2-C2-C3	6.54	137.95	109.12
4	B	1260	GOL	O2-C2-C3	6.53	137.90	109.12
4	B	1259	GOL	O2-C2-C3	6.52	137.84	109.12
4	B	1256	GOL	O2-C2-C3	6.51	137.78	109.12
4	A	1258	GOL	O2-C2-C3	6.45	137.54	109.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	1257	GOL	O2-C2-C3	6.45	137.53	109.12
4	A	1256	GOL	O1-C1-C2	3.37	126.36	110.20
4	A	1258	GOL	O1-C1-C2	3.36	126.30	110.20
4	B	1258	GOL	O1-C1-C2	3.26	125.81	110.20
4	B	1259	GOL	O1-C1-C2	3.25	125.80	110.20
4	A	1257	GOL	O1-C1-C2	3.24	125.72	110.20
4	A	1259	GOL	O1-C1-C2	3.24	125.72	110.20
4	B	1256	GOL	O1-C1-C2	3.21	125.59	110.20
4	B	1257	GOL	O1-C1-C2	3.21	125.59	110.20
4	B	1260	GOL	O1-C1-C2	3.20	125.53	110.20

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1257	GOL	C1-C2-C3-O3
4	A	1258	GOL	O1-C1-C2-C3
4	A	1259	GOL	O1-C1-C2-C3
4	B	1257	GOL	C1-C2-C3-O3
4	B	1258	GOL	O2-C2-C3-O3
4	A	1257	GOL	O1-C1-C2-C3
4	A	1258	GOL	C1-C2-C3-O3
4	A	1259	GOL	C1-C2-C3-O3
4	B	1256	GOL	C1-C2-C3-O3
4	B	1258	GOL	O1-C1-C2-C3
4	B	1259	GOL	C1-C2-C3-O3
4	B	1260	GOL	C1-C2-C3-O3
4	A	1256	GOL	O1-C1-C2-O2
4	A	1256	GOL	O2-C2-C3-O3
4	B	1256	GOL	O1-C1-C2-O2
4	B	1257	GOL	O1-C1-C2-O2
4	B	1259	GOL	O1-C1-C2-O2
4	B	1260	GOL	O1-C1-C2-O2
4	B	1256	GOL	O1-C1-C2-C3
4	B	1258	GOL	O1-C1-C2-O2
4	B	1257	GOL	O2-C2-C3-O3
4	B	1260	GOL	O1-C1-C2-C3

There are no ring outliers.

9 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	ACT	5	0
2	A	300	ACT	3	0
4	A	1258	GOL	3	0
4	A	1259	GOL	1	0
4	A	1256	GOL	1	0
4	B	1257	GOL	1	0
2	B	301	ACT	7	0
4	B	1258	GOL	1	0
2	B	300	ACT	3	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 ⓘ

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	252/254 (99%)	0.30	9 (3%)	42	41	16, 28, 47, 66	0
1	B	252/254 (99%)	0.33	8 (3%)	47	45	16, 29, 49, 60	0
All	All	504/508 (99%)	0.31	17 (3%)	45	43	16, 29, 48, 66	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	254	CYS	5.7
1	A	2	GLN	3.7
1	B	189	ARG	3.6
1	B	106	SER	2.9
1	B	188	CYS	2.9
1	B	254	CYS	2.9
1	B	105	PRO	2.8
1	A	121	THR	2.5
1	A	114	LEU	2.4
1	B	238	ASN	2.4
1	A	53	SER	2.2
1	A	123	VAL	2.2
1	A	210	HIS	2.2
1	B	123	VAL	2.1
1	B	192	TYR	2.1
1	A	67	GLU	2.0
1	A	63	ASN	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3   Carbohydrates ⓘ

There are no monosaccharides 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
4	GOL	B	1259	6/6	0.55	0.38	71,71,71,71	0
4	GOL	B	1260	6/6	0.67	0.24	45,46,46,46	0
4	GOL	B	1257	6/6	0.71	0.38	64,65,65,65	0
4	GOL	A	1256	6/6	0.73	0.33	56,57,57,58	0
2	ACT	B	301	4/4	0.76	0.23	41,41,41,42	0
4	GOL	A	1257	6/6	0.77	0.25	61,61,61,61	0
4	GOL	B	1258	6/6	0.78	0.24	70,70,70,70	0
4	GOL	A	1258	6/6	0.80	0.23	49,49,50,50	0
4	GOL	A	1259	6/6	0.83	0.27	52,52,53,53	0
2	ACT	A	301	4/4	0.84	0.16	41,42,42,42	0
4	GOL	B	1256	6/6	0.87	0.21	34,38,38,39	0
3	SO4	B	1255	5/5	0.88	0.32	78,78,78,78	0
2	ACT	A	300	4/4	0.91	0.21	33,33,34,34	0
2	ACT	B	300	4/4	0.96	0.14	34,35,35,36	0
3	SO4	A	1255	5/5	0.99	0.11	26,26,27,27	0

6.5   Other polymers ⓘ

There are no such residues in this entry.