



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 02:21 am GMT

PDB ID : 1BKX
Title : A BINARY COMPLEX OF THE CATALYTIC SUBUNIT OF CAMP-DEPENDENT PROTEIN KINASE AND ADENOSINE FURTHER DEFINES CONFORMATIONAL FLEXIBILITY
Authors : Narayana, N.; Cox, S.; Xuong, N.; Ten Eyck, L.F.; Taylor, S.S.
Deposited on : 1997-07-01
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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

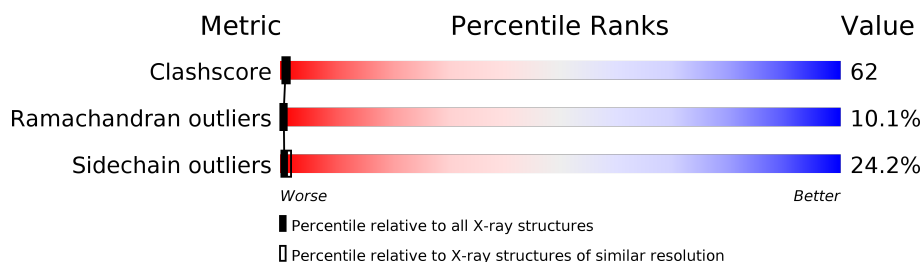
1 Overall quality at a glance

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))
Clashscore	112137	2895 (2.60-2.60)
Ramachandran outliers	110173	2848 (2.60-2.60)
Sidechain outliers	110143	2848 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	350	

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
1	SEP	A	338	-	-	X	-

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2832 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.

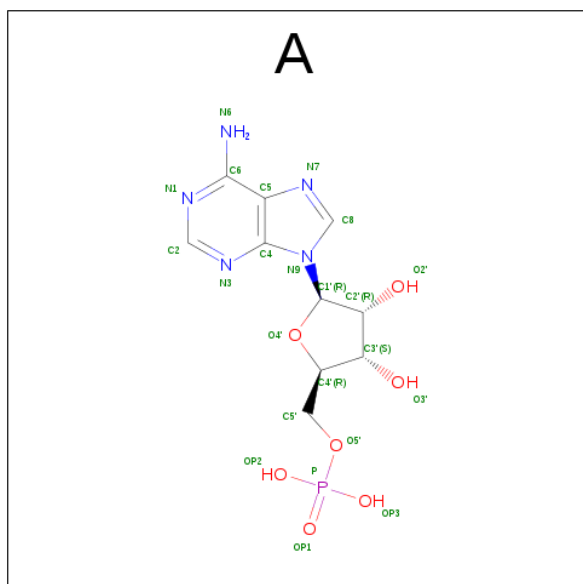
- Molecule 1 is a protein called CAMP-DEPENDENT PROTEIN KINASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	339	2801	1813	469	509	2	8	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	10	SEP	SER	CONFLICT	UNP P05132
A	197	TPO	THR	MODIFIED RESIDUE	UNP P05132
A	338	SEP	SER	MODIFIED RESIDUE	UNP P05132

- Molecule 2 is ADENOSINE-5'-MONOPHOSPHATE (three-letter code: A) (formula: $C_{10}H_{14}N_5O_7P$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	19	10	5	4	0	0

- Molecule 3 is water.

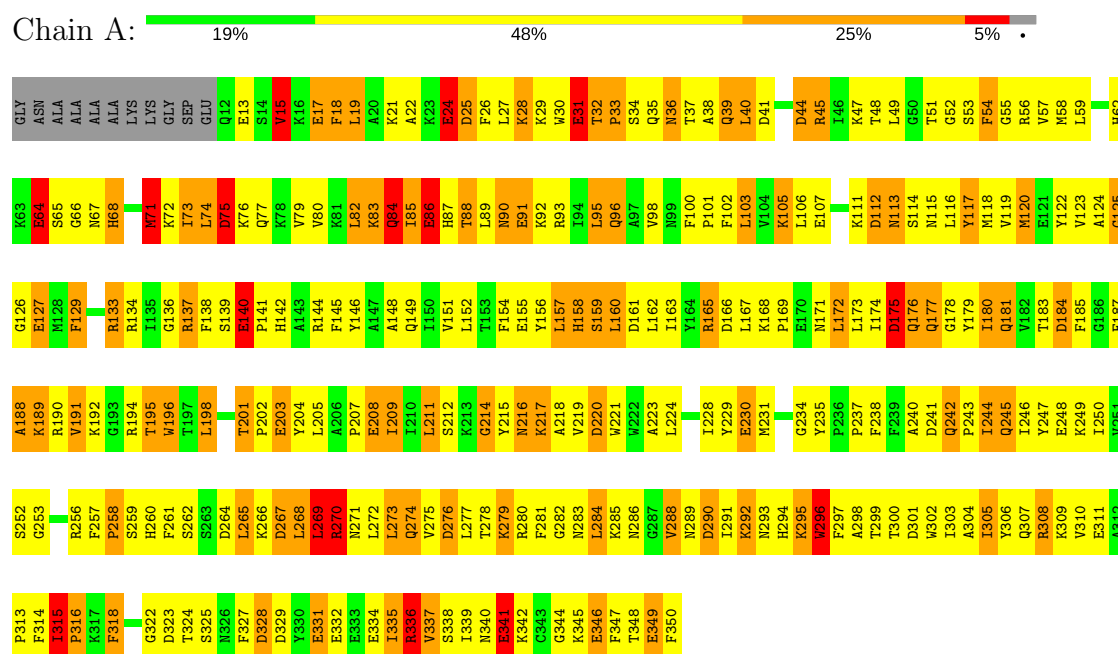
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	12	Total	O	0	0
			12	12		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

Note EDS was not executed.

• Molecule 1: CAMP-DEPENDENT PROTEIN KINASE



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	55.85Å 73.23Å 98.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.60	Depositor
% Data completeness (in resolution range)	86.0 (10.00-2.60)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
Refinement program	TNT V. 5-E, X-PLOR	Depositor
R, R_{free}	0.205 , 0.340	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2832	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: TPO, SEP

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	1.39	25/2849 (0.9%)	1.20	40/3836 (1.0%)

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	31	GLU	CD-OE1	9.99	1.36	1.25
1	A	91	GLU	CD-OE2	8.79	1.35	1.25
1	A	349	GLU	CD-OE2	8.49	1.34	1.25
1	A	13	GLU	CD-OE2	8.10	1.34	1.25
1	A	17	GLU	CD-OE2	7.48	1.33	1.25
1	A	86	GLU	CD-OE2	7.47	1.33	1.25
1	A	140	GLU	CD-OE2	7.45	1.33	1.25
1	A	155	GLU	CD-OE2	7.33	1.33	1.25
1	A	24	GLU	CD-OE2	7.25	1.33	1.25
1	A	248	GLU	CD-OE2	7.24	1.33	1.25
1	A	203	GLU	CD-OE2	6.84	1.33	1.25
1	A	127	GLU	CD-OE2	6.77	1.33	1.25
1	A	341	GLU	CD-OE2	6.74	1.33	1.25
1	A	140	GLU	CD-OE1	-6.45	1.18	1.25
1	A	346	GLU	CD-OE2	6.43	1.32	1.25
1	A	311	GLU	CD-OE2	6.25	1.32	1.25
1	A	64	GLU	CD-OE2	6.04	1.32	1.25
1	A	136	GLY	N-CA	5.89	1.54	1.46
1	A	230	GLU	CD-OE2	5.73	1.31	1.25
1	A	329	ASP	CG-OD2	5.62	1.38	1.25
1	A	331	GLU	CD-OE1	5.54	1.31	1.25
1	A	328	ASP	CG-OD2	5.53	1.38	1.25
1	A	332	GLU	CD-OE1	5.53	1.31	1.25
1	A	208	GLU	CD-OE2	5.16	1.31	1.25
1	A	258	PRO	N-CA	-5.04	1.38	1.47

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	315	ILE	C-N-CD	-10.03	98.54	120.60
1	A	329	ASP	CB-CG-OD2	-9.90	109.39	118.30
1	A	328	ASP	CB-CG-OD2	-8.65	110.52	118.30
1	A	290	ASP	CB-CG-OD2	-8.24	110.89	118.30
1	A	175	ASP	CB-CG-OD2	-7.88	111.21	118.30
1	A	290	ASP	CB-CG-OD1	7.36	124.92	118.30
1	A	44	ASP	CB-CG-OD2	-7.27	111.76	118.30
1	A	264	ASP	CB-CG-OD2	-7.01	111.99	118.30
1	A	75	ASP	CB-CG-OD2	-6.84	112.14	118.30
1	A	323	ASP	CB-CG-OD2	-6.84	112.15	118.30
1	A	75	ASP	CB-CG-OD1	6.73	124.36	118.30
1	A	264	ASP	CB-CG-OD1	6.65	124.29	118.30
1	A	41	ASP	CB-CG-OD2	-6.65	112.31	118.30
1	A	166	ASP	CB-CG-OD2	-6.53	112.42	118.30
1	A	329	ASP	CB-CG-OD1	6.38	124.04	118.30
1	A	241	ASP	CB-CG-OD2	-6.30	112.63	118.30
1	A	301	ASP	CB-CG-OD1	6.20	123.88	118.30
1	A	184	ASP	CB-CG-OD2	-6.17	112.75	118.30
1	A	301	ASP	CB-CG-OD2	-6.03	112.87	118.30
1	A	276	ASP	CB-CG-OD2	-5.76	113.11	118.30
1	A	184	ASP	CB-CG-OD1	5.74	123.46	118.30
1	A	71	MET	CG-SD-CE	5.73	109.36	100.20
1	A	194	ARG	NE-CZ-NH2	-5.66	117.47	120.30
1	A	165	ARG	NE-CZ-NH1	5.56	123.08	120.30
1	A	166	ASP	CB-CG-OD1	5.53	123.28	118.30
1	A	328	ASP	CB-CG-OD1	5.50	123.25	118.30
1	A	276	ASP	CB-CG-OD1	5.46	123.22	118.30
1	A	112	ASP	CB-CG-OD2	-5.44	113.41	118.30
1	A	241	ASP	CB-CG-OD1	5.44	123.19	118.30
1	A	41	ASP	CB-CG-OD1	5.43	123.18	118.30
1	A	25	ASP	CB-CG-OD2	-5.42	113.42	118.30
1	A	175	ASP	CB-CG-OD1	5.42	123.18	118.30
1	A	44	ASP	CB-CG-OD1	5.39	123.15	118.30
1	A	336	ARG	NE-CZ-NH2	-5.35	117.62	120.30
1	A	25	ASP	CB-CG-OD1	5.24	123.02	118.30
1	A	336	ARG	NE-CZ-NH1	5.20	122.90	120.30
1	A	133	ARG	NE-CZ-NH1	5.19	122.89	120.30
1	A	323	ASP	CB-CG-OD1	5.16	122.94	118.30
1	A	220	ASP	CB-CG-OD2	-5.15	113.67	118.30
1	A	267	ASP	CB-CG-OD2	-5.02	113.79	118.30

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	2801	0	2781	349	0
2	A	19	0	13	1	0
3	A	12	0	0	2	0
All	All	2832	0	2794	350	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 62.

All (350) 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:A:295:LYS:H	1:A:295:LYS:HD2	1.27	0.98
1:A:274:GLN:HE21	1:A:274:GLN:HA	1.34	0.92
1:A:337:VAL:O	1:A:338:SEP:O	1.88	0.92
1:A:242:GLN:HG2	1:A:243:PRO:HD2	1.48	0.92
1:A:167:LEU:HD11	1:A:172:LEU:HD21	1.52	0.89
1:A:189:LYS:HE2	1:A:191:VAL:CG1	2.02	0.89
1:A:72:LYS:HD2	1:A:118:MET:CE	2.03	0.89
1:A:116:LEU:HD22	1:A:350:PHE:CD2	2.08	0.88
1:A:90:ASN:H	1:A:90:ASN:ND2	1.70	0.88
1:A:93:ARG:HA	1:A:96:GLN:HE21	1.36	0.88
1:A:167:LEU:HD12	1:A:168:LYS:H	1.40	0.86
1:A:75:ASP:HA	1:A:115:ASN:HB3	1.58	0.86
1:A:154:PHE:HZ	1:A:167:LEU:HD22	1.38	0.85
1:A:274:GLN:NE2	1:A:274:GLN:HA	1.92	0.84
1:A:261:PHE:CD2	1:A:265:LEU:HD13	2.13	0.84
1:A:209:ILE:HD13	1:A:215:TYR:CD1	2.13	0.83
1:A:277:LEU:HB2	1:A:283:ASN:ND2	1.93	0.83
1:A:77:GLN:HG3	1:A:342:LYS:HE3	1.60	0.83
1:A:137:ARG:HE	1:A:260:HIS:CE1	1.97	0.83
1:A:201:THR:HG22	1:A:202:PRO:HD2	1.60	0.82
1:A:72:LYS:HD2	1:A:118:MET:HE3	1.60	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:GLN:CG	1:A:342:LYS:HE3	2.10	0.82
1:A:158:HIS:ND1	1:A:217:LYS:HB3	1.94	0.82
1:A:123:VAL:HG21	1:A:173:LEU:HD13	1.60	0.81
1:A:242:GLN:H	1:A:245:GLN:HE22	1.27	0.81
1:A:91:GLU:HG3	1:A:185:PHE:HB2	1.61	0.80
1:A:258:PRO:HG2	1:A:261:PHE:CE1	2.16	0.79
1:A:123:VAL:CG2	1:A:173:LEU:HD13	2.13	0.79
1:A:167:LEU:HD12	1:A:168:LYS:N	1.98	0.77
1:A:90:ASN:N	1:A:90:ASN:ND2	2.29	0.77
1:A:189:LYS:HE2	1:A:191:VAL:HG11	1.66	0.77
1:A:161:ASP:HB3	1:A:191:VAL:O	1.84	0.77
1:A:315:ILE:HD13	1:A:316:PRO:HD2	1.67	0.77
1:A:77:GLN:NE2	1:A:342:LYS:HG3	2.00	0.76
1:A:35:GLN:O	1:A:36:ASN:C	2.24	0.76
1:A:176:GLN:HA	1:A:318:PHE:CZ	2.21	0.76
1:A:172:LEU:HD12	1:A:180:ILE:HD12	1.69	0.75
1:A:95:LEU:HD11	1:A:185:PHE:CD1	2.22	0.75
1:A:163:ILE:HG22	1:A:165:ARG:HG3	1.68	0.74
1:A:281:PHE:HB3	1:A:291:ILE:HG13	1.69	0.74
1:A:154:PHE:CZ	1:A:167:LEU:HD22	2.22	0.74
1:A:168:LYS:O	1:A:172:LEU:HD23	1.86	0.74
1:A:277:LEU:H	1:A:277:LEU:HD23	1.53	0.74
1:A:93:ARG:HA	1:A:96:GLN:NE2	2.00	0.74
1:A:242:GLN:H	1:A:245:GLN:NE2	1.85	0.74
1:A:337:VAL:O	1:A:338:SEP:C	2.36	0.74
1:A:335:ILE:HD12	1:A:335:ILE:H	1.54	0.73
1:A:256:ARG:HG2	1:A:256:ARG:HH11	1.53	0.72
1:A:59:LEU:HD22	1:A:324:THR:CG2	2.18	0.72
1:A:163:ILE:CG2	1:A:165:ARG:HG3	2.20	0.71
1:A:274:GLN:HG3	1:A:279:LYS:O	1.90	0.71
1:A:113:ASN:ND2	1:A:341:GLU:HA	2.06	0.69
1:A:40:LEU:HD22	1:A:45:ARG:CZ	2.23	0.69
1:A:82:LEU:HB2	1:A:84:GLN:HG2	1.74	0.69
1:A:85:ILE:HG22	1:A:89:LEU:HD11	1.74	0.69
1:A:336:ARG:HG2	1:A:336:ARG:HH11	1.57	0.69
1:A:75:ASP:HA	1:A:115:ASN:CB	2.21	0.69
1:A:74:LEU:HD12	1:A:74:LEU:H	1.58	0.69
1:A:221:TRP:CD1	1:A:282:GLY:HA3	2.28	0.69
1:A:158:HIS:CE1	1:A:217:LYS:HB3	2.28	0.69
1:A:87:HIS:O	1:A:89:LEU:N	2.26	0.68
1:A:230:GLU:HG3	1:A:234:GLY:O	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:48:THR:HA	1:A:58:MET:HB2	1.75	0.67
1:A:86:GLU:O	1:A:90:ASN:ND2	2.28	0.67
2:A:351:A:H5'	2:A:351:A:H8	1.59	0.67
1:A:83:LYS:O	1:A:85:ILE:N	2.27	0.67
1:A:307:GLN:HB3	1:A:309:LYS:HG2	1.76	0.67
1:A:31:GLU:HA	1:A:93:ARG:NH2	2.09	0.67
1:A:195:THR:O	1:A:214:GLY:HA2	1.96	0.66
1:A:217:LYS:O	1:A:220:ASP:HB2	1.95	0.65
1:A:85:ILE:O	1:A:89:LEU:HD12	1.96	0.65
1:A:71:MET:HG3	1:A:73:ILE:CG2	2.26	0.65
1:A:18:PHE:HZ	1:A:306:TYR:HH	1.42	0.65
1:A:262:SER:OG	1:A:265:LEU:HB2	1.96	0.65
1:A:349:GLU:HG2	1:A:349:GLU:O	1.97	0.65
1:A:47:LYS:O	1:A:58:MET:HB2	1.96	0.64
1:A:201:THR:HG22	1:A:203:GLU:OE1	1.97	0.64
1:A:279:LYS:HA	1:A:284:LEU:HD11	1.79	0.64
1:A:256:ARG:HG2	1:A:256:ARG:NH1	2.10	0.64
1:A:39:GLN:HA	3:A:355:HOH:O	1.97	0.64
1:A:173:LEU:HD11	1:A:183:THR:HG21	1.79	0.64
1:A:28:LYS:O	1:A:31:GLU:N	2.31	0.64
1:A:144:ARG:HD3	1:A:300:THR:HG23	1.80	0.64
1:A:142:HIS:NE2	1:A:314:PHE:HB2	2.12	0.64
1:A:215:TYR:HB2	1:A:219:VAL:CG1	2.28	0.63
1:A:273:LEU:H	1:A:273:LEU:HD12	1.63	0.63
1:A:305:ILE:HG22	1:A:306:TYR:N	2.13	0.63
1:A:102:PHE:O	1:A:181:GLN:HA	1.98	0.63
1:A:129:PHE:HB2	1:A:169:PRO:HB2	1.80	0.63
1:A:165:ARG:NE	1:A:187:PHE:O	2.28	0.62
1:A:244:ILE:O	1:A:247:TYR:HB2	1.99	0.62
1:A:82:LEU:O	1:A:84:GLN:N	2.31	0.62
1:A:304:ALA:CB	1:A:310:VAL:HG23	2.29	0.62
1:A:112:ASP:O	1:A:114:SER:N	2.33	0.62
1:A:65:SER:O	1:A:67:ASN:N	2.32	0.62
1:A:62:HIS:HE1	1:A:64:GLU:HB2	1.65	0.62
1:A:176:GLN:O	1:A:315:ILE:HD11	1.99	0.61
1:A:18:PHE:O	1:A:21:LYS:N	2.33	0.61
1:A:243:PRO:HA	1:A:246:ILE:HD12	1.83	0.61
1:A:83:LYS:C	1:A:85:ILE:H	2.03	0.61
1:A:335:ILE:HD12	1:A:335:ILE:N	2.14	0.61
1:A:123:VAL:HG21	1:A:173:LEU:CD1	2.30	0.61
1:A:82:LEU:HD12	1:A:84:GLN:HG3	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:27:LEU:O	1:A:30:TRP:HB3	2.00	0.61
1:A:146:TYR:O	1:A:149:GLN:N	2.28	0.61
1:A:95:LEU:HD11	1:A:185:PHE:CE1	2.35	0.61
1:A:201:THR:CG2	1:A:202:PRO:HD2	2.30	0.61
1:A:303:ILE:O	1:A:307:GLN:N	2.27	0.61
1:A:295:LYS:HD2	1:A:295:LYS:N	2.07	0.61
1:A:48:THR:HA	1:A:58:MET:CB	2.31	0.61
1:A:246:ILE:O	1:A:250:ILE:HG13	2.01	0.60
1:A:89:LEU:HB3	1:A:349:GLU:OE1	2.01	0.60
1:A:116:LEU:HD22	1:A:350:PHE:CG	2.36	0.60
1:A:189:LYS:HE2	1:A:191:VAL:HG13	1.83	0.60
1:A:295:LYS:O	1:A:298:ALA:N	2.35	0.60
1:A:304:ALA:HB1	1:A:310:VAL:HG23	1.83	0.60
1:A:276:ASP:OD1	1:A:278:THR:N	2.34	0.59
1:A:159:SER:OG	1:A:160:LEU:HD13	2.01	0.59
1:A:57:VAL:HG23	1:A:72:LYS:HG3	1.84	0.59
1:A:100:PHE:HB3	1:A:103:LEU:HD22	1.83	0.59
1:A:82:LEU:CD1	1:A:84:GLN:HG3	2.32	0.59
1:A:93:ARG:HG3	1:A:96:GLN:HE22	1.68	0.58
1:A:268:LEU:O	1:A:271:ASN:HB2	2.03	0.58
1:A:33:PRO:HB3	1:A:96:GLN:NE2	2.19	0.58
1:A:35:GLN:NE2	1:A:350:PHE:OXT	2.37	0.58
1:A:142:HIS:CD2	1:A:313:PRO:HB2	2.39	0.58
1:A:161:ASP:O	1:A:191:VAL:N	2.37	0.58
1:A:277:LEU:HB2	1:A:283:ASN:HD22	1.68	0.58
1:A:336:ARG:HG2	1:A:336:ARG:NH1	2.15	0.58
1:A:71:MET:HG3	1:A:73:ILE:HG23	1.84	0.58
1:A:205:LEU:HD12	1:A:247:TYR:HE1	1.67	0.58
1:A:209:ILE:HD13	1:A:215:TYR:CE1	2.38	0.58
1:A:337:VAL:HG12	1:A:337:VAL:O	2.04	0.58
1:A:123:VAL:HG11	1:A:181:GLN:HG3	1.85	0.57
1:A:59:LEU:HD22	1:A:324:THR:HG21	1.85	0.57
1:A:295:LYS:CD	1:A:295:LYS:H	2.08	0.57
1:A:100:PHE:CG	1:A:101:PRO:HD2	2.40	0.56
1:A:28:LYS:O	1:A:29:LYS:C	2.42	0.56
1:A:71:MET:HB2	1:A:119:VAL:HG22	1.86	0.56
1:A:273:LEU:HD12	1:A:273:LEU:N	2.19	0.56
1:A:85:ILE:HG22	1:A:89:LEU:CD1	2.35	0.56
1:A:304:ALA:O	1:A:308:ARG:N	2.38	0.56
1:A:137:ARG:HH21	1:A:260:HIS:CE1	2.22	0.56
1:A:280:ARG:O	1:A:281:PHE:C	2.42	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:GLN:HG3	1:A:342:LYS:CE	2.33	0.56
1:A:315:ILE:HG23	1:A:316:PRO:N	2.21	0.56
1:A:56:ARG:NH2	1:A:331:GLU:O	2.26	0.55
1:A:24:GLU:O	1:A:25:ASP:C	2.44	0.55
1:A:106:LEU:HD12	1:A:107:GLU:H	1.71	0.55
1:A:240:ALA:H	1:A:246:ILE:HG12	1.72	0.55
1:A:215:TYR:HB2	1:A:219:VAL:HG13	1.88	0.54
1:A:127:GLU:HG2	3:A:363:HOH:O	2.06	0.54
1:A:277:LEU:HB2	1:A:283:ASN:HD21	1.69	0.54
1:A:297:PHE:CD1	1:A:302:TRP:CZ2	2.96	0.54
1:A:106:LEU:HD12	1:A:107:GLU:N	2.22	0.54
1:A:173:LEU:HD11	1:A:183:THR:CG2	2.38	0.54
1:A:234:GLY:O	1:A:235:TYR:C	2.45	0.54
1:A:29:LYS:O	1:A:30:TRP:C	2.44	0.54
1:A:125:GLY:HA3	1:A:174:ILE:O	2.09	0.53
1:A:57:VAL:CG2	1:A:72:LYS:HA	2.38	0.53
1:A:138:PHE:CE2	1:A:146:TYR:HE2	2.27	0.53
1:A:62:HIS:CE1	1:A:64:GLU:HB2	2.42	0.53
1:A:76:LYS:HG3	1:A:114:SER:O	2.09	0.53
1:A:288:VAL:O	1:A:292:LYS:HB2	2.07	0.53
1:A:336:ARG:CG	1:A:336:ARG:HH11	2.21	0.53
1:A:314:PHE:CG	1:A:315:ILE:N	2.77	0.53
1:A:305:ILE:O	1:A:308:ARG:N	2.37	0.52
1:A:341:GLU:CD	1:A:344:GLY:HA3	2.28	0.52
1:A:93:ARG:HG3	1:A:96:GLN:NE2	2.24	0.52
1:A:162:LEU:HD23	1:A:190:ARG:HA	1.91	0.52
1:A:208:GLU:OE1	1:A:219:VAL:HG12	2.10	0.52
1:A:71:MET:CG	1:A:73:ILE:CG2	2.87	0.52
1:A:92:LYS:O	1:A:96:GLN:HB3	2.09	0.52
1:A:74:LEU:O	1:A:115:ASN:HB2	2.10	0.52
1:A:119:VAL:O	1:A:119:VAL:HG12	2.09	0.52
1:A:216:ASN:O	1:A:218:ALA:N	2.43	0.51
1:A:306:TYR:C	1:A:308:ARG:H	2.13	0.51
1:A:90:ASN:N	1:A:90:ASN:HD22	2.08	0.51
1:A:146:TYR:HD2	1:A:231:MET:SD	2.33	0.51
1:A:257:PHE:HE1	1:A:269:LEU:HD23	1.75	0.51
1:A:272:LEU:C	1:A:274:GLN:H	2.14	0.51
1:A:202:PRO:HA	1:A:205:LEU:CD1	2.41	0.51
1:A:242:GLN:CG	1:A:243:PRO:HD2	2.33	0.51
1:A:276:ASP:HB3	1:A:279:LYS:CG	2.41	0.51
1:A:57:VAL:HG22	1:A:72:LYS:HA	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142:HIS:CD2	1:A:313:PRO:HG2	2.45	0.51
1:A:187:PHE:O	1:A:188:ALA:O	2.29	0.51
1:A:295:LYS:O	1:A:297:PHE:N	2.44	0.51
1:A:215:TYR:HB2	1:A:219:VAL:HG11	1.93	0.50
1:A:261:PHE:CE2	1:A:265:LEU:HD13	2.46	0.50
1:A:113:ASN:HD22	1:A:341:GLU:HA	1.73	0.50
1:A:142:HIS:CE1	1:A:314:PHE:HB2	2.46	0.50
1:A:161:ASP:O	1:A:190:ARG:HA	2.12	0.50
1:A:154:PHE:CD1	1:A:154:PHE:N	2.78	0.50
1:A:346:GLU:H	1:A:346:GLU:CD	2.15	0.50
1:A:57:VAL:HG22	1:A:72:LYS:CA	2.41	0.50
1:A:91:GLU:O	1:A:95:LEU:HD22	2.12	0.50
1:A:286:ASN:HB3	1:A:290:ASP:OD1	2.12	0.49
1:A:216:ASN:O	1:A:219:VAL:HG22	2.12	0.49
1:A:284:LEU:HB2	1:A:290:ASP:OD2	2.11	0.49
1:A:74:LEU:N	1:A:74:LEU:HD12	2.25	0.49
1:A:33:PRO:O	1:A:34:SER:C	2.49	0.49
1:A:84:GLN:HA	1:A:84:GLN:HE21	1.77	0.49
1:A:111:LYS:NZ	1:A:347:PHE:O	2.29	0.49
1:A:98:VAL:HG22	1:A:103:LEU:HD23	1.94	0.49
1:A:267:ASP:HB3	1:A:294:HIS:CE1	2.47	0.49
1:A:76:LYS:O	1:A:80:VAL:HG23	2.11	0.49
1:A:261:PHE:HB3	1:A:266:LYS:HG3	1.94	0.49
1:A:234:GLY:O	1:A:235:TYR:O	2.31	0.48
1:A:76:LYS:HE3	1:A:113:ASN:O	2.13	0.48
1:A:139:SER:O	1:A:142:HIS:N	2.46	0.48
1:A:228:ILE:O	1:A:229:TYR:C	2.47	0.48
1:A:207:PRO:O	1:A:211:LEU:HD22	2.12	0.48
1:A:82:LEU:C	1:A:84:GLN:H	2.15	0.48
1:A:142:HIS:CD2	1:A:313:PRO:CG	2.96	0.48
1:A:18:PHE:HZ	1:A:306:TYR:OH	1.96	0.48
1:A:295:LYS:O	1:A:296:TRP:C	2.49	0.48
1:A:267:ASP:OD2	1:A:294:HIS:NE2	2.42	0.48
1:A:160:LEU:HD13	1:A:160:LEU:N	2.29	0.47
1:A:198:LEU:HD23	1:A:209:ILE:HG22	1.96	0.47
1:A:252:SER:OG	1:A:253:GLY:N	2.47	0.47
1:A:267:ASP:HB3	1:A:294:HIS:NE2	2.29	0.47
1:A:100:PHE:CD1	1:A:156:TYR:CD2	3.03	0.47
1:A:154:PHE:HD1	1:A:154:PHE:N	2.11	0.47
1:A:271:ASN:O	1:A:274:GLN:HB2	2.13	0.47
1:A:87:HIS:C	1:A:89:LEU:H	2.17	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:158:HIS:HE1	1:A:220:ASP:HB2	1.79	0.47
1:A:37:THR:HG22	1:A:37:THR:O	2.15	0.47
1:A:297:PHE:CE1	1:A:302:TRP:CH2	3.03	0.47
1:A:85:ILE:O	1:A:86:GLU:C	2.52	0.47
1:A:151:VAL:CG2	1:A:224:LEU:HD21	2.44	0.47
1:A:15:VAL:HG11	1:A:292:LYS:NZ	2.30	0.47
1:A:175:ASP:OD1	1:A:177:GLN:HG2	2.15	0.47
1:A:204:TYR:OH	1:A:230:GLU:OE1	2.25	0.47
1:A:68:HIS:N	1:A:68:HIS:ND1	2.63	0.47
1:A:91:GLU:HG3	1:A:185:PHE:CB	2.38	0.47
1:A:26:PHE:O	1:A:27:LEU:C	2.53	0.46
1:A:74:LEU:HD22	1:A:88:THR:HG23	1.96	0.46
1:A:116:LEU:CD2	1:A:350:PHE:CG	2.99	0.46
1:A:54:PHE:HB2	1:A:79:VAL:HG12	1.97	0.46
1:A:272:LEU:O	1:A:274:GLN:N	2.34	0.46
1:A:168:LYS:HB2	1:A:169:PRO:CD	2.46	0.46
1:A:285:LYS:HA	1:A:285:LYS:HD3	1.59	0.46
1:A:171:ASN:N	1:A:171:ASN:OD1	2.45	0.46
1:A:224:LEU:O	1:A:224:LEU:HD12	2.15	0.46
1:A:140:GLU:OE1	1:A:262:SER:HB3	2.16	0.46
1:A:163:ILE:HG21	1:A:165:ARG:HG3	1.96	0.46
1:A:189:LYS:HG2	1:A:191:VAL:HG13	1.98	0.46
1:A:168:LYS:HB2	1:A:169:PRO:HD2	1.98	0.46
1:A:37:THR:O	1:A:38:ALA:HB2	2.16	0.46
1:A:159:SER:C	1:A:160:LEU:HD13	2.36	0.45
1:A:267:ASP:HB3	1:A:294:HIS:HE2	1.80	0.45
1:A:77:GLN:CD	1:A:342:LYS:HE3	2.35	0.45
1:A:30:TRP:NE1	1:A:93:ARG:NH1	2.64	0.45
1:A:129:PHE:CA	1:A:169:PRO:HB2	2.46	0.45
1:A:325:SER:C	1:A:327:PHE:H	2.20	0.45
1:A:216:ASN:O	1:A:217:LYS:C	2.55	0.45
1:A:202:PRO:HA	1:A:205:LEU:HD12	1.99	0.45
1:A:73:ILE:CG2	1:A:117:TYR:CD2	2.99	0.45
1:A:167:LEU:CD1	1:A:172:LEU:HD21	2.35	0.45
1:A:266:LYS:O	1:A:270:ARG:HG3	2.16	0.45
1:A:113:ASN:ND2	1:A:341:GLU:CA	2.76	0.45
1:A:82:LEU:HB2	1:A:84:GLN:CG	2.43	0.45
1:A:177:GLN:O	1:A:179:TYR:N	2.50	0.45
1:A:93:ARG:O	1:A:96:GLN:NE2	2.50	0.45
1:A:261:PHE:CG	1:A:265:LEU:HD13	2.52	0.44
1:A:111:LYS:HE2	1:A:350:PHE:OXT	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:ARG:CG	1:A:96:GLN:HE22	2.29	0.44
1:A:243:PRO:O	1:A:244:ILE:C	2.53	0.44
1:A:55:GLY:O	1:A:56:ARG:HG3	2.17	0.44
1:A:57:VAL:HG23	1:A:72:LYS:CG	2.46	0.44
1:A:172:LEU:CD2	1:A:172:LEU:N	2.79	0.44
1:A:198:LEU:HD23	1:A:209:ILE:CG2	2.47	0.44
1:A:256:ARG:CG	1:A:256:ARG:HH11	2.26	0.44
1:A:73:ILE:HA	1:A:116:LEU:O	2.18	0.44
1:A:148:ALA:HA	1:A:302:TRP:CZ3	2.53	0.44
1:A:229:TYR:CD1	1:A:229:TYR:C	2.91	0.44
1:A:87:HIS:O	1:A:90:ASN:ND2	2.51	0.44
1:A:274:GLN:NE2	1:A:274:GLN:CA	2.74	0.43
1:A:337:VAL:C	1:A:338:SEP:O	2.52	0.43
1:A:142:HIS:CD2	1:A:313:PRO:CB	3.01	0.43
1:A:315:ILE:HA	1:A:316:PRO:HD3	1.70	0.43
1:A:49:LEU:HB2	1:A:57:VAL:HG12	2.00	0.43
1:A:269:LEU:O	1:A:271:ASN:N	2.51	0.43
1:A:304:ALA:HB3	1:A:310:VAL:HG23	2.00	0.43
1:A:122:TYR:HE2	1:A:322:GLY:HA2	1.84	0.43
1:A:88:THR:HG22	1:A:88:THR:O	2.19	0.43
1:A:145:PHE:C	1:A:149:GLN:HE21	2.21	0.43
1:A:183:THR:OG1	1:A:184:ASP:N	2.51	0.43
1:A:195:THR:C	1:A:196:TRP:CE3	2.92	0.43
1:A:91:GLU:HG2	1:A:95:LEU:CD2	2.49	0.43
1:A:237:PRO:HB2	1:A:238:PHE:CE2	2.54	0.43
1:A:265:LEU:HD23	1:A:265:LEU:HA	1.88	0.43
1:A:306:TYR:C	1:A:306:TYR:CD1	2.92	0.43
1:A:83:LYS:C	1:A:85:ILE:N	2.72	0.43
1:A:144:ARG:HD3	1:A:300:THR:CG2	2.46	0.42
1:A:75:ASP:OD1	1:A:77:GLN:N	2.36	0.42
1:A:18:PHE:O	1:A:22:ALA:N	2.30	0.42
1:A:27:LEU:O	1:A:28:LYS:C	2.56	0.42
1:A:220:ASP:O	1:A:223:ALA:N	2.51	0.42
1:A:289:ASN:O	1:A:293:ASN:HB2	2.19	0.42
1:A:47:LYS:O	1:A:59:LEU:N	2.34	0.42
1:A:205:LEU:HA	1:A:205:LEU:HD23	1.88	0.42
1:A:82:LEU:C	1:A:84:GLN:N	2.73	0.42
1:A:103:LEU:HA	1:A:103:LEU:HD12	1.86	0.42
1:A:122:TYR:CE2	1:A:322:GLY:HA2	2.55	0.42
1:A:160:LEU:CD1	1:A:160:LEU:N	2.82	0.42
1:A:27:LEU:O	1:A:28:LYS:O	2.38	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:137:ARG:HE	1:A:260:HIS:HE1	1.60	0.42
1:A:139:SER:O	1:A:141:PRO:N	2.53	0.42
1:A:129:PHE:CB	1:A:169:PRO:HB2	2.46	0.42
1:A:51:THR:HB	1:A:52:GLY:H	1.72	0.42
1:A:49:LEU:HB2	1:A:57:VAL:O	2.19	0.42
1:A:133:ARG:NH2	1:A:230:GLU:OE2	2.53	0.42
1:A:134:ARG:HB3	1:A:134:ARG:CZ	2.48	0.42
1:A:204:TYR:CD1	1:A:204:TYR:N	2.88	0.42
1:A:244:ILE:HA	1:A:247:TYR:HD2	1.84	0.42
1:A:73:ILE:CG2	1:A:117:TYR:HD2	2.33	0.42
1:A:19:LEU:H	1:A:19:LEU:HG	1.61	0.42
1:A:35:GLN:HG3	1:A:36:ASN:N	2.34	0.42
1:A:244:ILE:HA	1:A:247:TYR:CD2	2.55	0.41
1:A:30:TRP:CE2	1:A:93:ARG:NH1	2.88	0.41
1:A:175:ASP:C	1:A:177:GLN:H	2.22	0.41
1:A:338:SEP:O2P	1:A:338:SEP:HA	2.20	0.41
1:A:124:ALA:O	1:A:126:GLY:N	2.53	0.41
1:A:306:TYR:C	1:A:308:ARG:N	2.73	0.41
1:A:268:LEU:O	1:A:269:LEU:C	2.59	0.41
1:A:129:PHE:HA	1:A:169:PRO:HB2	2.02	0.41
1:A:144:ARG:CD	1:A:300:THR:CG2	2.98	0.41
1:A:95:LEU:HD12	1:A:95:LEU:HA	1.88	0.41
1:A:105:LYS:O	1:A:120:MET:HA	2.21	0.41
1:A:277:LEU:N	1:A:277:LEU:HD23	2.30	0.41
1:A:31:GLU:HA	1:A:93:ARG:HH21	1.84	0.41
1:A:154:PHE:HB3	1:A:158:HIS:CD2	2.56	0.41
1:A:297:PHE:CG	1:A:302:TRP:CZ2	3.09	0.41
1:A:177:GLN:C	1:A:179:TYR:H	2.24	0.41
1:A:157:LEU:O	1:A:159:SER:N	2.54	0.41
1:A:215:TYR:CB	1:A:219:VAL:HG11	2.50	0.40
1:A:267:ASP:O	1:A:268:LEU:C	2.60	0.40
1:A:75:ASP:OD1	1:A:342:LYS:NZ	2.38	0.40
1:A:82:LEU:O	1:A:84:GLN:HG2	2.21	0.40
1:A:208:GLU:O	1:A:209:ILE:C	2.59	0.40
1:A:27:LEU:HA	1:A:27:LEU:HD23	1.88	0.40
1:A:297:PHE:CG	1:A:302:TRP:HZ2	2.39	0.40
1:A:340:ASN:O	1:A:342:LYS:N	2.54	0.40
1:A:154:PHE:O	1:A:158:HIS:HB2	2.21	0.40
1:A:209:ILE:HD13	1:A:215:TYR:CG	2.55	0.40
1:A:237:PRO:HB2	1:A:238:PHE:CD2	2.56	0.40
1:A:280:ARG:HG2	1:A:281:PHE:O	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:54:PHE:O	1:A:74:LEU:HB3	2.20	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	335/350 (96%)	235 (70%)	66 (20%)	34 (10%)	1 0

All (34) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	32	THR
1	A	64	GLU
1	A	83	LYS
1	A	84	GLN
1	A	88	THR
1	A	113	ASN
1	A	188	ALA
1	A	269	LEU
1	A	279	LYS
1	A	316	PRO
1	A	28	LYS
1	A	66	GLY
1	A	125	GLY
1	A	158	HIS
1	A	178	GLY
1	A	214	GLY
1	A	217	LYS
1	A	270	ARG
1	A	273	LEU
1	A	341	GLU

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Mol	Chain	Res	Type
1	A	129	PHE
1	A	157	LEU
1	A	15	VAL
1	A	19	LEU
1	A	36	ASN
1	A	140	GLU
1	A	189	LYS
1	A	292	LYS
1	A	337	VAL
1	A	18	PHE
1	A	33	PRO
1	A	296	TRP
1	A	209	ILE
1	A	305	ILE

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	298/302 (99%)	226 (76%)	72 (24%)	1 1

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	VAL
1	A	17	GLU
1	A	24	GLU
1	A	31	GLU
1	A	32	THR
1	A	39	GLN
1	A	40	LEU
1	A	44	ASP
1	A	45	ARG
1	A	53	SER
1	A	54	PHE
1	A	68	HIS

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Mol	Chain	Res	Type
1	A	71	MET
1	A	73	ILE
1	A	74	LEU
1	A	75	ASP
1	A	82	LEU
1	A	84	GLN
1	A	85	ILE
1	A	86	GLU
1	A	90	ASN
1	A	95	LEU
1	A	96	GLN
1	A	103	LEU
1	A	105	LYS
1	A	117	TYR
1	A	120	MET
1	A	137	ARG
1	A	152	LEU
1	A	159	SER
1	A	160	LEU
1	A	172	LEU
1	A	175	ASP
1	A	176	GLN
1	A	177	GLN
1	A	180	ILE
1	A	181	GLN
1	A	191	VAL
1	A	192	LYS
1	A	195	THR
1	A	196	TRP
1	A	198	LEU
1	A	201	THR
1	A	211	LEU
1	A	212	SER
1	A	216	ASN
1	A	242	GLN
1	A	244	ILE
1	A	245	GLN
1	A	249	LYS
1	A	259	SER
1	A	265	LEU
1	A	268	LEU
1	A	269	LEU

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Mol	Chain	Res	Type
1	A	270	ARG
1	A	274	GLN
1	A	275	VAL
1	A	284	LEU
1	A	288	VAL
1	A	295	LYS
1	A	296	TRP
1	A	299	THR
1	A	308	ARG
1	A	315	ILE
1	A	318	PHE
1	A	328	ASP
1	A	334	GLU
1	A	335	ILE
1	A	336	ARG
1	A	339	ILE
1	A	345	LYS
1	A	348	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	35	GLN
1	A	39	GLN
1	A	67	ASN
1	A	77	GLN
1	A	84	GLN
1	A	90	ASN
1	A	96	GLN
1	A	113	ASN
1	A	216	ASN
1	A	245	GLN
1	A	274	GLN
1	A	307	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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
1	TPO	A	197	1	9,10,11	2.02	3 (33%)	10,14,16	1.17	1 (10%)
1	SEP	A	338	1	9,9,10	1.26	1 (11%)	9,12,14	1.49	1 (11%)

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
1	TPO	A	197	1	-	0/8/11/13	0/0/0/0
1	SEP	A	338	1	-	0/5/8/10	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	197	TPO	P-O3P	-2.09	1.46	1.54
1	A	197	TPO	P-O2P	-2.08	1.46	1.54
1	A	338	SEP	CA-C	2.64	1.53	1.50
1	A	197	TPO	CA-C	5.04	1.56	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	338	SEP	P-OG-CB	-3.37	109.01	118.30
1	A	197	TPO	C-CA-N	3.07	116.06	109.86

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	338	SEP	4	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	$\# Z > 2$
2	A	A	351	-	18,21,25	1.14	1 (5%)	17,31,38	0.90	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
2	A	A	351	-	-	0/2/22/26	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	351	A	O4'-C4'	-2.15	1.40	1.45

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	351	A	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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.