



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:53 AM UTC

PDB ID : 1SYK / pdb_00001syk
Title : Crystal structure of E230Q mutant of cAMP-dependent protein kinase reveals unexpected apoenzyme conformation
Authors : Wu, J.; Yang, J.; Madhusudan, N.; Xuong, N.H.; Ten Eyck, L.F.; Taylor, S.S.
Deposited on : 2004-04-01
Resolution : 2.80 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

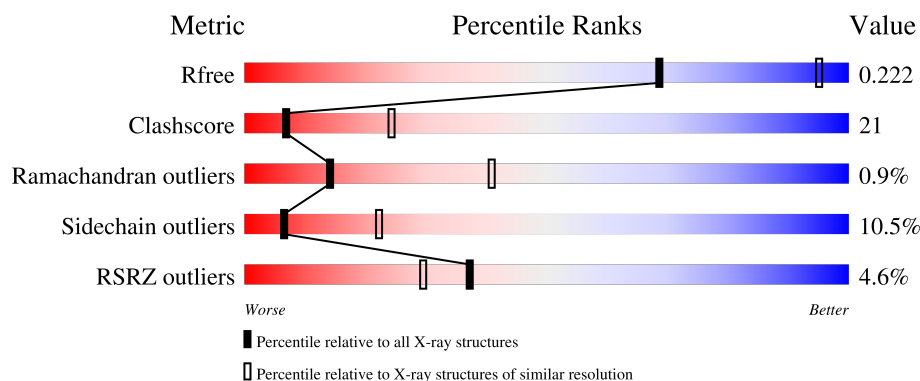
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	350	5% 56% 41% ..
1	B	350	4% 53% 33% 5% 7%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5584 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, alpha-catalytic subunit.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	350	Total	C	N	O	P	S	0	0	0
			2803	1806	478	509	2	8			
1	B	325	Total	C	N	O	P	S	0	0	0
			2668	1730	449	479	2	8			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	197	TPO	THR	modified residue	UNP P05132
A	230	GLN	GLU	engineered mutation	UNP P05132
A	338	SEP	SER	modified residue	UNP P05132
B	197	TPO	THR	modified residue	UNP P05132
B	230	GLN	GLU	engineered mutation	UNP P05132
B	338	SEP	SER	modified residue	UNP P05132

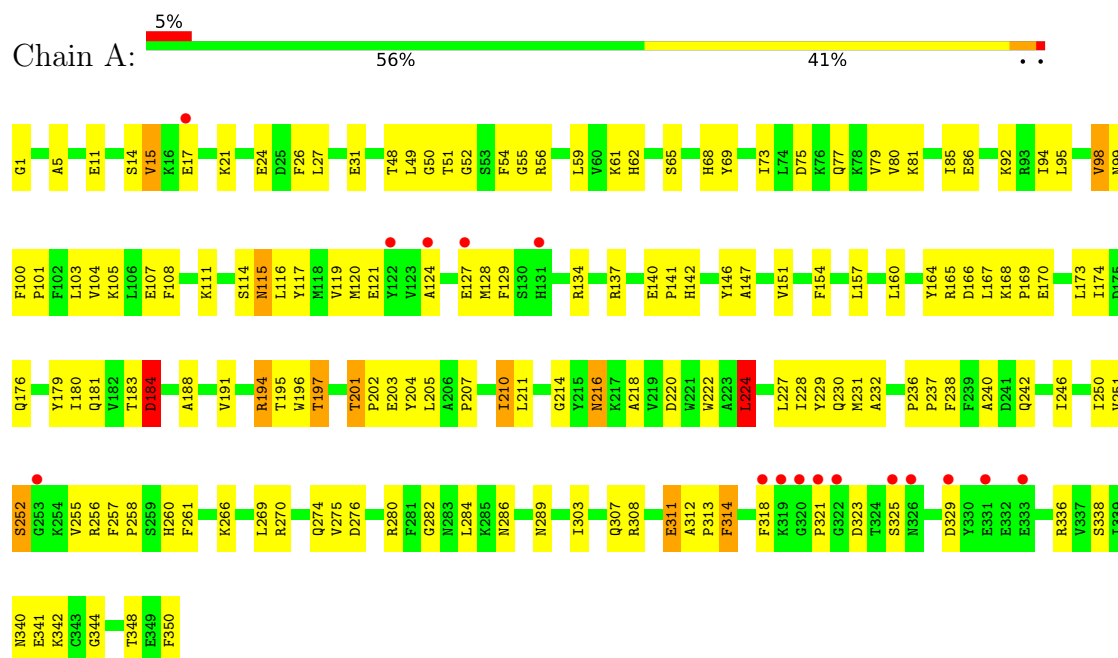
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	64	Total	O	0	0
			64	64		
2	B	49	Total	O	0	0
			49	49		

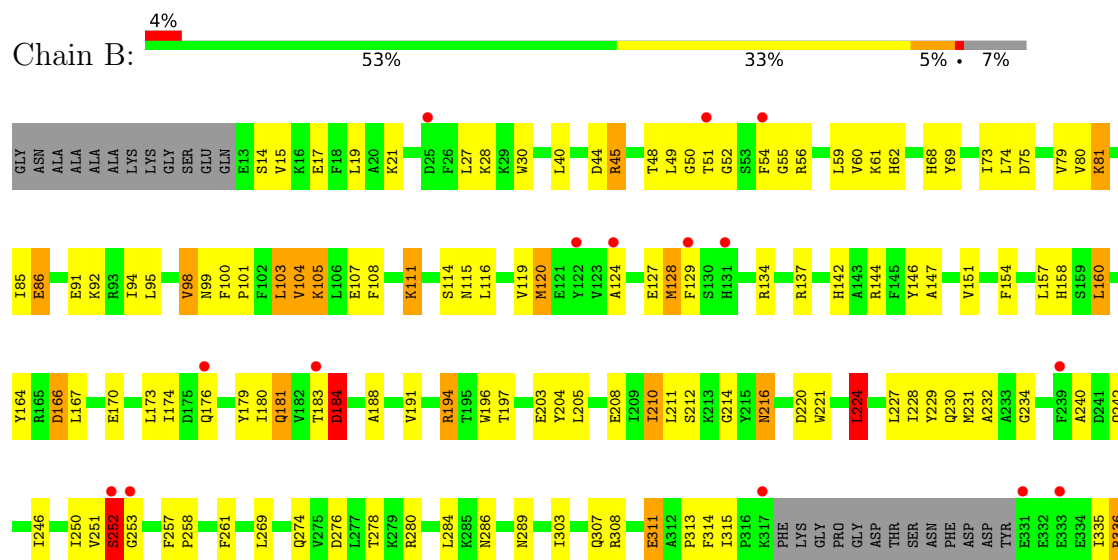
3 Residue-property plots

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: cAMP-dependent protein kinase, alpha-catalytic subunit



- Molecule 1: cAMP-dependent protein kinase, alpha-catalytic subunit



Y337
S338
I339
N340
E341
K342
C343
G344
K345
E346
F350

4 Data and refinement statistics

Property	Value	Source
Space group	P 42	Depositor
Cell constants a, b, c, α , β , γ	120.30Å 120.30Å 58.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.80 50.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.80) 92.4 (50.00-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.93 (at 2.81Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.202 , 0.249 (Not available) , 0.222	Depositor DCC
R_{free} test set	983 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	30.9	Xtriage
Anisotropy	0.553	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 41.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.039 for h,-k,-l	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	5584	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.07% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.47	0/2847	0.98	12/3832 (0.3%)
1	B	0.48	0/2711	1.00	11/3651 (0.3%)
All	All	0.47	0/5558	0.99	23/7483 (0.3%)

There are no bond length outliers.

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	15	VAL	N-CA-C	8.31	119.08	110.36
1	A	252	SER	N-CA-C	-7.12	103.21	110.97
1	A	15	VAL	N-CA-C	-6.89	104.06	110.53
1	B	166	ASP	N-CA-C	6.86	119.19	110.61
1	B	114	SER	N-CA-C	6.82	121.64	113.12
1	B	252	SER	N-CA-C	-6.61	103.99	111.07
1	A	114	SER	N-CA-C	6.49	121.23	113.12
1	B	224	LEU	N-CA-C	-6.47	104.22	111.28
1	A	166	ASP	N-CA-C	6.37	118.57	110.61
1	B	105	LYS	N-CA-C	5.89	118.11	108.52
1	A	224	LEU	N-CA-C	-5.88	104.87	111.28
1	A	115	ASN	N-CA-C	5.51	117.01	109.18
1	A	105	LYS	N-CA-C	5.50	117.70	108.73
1	A	282	GLY	N-CA-C	-5.49	108.16	114.69
1	B	14	SER	N-CA-C	5.46	122.43	110.80
1	B	257	PHE	N-CA-C	5.43	116.51	109.72
1	A	257	PHE	N-CA-C	5.39	116.46	109.72
1	B	115	ASN	N-CA-C	5.37	117.58	109.41
1	A	201	THR	CA-C-N	5.25	126.41	119.84
1	A	201	THR	C-N-CA	5.25	126.41	119.84
1	A	214	GLY	N-CA-C	-5.10	106.58	112.29
1	B	214	GLY	N-CA-C	-5.09	106.17	112.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	234	GLY	N-CA-C	-5.07	107.55	114.64

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	2803	0	2755	131	0
1	B	2668	0	2653	106	0
2	A	64	0	0	9	0
2	B	49	0	0	4	0
All	All	5584	0	5408	231	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 21.

All (231) 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:227:LEU:HG	1:A:231:MET:HE2	1.61	0.83
1:A:127:GLU:HG2	1:A:129:PHE:H	1.44	0.83
1:B:51:THR:HG22	1:B:56:ARG:HB2	1.62	0.82
1:B:95:LEU:HD13	1:B:120:MET:HE1	1.63	0.79
1:B:127:GLU:HG2	1:B:129:PHE:H	1.47	0.79
1:A:313:PRO:O	1:A:314:PHE:HB3	1.82	0.78
1:B:52:GLY:HA3	1:B:54:PHE:CE1	2.19	0.78
1:B:227:LEU:HG	1:B:231:MET:HE2	1.64	0.78
1:A:77:GLN:HG3	2:A:850:HOH:O	1.85	0.76
1:B:75:ASP:O	1:B:79:VAL:HG23	1.85	0.76
1:A:52:GLY:HA3	1:A:54:PHE:CE1	2.20	0.76
1:A:127:GLU:CD	1:A:129:PHE:HB3	2.10	0.75
1:A:51:THR:HG22	1:A:56:ARG:HB2	1.69	0.75
1:B:194:ARG:HD3	1:B:194:ARG:H	1.51	0.74
1:A:95:LEU:HD13	1:A:120:MET:HE1	1.70	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:194:ARG:H	1:A:194:ARG:HD3	1.54	0.72
1:A:196:TRP:CD2	1:B:345:LYS:HD3	2.24	0.72
1:B:61:LYS:HE2	1:B:68:HIS:CE1	2.24	0.72
1:B:127:GLU:CD	1:B:129:PHE:HB3	2.15	0.71
1:A:127:GLU:OE1	1:A:129:PHE:HB3	1.91	0.70
1:B:142:HIS:CD2	1:B:313:PRO:HB3	2.26	0.70
1:A:75:ASP:O	1:A:79:VAL:HG23	1.91	0.69
1:B:17:GLU:HG2	1:B:21:LYS:HE3	1.73	0.69
1:B:183:THR:O	1:B:184:ASP:HB2	1.93	0.69
1:A:280:ARG:O	1:A:284:LEU:HD13	1.94	0.68
1:B:127:GLU:OE1	1:B:129:PHE:HB3	1.94	0.68
1:A:80:VAL:HG22	1:A:85:ILE:HD11	1.76	0.67
1:A:311:GLU:O	1:A:311:GLU:HG3	1.93	0.67
1:A:173:LEU:HD23	1:A:183:THR:HG21	1.76	0.67
1:A:183:THR:O	1:A:184:ASP:HB2	1.96	0.66
1:B:127:GLU:HG2	1:B:128:MET:N	2.11	0.65
1:B:216:ASN:HD22	1:B:216:ASN:H	1.40	0.65
1:A:127:GLU:HG2	1:A:128:MET:N	2.10	0.65
1:B:341:GLU:OE2	1:B:344:GLY:HA3	1.97	0.65
1:B:280:ARG:O	1:B:284:LEU:HD13	1.96	0.65
1:A:216:ASN:HD22	1:A:216:ASN:H	1.42	0.64
1:A:61:LYS:HE2	1:A:68:HIS:CE1	2.32	0.64
1:A:17:GLU:HG2	1:A:21:LYS:HE3	1.81	0.63
1:A:69:TYR:CE2	1:A:107:GLU:HG2	2.33	0.63
1:A:216:ASN:ND2	2:A:832:HOH:O	2.32	0.62
1:B:173:LEU:HD23	1:B:183:THR:HG21	1.81	0.62
1:A:49:LEU:HD11	1:A:59:LEU:HB2	1.82	0.62
1:A:303:ILE:HD12	1:A:303:ILE:H	1.64	0.62
1:B:69:TYR:CE2	1:B:107:GLU:HG2	2.34	0.61
1:B:303:ILE:O	1:B:307:GLN:HG3	2.00	0.61
1:A:100:PHE:CD1	1:A:101:PRO:HD2	2.36	0.61
1:A:236:PRO:HB2	2:A:856:HOH:O	2.01	0.61
1:B:49:LEU:HD11	1:B:59:LEU:HB2	1.82	0.61
1:B:86:GLU:H	1:B:86:GLU:CD	2.10	0.60
1:B:303:ILE:HD12	1:B:303:ILE:H	1.66	0.60
1:B:147:ALA:O	1:B:151:VAL:HG23	2.02	0.60
1:A:303:ILE:O	1:A:307:GLN:HG3	2.01	0.59
1:B:194:ARG:HG3	1:B:194:ARG:HH11	1.66	0.59
1:A:303:ILE:HD12	1:A:303:ILE:N	2.16	0.59
1:A:86:GLU:CD	1:A:86:GLU:H	2.10	0.59
1:A:341:GLU:OE2	1:A:344:GLY:HA3	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1:GLY:H2	1:A:5:ALA:H	1.51	0.58
1:A:14:SER:O	1:A:17:GLU:HB3	2.03	0.58
1:B:194:ARG:HD3	1:B:194:ARG:N	2.17	0.58
1:B:303:ILE:HD12	1:B:303:ILE:N	2.17	0.58
1:B:80:VAL:HG22	1:B:85:ILE:HD11	1.85	0.58
1:B:92:LYS:C	1:B:92:LYS:HD3	2.29	0.58
1:A:100:PHE:CG	1:A:101:PRO:HD2	2.39	0.58
1:B:98:VAL:HG13	1:B:103:LEU:HD23	1.86	0.58
1:A:48:THR:HG22	1:A:50:GLY:H	1.69	0.57
1:A:146:TYR:HB3	1:A:180:ILE:HD11	1.85	0.57
1:B:100:PHE:CD1	1:B:101:PRO:HD2	2.40	0.57
1:B:100:PHE:CG	1:B:101:PRO:HD2	2.40	0.57
1:A:194:ARG:HG3	1:A:194:ARG:HH11	1.70	0.57
1:A:92:LYS:HD3	1:A:92:LYS:C	2.29	0.57
1:A:323:ASP:C	1:A:325:SER:H	2.13	0.56
1:B:137:ARG:HD2	1:B:232:ALA:O	2.06	0.56
1:B:144:ARG:HD2	2:B:912:HOH:O	2.05	0.56
1:A:197:TPO:HG22	2:A:831:HOH:O	2.05	0.56
1:A:284:LEU:HB2	2:A:836:HOH:O	2.04	0.56
1:A:142:HIS:CD2	1:A:313:PRO:HB3	2.41	0.55
1:A:92:LYS:HG3	1:A:350:PHE:CE2	2.42	0.55
1:A:194:ARG:HD3	1:A:194:ARG:N	2.20	0.55
1:B:124:ALA:HB3	1:B:176:GLN:HG2	1.87	0.55
1:A:81:LYS:HZ2	1:A:81:LYS:HB2	1.71	0.55
1:B:146:TYR:HB3	1:B:180:ILE:HD11	1.87	0.55
1:B:311:GLU:HA	1:B:311:GLU:OE1	2.06	0.54
1:A:81:LYS:NZ	1:A:81:LYS:HA	2.21	0.54
1:A:137:ARG:HD2	1:A:232:ALA:O	2.07	0.54
1:B:61:LYS:HE2	1:B:68:HIS:NE2	2.21	0.54
1:A:147:ALA:O	1:A:151:VAL:HG23	2.08	0.54
1:A:183:THR:O	1:A:183:THR:HG23	2.08	0.54
1:A:94:ILE:CD1	1:A:188:ALA:HB3	2.38	0.53
1:A:98:VAL:HG13	1:A:103:LEU:HD23	1.90	0.53
1:B:108:PHE:HB2	1:B:119:VAL:HB	1.90	0.53
1:B:183:THR:O	1:B:183:THR:HG23	2.08	0.53
1:A:81:LYS:HA	1:A:81:LYS:HZ1	1.73	0.53
1:A:69:TYR:HB3	1:A:120:MET:O	2.09	0.53
1:A:179:TYR:CZ	1:A:308:ARG:HA	2.45	0.52
1:B:179:TYR:CZ	1:B:308:ARG:HA	2.45	0.52
1:B:314:PHE:CD1	1:B:315:ILE:N	2.78	0.51
1:A:51:THR:HG22	1:A:56:ARG:CB	2.39	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:124:ALA:HB3	1:A:176:GLN:HG2	1.92	0.51
1:A:336:ARG:HD3	1:A:336:ARG:C	2.35	0.51
1:B:92:LYS:HG3	1:B:350:PHE:CE2	2.45	0.51
1:A:31:GLU:HG2	1:B:30:TRP:CD1	2.45	0.51
1:A:170:GLU:OE1	1:A:170:GLU:N	2.36	0.51
1:A:314:PHE:CD1	1:A:314:PHE:C	2.89	0.51
1:B:48:THR:HG22	1:B:50:GLY:H	1.75	0.51
1:A:81:LYS:NZ	1:A:81:LYS:CA	2.73	0.51
1:A:201:THR:HG23	1:A:202:PRO:HD2	1.94	0.50
1:A:31:GLU:HG3	2:A:806:HOH:O	2.11	0.50
1:A:204:TYR:OH	1:A:230:GLN:NE2	2.45	0.49
1:A:303:ILE:H	1:A:303:ILE:CD1	2.25	0.49
1:B:210:ILE:HD11	1:B:251:VAL:HG21	1.95	0.49
1:B:340:ASN:HB2	1:B:342:LYS:NZ	2.27	0.49
1:B:94:ILE:CD1	1:B:188:ALA:HB3	2.43	0.49
1:B:194:ARG:HG3	1:B:194:ARG:NH1	2.27	0.49
1:A:111:LYS:HB3	1:A:116:LEU:HA	1.94	0.49
1:A:224:LEU:HD22	1:A:228:ILE:HG13	1.94	0.49
1:A:104:VAL:CG1	1:A:120:MET:HE2	2.42	0.48
1:B:286:ASN:O	1:B:289:ASN:HB2	2.13	0.48
1:B:98:VAL:CG1	1:B:103:LEU:HD23	2.43	0.48
1:B:180:ILE:HG22	1:B:181:GLN:N	2.28	0.48
1:A:266:LYS:O	1:A:270:ARG:HG3	2.14	0.48
1:A:98:VAL:HG13	1:A:99:ASN:N	2.28	0.47
1:A:195:THR:OG1	1:A:197:TPO:O3P	2.32	0.47
1:A:258:PRO:HD2	1:A:261:PHE:CE2	2.49	0.47
1:B:204:TYR:OH	1:B:230:GLN:NE2	2.46	0.47
1:A:240:ALA:HB3	1:A:246:ILE:HG13	1.96	0.47
1:B:111:LYS:HB3	1:B:116:LEU:HA	1.95	0.47
1:A:224:LEU:HD22	1:A:224:LEU:O	2.15	0.47
1:A:180:ILE:HG22	1:A:181:GLN:N	2.29	0.47
1:A:210:ILE:HD11	1:A:251:VAL:HG21	1.96	0.47
1:A:81:LYS:HA	1:A:81:LYS:CE	2.44	0.47
1:A:121:GLU:HG3	2:A:860:HOH:O	2.15	0.47
1:A:165:ARG:H	1:A:165:ARG:HD3	1.80	0.47
1:B:73:ILE:C	1:B:74:LEU:HD12	2.40	0.47
1:B:54:PHE:H	1:B:54:PHE:HD1	1.59	0.47
1:A:11:GLU:O	1:A:15:VAL:HG23	2.15	0.47
1:B:258:PRO:HD2	1:B:261:PHE:CE2	2.50	0.47
1:A:108:PHE:HB2	1:A:119:VAL:HB	1.97	0.46
1:A:98:VAL:CG1	1:A:103:LEU:HD23	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:228:ILE:HA	1:A:231:MET:HE3	1.97	0.46
1:A:24:GLU:CD	1:B:28:LYS:HZ2	2.23	0.46
1:B:134:ARG:HG3	1:B:134:ARG:HH11	1.80	0.46
1:A:61:LYS:HE2	1:A:68:HIS:NE2	2.31	0.46
1:A:196:TRP:CG	1:B:345:LYS:HD3	2.50	0.46
1:B:164:TYR:O	1:B:220:ASP:OD1	2.34	0.46
1:B:51:THR:HA	1:B:56:ARG:HA	1.97	0.46
1:B:69:TYR:HB3	1:B:120:MET:O	2.15	0.46
1:B:85:ILE:HD13	1:B:346:GLU:HB3	1.98	0.46
1:A:207:PRO:HG2	1:A:275:VAL:HA	1.98	0.45
1:A:222:TRP:CD1	1:A:222:TRP:C	2.94	0.45
1:A:104:VAL:HG21	1:A:183:THR:HB	1.97	0.45
1:B:229:TYR:CD1	1:B:229:TYR:C	2.94	0.45
1:A:216:ASN:HD22	1:A:216:ASN:N	2.05	0.45
1:B:180:ILE:CG2	1:B:181:GLN:N	2.79	0.45
1:B:252:SER:OG	1:B:253:GLY:N	2.49	0.45
1:B:276:ASP:OD1	1:B:278:THR:OG1	2.32	0.45
1:A:205:LEU:O	1:A:250:ILE:HD13	2.17	0.45
1:A:140:GLU:HB2	1:A:141:PRO:HD3	1.98	0.45
1:B:151:VAL:HG22	1:B:224:LEU:HD11	1.97	0.45
1:A:340:ASN:HA	2:A:866:HOH:O	2.16	0.45
1:A:348:THR:HG21	1:B:196:TRP:HZ3	1.82	0.45
1:B:303:ILE:H	1:B:303:ILE:CD1	2.28	0.45
1:A:24:GLU:CD	1:B:28:LYS:NZ	2.75	0.45
1:A:169:PRO:HD3	1:A:204:TYR:OH	2.17	0.45
1:A:229:TYR:CD1	1:A:229:TYR:C	2.95	0.45
1:A:180:ILE:CG2	1:A:181:GLN:N	2.80	0.44
1:B:158:HIS:HE1	1:B:220:ASP:OD2	1.99	0.44
1:A:128:MET:HG3	1:A:174:ILE:HD11	1.99	0.44
1:A:194:ARG:HG3	1:A:194:ARG:NH1	2.32	0.44
1:A:69:TYR:HE2	1:A:107:GLU:HG2	1.80	0.44
1:A:183:THR:O	1:A:184:ASP:CB	2.65	0.44
1:A:164:TYR:O	1:A:220:ASP:OD1	2.35	0.44
1:B:98:VAL:HG13	1:B:99:ASN:N	2.33	0.43
1:B:205:LEU:O	1:B:250:ILE:HD13	2.18	0.43
1:B:314:PHE:CD1	1:B:314:PHE:C	2.96	0.43
1:B:55:GLY:HA3	1:B:73:ILE:O	2.17	0.43
1:A:232:ALA:O	1:A:260:HIS:HE1	2.01	0.43
1:A:62:HIS:HB3	1:A:65:SER:OG	2.19	0.43
1:B:81:LYS:NZ	1:B:81:LYS:HA	2.34	0.43
1:A:216:ASN:H	1:A:216:ASN:ND2	2.15	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:208:GLU:HG3	2:B:921:HOH:O	2.19	0.43
1:A:55:GLY:HA3	1:A:73:ILE:O	2.20	0.42
1:A:312:ALA:C	1:A:314:PHE:H	2.26	0.42
1:A:340:ASN:HB2	1:A:342:LYS:NZ	2.34	0.42
1:B:91:GLU:OE2	1:B:184:ASP:HA	2.19	0.42
1:B:183:THR:O	1:B:184:ASP:CB	2.63	0.42
1:A:218:ALA:HB3	2:A:832:HOH:O	2.18	0.42
1:B:124:ALA:HB3	1:B:176:GLN:CG	2.48	0.42
1:B:69:TYR:HE2	1:B:107:GLU:HG2	1.83	0.42
1:B:216:ASN:HD22	1:B:216:ASN:N	2.06	0.42
1:A:26:PHE:CD1	1:A:160:LEU:HG	2.54	0.42
1:A:237:PRO:HG2	1:A:238:PHE:CD1	2.54	0.42
1:B:127:GLU:OE2	1:B:170:GLU:HA	2.19	0.42
1:A:173:LEU:HD23	1:A:183:THR:CG2	2.46	0.42
1:A:255:VAL:HG12	1:A:256:ARG:N	2.35	0.42
1:A:286:ASN:O	1:A:289:ASN:HB2	2.19	0.42
1:B:128:MET:HG3	1:B:174:ILE:HD11	2.02	0.42
1:A:115:ASN:HB2	1:A:117:TYR:CE1	2.55	0.42
1:A:201:THR:HA	1:A:202:PRO:HD3	1.90	0.41
1:A:276:ASP:OD1	1:A:276:ASP:C	2.63	0.41
1:B:52:GLY:HA3	1:B:54:PHE:HE1	1.79	0.41
1:A:117:TYR:N	1:A:117:TYR:CD1	2.88	0.41
1:A:134:ARG:HH11	1:A:134:ARG:HG3	1.86	0.41
1:A:179:TYR:CE2	1:A:308:ARG:HA	2.55	0.41
1:B:221:TRP:CE3	1:B:221:TRP:HA	2.55	0.41
1:B:335:ILE:HG22	1:B:336:ARG:N	2.35	0.41
1:A:154:PHE:CZ	1:A:167:LEU:HD22	2.56	0.41
1:B:179:TYR:CE2	1:B:308:ARG:HA	2.55	0.41
1:A:1:GLY:H1	1:A:5:ALA:HB2	1.85	0.41
1:B:158:HIS:C	1:B:160:LEU:N	2.79	0.41
1:B:212:SER:HA	2:B:922:HOH:O	2.21	0.41
1:A:127:GLU:OE2	1:A:170:GLU:HA	2.21	0.41
1:A:167:LEU:O	1:A:168:LYS:HB3	2.20	0.41
1:B:216:ASN:H	1:B:216:ASN:ND2	2.14	0.41
1:B:224:LEU:HD22	1:B:228:ILE:HG13	2.02	0.41
1:B:60:VAL:O	1:B:68:HIS:HA	2.20	0.41
1:B:81:LYS:HA	1:B:81:LYS:CE	2.50	0.41
1:A:51:THR:HA	1:A:56:ARG:HA	2.03	0.41
1:A:224:LEU:O	1:A:228:ILE:HG13	2.21	0.41
1:B:45:ARG:H	1:B:45:ARG:HG2	1.26	0.41
1:B:81:LYS:HA	1:B:81:LYS:HZ1	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:240:ALA:HB3	1:B:246:ILE:HG13	2.03	0.41
1:B:276:ASP:OD1	1:B:276:ASP:C	2.64	0.41
1:A:227:LEU:O	1:A:228:ILE:C	2.63	0.40
1:B:62:HIS:HB2	1:B:69:TYR:HE1	1.85	0.40
1:A:103:LEU:HD21	1:A:157:LEU:HD11	2.03	0.40
1:A:140:GLU:N	1:A:141:PRO:CD	2.84	0.40
1:B:104:VAL:CG1	1:B:120:MET:HE2	2.51	0.40
1:A:49:LEU:CD1	1:A:59:LEU:HB2	2.51	0.40
1:B:154:PHE:CZ	1:B:167:LEU:HD22	2.56	0.40
1:B:166:ASP:HA	2:B:915:HOH:O	2.20	0.40
1:B:303:ILE:N	1:B:303:ILE:CD1	2.84	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	346/350 (99%)	314 (91%)	27 (8%)	5 (1%)	9	30
1	B	319/350 (91%)	296 (93%)	22 (7%)	1 (0%)	36	66
All	All	665/700 (95%)	610 (92%)	49 (7%)	6 (1%)	14	41

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	184	ASP
1	A	318	PHE
1	A	321	PRO
1	B	184	ASP
1	A	314	PHE
1	A	329	ASP

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	156/303 (52%)	141 (90%)	15 (10%)	8	26
1	B	281/303 (93%)	250 (89%)	31 (11%)	6	20
All	All	437/606 (72%)	391 (90%)	46 (10%)	6	22

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	LEU
1	A	98	VAL
1	A	184	ASP
1	A	191	VAL
1	A	194	ARG
1	A	203	GLU
1	A	210	ILE
1	A	211	LEU
1	A	216	ASN
1	A	224	LEU
1	A	242	GLN
1	A	252	SER
1	A	269	LEU
1	A	274	GLN
1	A	311	GLU
1	B	19	LEU
1	B	27	LEU
1	B	40	LEU
1	B	44	ASP
1	B	45	ARG
1	B	81	LYS
1	B	86	GLU
1	B	98	VAL
1	B	103	LEU
1	B	104	VAL
1	B	105	LYS
1	B	111	LYS

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Mol	Chain	Res	Type
1	B	120	MET
1	B	128	MET
1	B	157	LEU
1	B	160	LEU
1	B	181	GLN
1	B	184	ASP
1	B	191	VAL
1	B	194	ARG
1	B	203	GLU
1	B	210	ILE
1	B	211	LEU
1	B	216	ASN
1	B	224	LEU
1	B	242	GLN
1	B	252	SER
1	B	269	LEU
1	B	274	GLN
1	B	311	GLU
1	B	336	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	87	HIS
1	A	90	ASN
1	A	177	GLN
1	A	181	GLN
1	A	216	ASN
1	A	230	GLN
1	A	283	ASN
1	A	289	ASN
1	B	36	ASN
1	B	39	GLN
1	B	42	GLN
1	B	67	ASN
1	B	87	HIS
1	B	90	ASN
1	B	142	HIS
1	B	158	HIS
1	B	177	GLN
1	B	181	GLN
1	B	216	ASN

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Mol	Chain	Res	Type
1	B	230	GLN
1	B	242	GLN
1	B	260	HIS
1	B	283	ASN
1	B	289	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 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	B	197	1	8,10,11	1.23	1 (12%)	10,14,16	1.86	2 (20%)
1	SEP	B	338	1	8,9,10	0.72	0	7,12,14	1.17	1 (14%)
1	SEP	A	338	1	8,9,10	0.73	0	7,12,14	1.16	1 (14%)
1	TPO	A	197	1	8,10,11	1.21	1 (12%)	10,14,16	1.74	2 (20%)

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	B	197	1	-	6/9/11/13	-
1	SEP	B	338	1	-	2/6/8/10	-
1	SEP	A	338	1	-	2/6/8/10	-
1	TPO	A	197	1	-	5/9/11/13	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	197	TPO	P-O3P	-2.27	1.46	1.54
1	B	197	TPO	P-O3P	-2.20	1.46	1.54

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	197	TPO	O3P-P-O1P	-4.24	94.30	110.83
1	A	197	TPO	O3P-P-O1P	-3.97	95.36	110.83
1	B	197	TPO	O3P-P-O2P	2.94	118.82	107.80
1	A	197	TPO	O3P-P-O2P	2.52	117.23	107.80
1	A	338	SEP	OG-CB-CA	2.39	110.47	108.14
1	B	338	SEP	OG-CB-CA	2.39	110.47	108.14

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	197	TPO	N-CA-CB-CG2
1	A	197	TPO	N-CA-CB-OG1
1	A	197	TPO	C-CA-CB-CG2
1	A	197	TPO	CG2-CB-OG1-P
1	A	338	SEP	CA-CB-OG-P
1	B	197	TPO	N-CA-CB-CG2
1	B	197	TPO	N-CA-CB-OG1
1	B	197	TPO	C-CA-CB-CG2
1	B	197	TPO	CG2-CB-OG1-P
1	B	338	SEP	CA-CB-OG-P
1	A	338	SEP	N-CA-CB-OG
1	B	338	SEP	N-CA-CB-OG
1	B	197	TPO	CB-OG1-P-O3P
1	A	197	TPO	O-C-CA-CB
1	B	197	TPO	O-C-CA-CB

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	197	TPO	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	348/350 (99%)	0.25	16 (4%) 37 29	12, 26, 57, 84	0
1	B	323/350 (92%)	0.22	15 (4%) 37 29	13, 26, 51, 70	0
All	All	671/700 (95%)	0.24	31 (4%) 37 29	12, 26, 54, 84	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	318	PHE	4.3
1	A	325	SER	4.1
1	A	326	ASN	3.8
1	B	122	TYR	3.6
1	B	239	PHE	3.6
1	B	124	ALA	3.5
1	A	331	GLU	3.4
1	A	329	ASP	3.4
1	A	319	LYS	3.1
1	B	253	GLY	3.0
1	A	131	HIS	3.0
1	B	333	GLU	3.0
1	A	122	TYR	2.9
1	A	321	PRO	2.8
1	A	333	GLU	2.8
1	B	131	HIS	2.8
1	A	320	GLY	2.8
1	B	317	LYS	2.7
1	B	252	SER	2.6
1	A	253	GLY	2.4
1	B	54	PHE	2.4
1	A	124	ALA	2.4
1	B	176	GLN	2.4
1	A	17	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	331	GLU	2.3
1	B	183	THR	2.2
1	A	322	GLY	2.2
1	B	51	THR	2.1
1	B	25	ASP	2.1
1	A	127	GLU	2.1
1	B	129	PHE	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	TPO	A	197	11/12	0.92	0.10	24,26,30,31	0
1	TPO	B	197	11/12	0.94	0.10	24,25,29,31	0
1	SEP	B	338	10/11	0.94	0.09	33,34,35,35	0
1	SEP	A	338	10/11	0.95	0.09	33,33,35,35	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.