



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:24 PM GMT

PDB ID : 4EOP
Title : Thr 160 phosphorylated CDK2 Q131E - human cyclin A3 complex with the inhibitor RO3306
Authors : Echalier, A.; Cot, E.; Camasses, A.; Hodimont, E.; Hoh, F.; Sheinerman, F.; Krasinska, L.; Fisher, D.
Deposited on : 2012-04-14
Resolution : 1.99 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

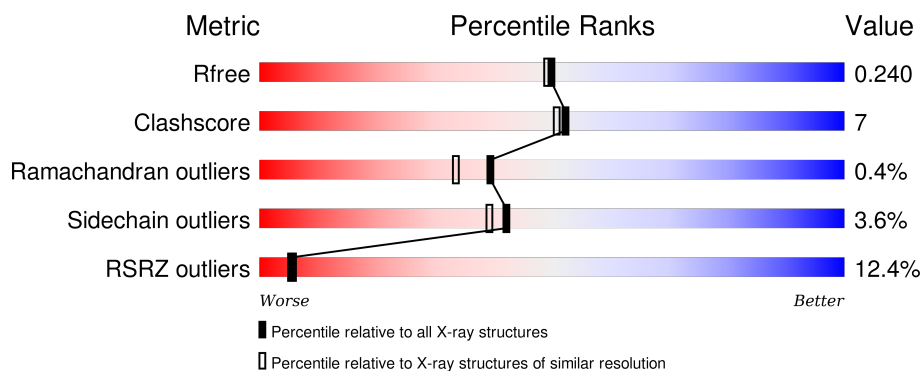
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.99 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}	91344	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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.

Mol	Chain	Length	Quality of chain
1	A	300	<div> <div>5%</div> <div>85%</div> <div>12%</div> <div>...</div> </div>
1	C	300	<div> <div>15%</div> <div>84%</div> <div>13%</div> <div>..</div> </div>
2	B	258	<div> <div>14%</div> <div>90%</div> <div>8%</div> <div>.</div> </div>
2	D	258	<div> <div>17%</div> <div>86%</div> <div>12%</div> <div>.</div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	1RO	A	301	-	-	X	X
3	1RO	C	301	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9518 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 Cyclin-dependent kinase 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	298	Total	C	N	O	P	S	0	4	0
			2420	1568	411	432	1	8			
1	C	297	Total	C	N	O	P	S	0	3	0
			2409	1561	406	433	1	8			

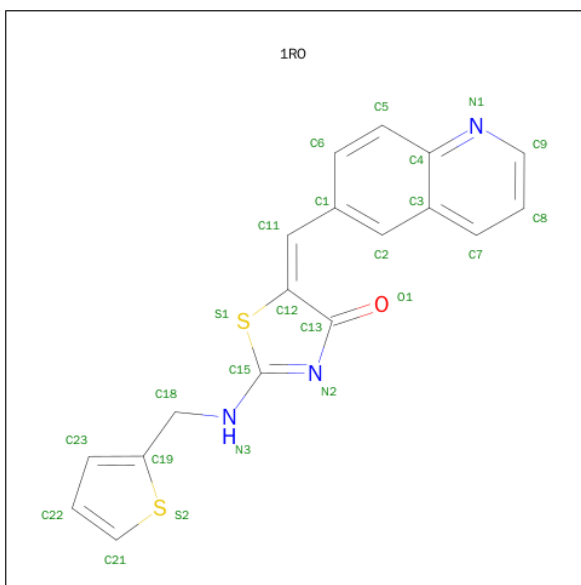
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	PRO	-	EXPRESSION TAG	UNP P24941
A	-1	GLY	-	EXPRESSION TAG	UNP P24941
A	0	SER	-	EXPRESSION TAG	UNP P24941
A	131	GLU	GLN	ENGINEERED MUTATION	UNP P24941
C	-2	PRO	-	EXPRESSION TAG	UNP P24941
C	-1	GLY	-	EXPRESSION TAG	UNP P24941
C	0	SER	-	EXPRESSION TAG	UNP P24941
C	131	GLU	GLN	ENGINEERED MUTATION	UNP P24941

- Molecule 2 is a protein called Cyclin-A2.

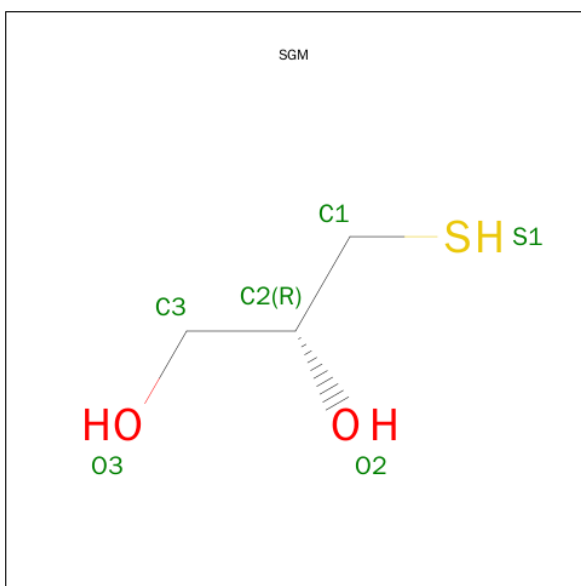
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	257	Total	C	N	O	S		0	2	0
			2094	1356	342	384	12				
2	D	255	Total	C	N	O	S		0	0	0
			2059	1334	335	379	11				

- Molecule 3 is (5E)-5-(QUINOLIN-6-YLMETHYLIDENE)-2-[(THIOPHEN-2-YLMETHYL) AMINO]-1,3-THIAZOL-4(5H)-ONE (three-letter code: 1RO) (formula: C₁₈H₁₃N₃OS₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			24	18	3	1	2		
3	C	1	Total	C	N	O	S	0	0
			24	18	3	1	2		

- Molecule 4 is MONOTHIOGLYCEROL (three-letter code: SGM) (formula: $C_3H_8O_2S$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	O	S	0	0
			6	3	2	1		

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	1	Total 1	Mg 1	0	0

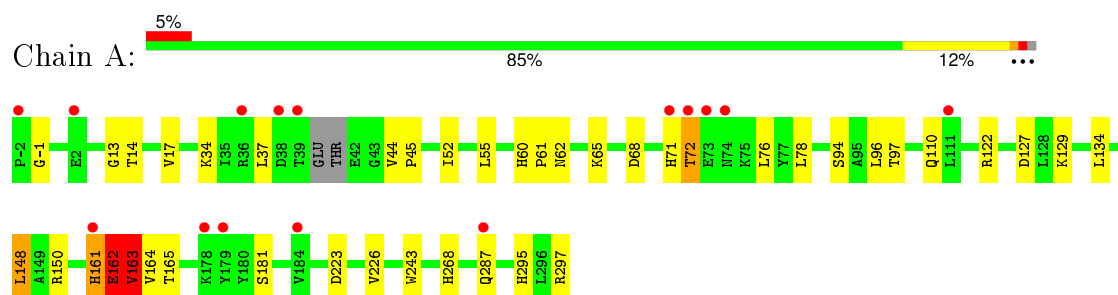
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	170	Total 170	O 170	0	0
6	B	113	Total 113	O 113	0	0
6	C	120	Total 120	O 120	0	0
6	D	78	Total 78	O 78	0	0

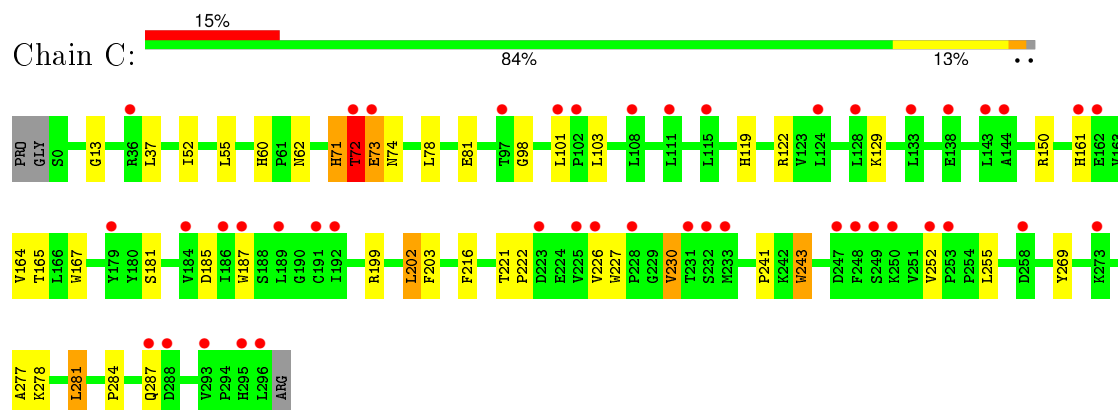
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

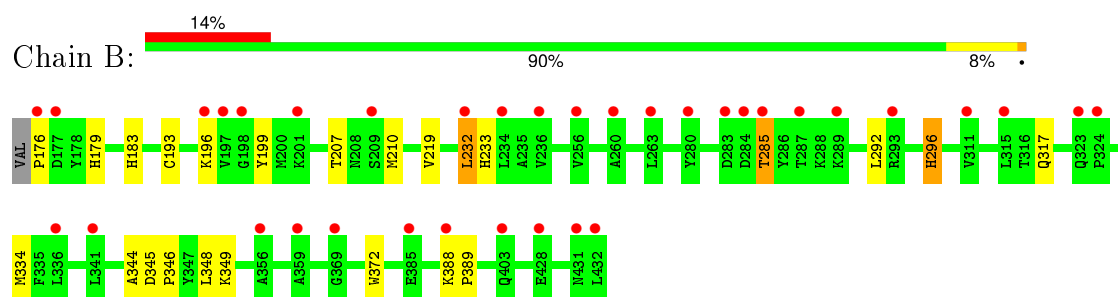
• Molecule 1: Cyclin-dependent kinase 2



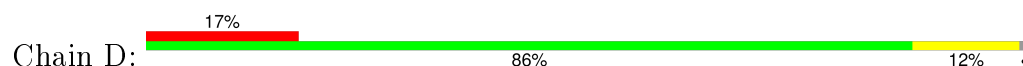
• Molecule 1: Cyclin-dependent kinase 2

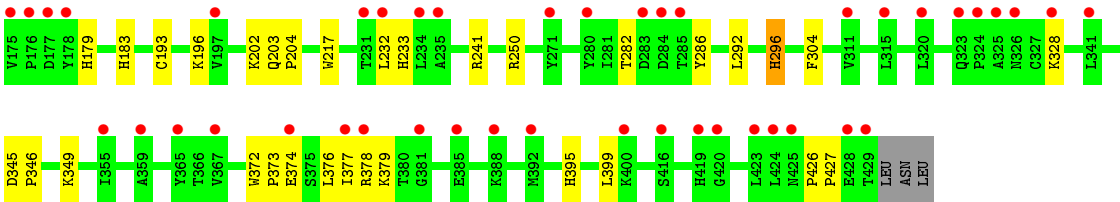


• Molecule 2: Cyclin-A2



• Molecule 2: Cyclin-A2





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	74.78Å 133.39Å 147.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.83 – 1.99 29.83 – 1.99	Depositor EDS
% Data completeness (in resolution range)	98.7 (29.83-1.99) 98.8 (29.83-1.99)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.35 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.216 , 0.241 0.214 , 0.240	Depositor DCC
R_{free} test set	5081 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	29.7	Xtriage
Anisotropy	0.065	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 44.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 100868 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9518	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.25% 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, 0.375 respectively for untwinned datasets, and 0.333, 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, MG, SGM, 1RO

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	0.58	1/2470 (0.0%)	0.63	0/3349
1	C	0.56	3/2459 (0.1%)	0.61	0/3337
2	B	0.50	1/2145 (0.0%)	0.55	0/2911
2	D	0.49	2/2109 (0.1%)	0.57	0/2864
All	All	0.54	7/9183 (0.1%)	0.60	0/12461

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	C	0	2

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	243	TRP	CD2-CE2	5.72	1.48	1.41
1	C	187	TRP	CD2-CE2	5.70	1.48	1.41
2	B	372	TRP	CD2-CE2	5.41	1.47	1.41
2	D	217	TRP	CD2-CE2	5.32	1.47	1.41
2	D	372	TRP	CD2-CE2	5.24	1.47	1.41
1	C	167	TRP	CD2-CE2	5.20	1.47	1.41
1	C	243	TRP	CD2-CE2	5.13	1.47	1.41

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	71	HIS	Peptide
1	C	72	THR	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	2420	0	2457	42	0
1	C	2409	0	2441	32	0
2	B	2094	0	2112	19	0
2	D	2059	0	2079	21	0
3	A	24	0	13	9	0
3	C	24	0	13	9	0
4	B	6	0	7	1	0
5	D	1	0	0	0	0
6	A	170	0	0	10	0
6	B	113	0	0	5	0
6	C	120	0	0	5	0
6	D	78	0	0	2	0
All	All	9518	0	9122	122	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 (122) 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)
2:B:193:CYS:SG	4:B:501:SGM:S1	2.30	1.29
3:A:301:1RO:S1	6:A:482:HOH:O	1.99	1.16
1:C:72:THR:CG2	2:D:296:HIS:NE2	2.11	1.13
1:C:72:THR:HG23	2:D:296:HIS:NE2	1.68	1.08
3:C:301:1RO:S1	6:C:462:HOH:O	2.17	0.99
3:A:301:1RO:O1	3:A:301:1RO:H13	1.62	0.99
3:A:301:1RO:O1	3:A:301:1RO:C2	2.11	0.99
1:C:226:VAL:HB	6:C:459:HOH:O	1.67	0.93
3:C:301:1RO:C2	3:C:301:1RO:O1	2.17	0.93
1:C:72:THR:HG21	2:D:296:HIS:NE2	1.81	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:301:1RO:H13	3:C:301:1RO:O1	1.71	0.88
3:A:301:1RO:N2	3:A:301:1RO:C19	2.43	0.81
1:A:71:HIS:CD2	1:A:72:THR:HB	2.18	0.78
1:A:97:THR:HG22	6:A:441:HOH:O	1.81	0.78
3:C:301:1RO:C19	3:C:301:1RO:N2	2.46	0.75
1:A:60:HIS:HD2	1:A:62:ASN:H	1.34	0.74
1:A:60:HIS:CD2	1:A:62:ASN:H	2.06	0.74
3:A:301:1RO:C13	3:A:301:1RO:H13	2.16	0.74
1:A:52:ILE:HD11	1:A:78:LEU:HD21	1.71	0.72
2:D:282:THR:HG21	2:D:286:TYR:CD2	2.25	0.71
1:C:221:THR:HG21	1:C:241:PRO:O	1.90	0.70
1:C:227:TRP:O	1:C:230:VAL:HG23	1.92	0.69
1:C:129:LYS:HD3	1:C:165[A]:THR:HG21	1.73	0.69
1:C:202:LEU:HD12	1:C:203:PHE:CZ	2.29	0.68
1:C:60:HIS:CD2	1:C:62:ASN:H	2.12	0.68
1:C:252:VAL:HG21	1:C:255:LEU:HD12	1.76	0.67
3:C:301:1RO:C13	3:C:301:1RO:H13	2.25	0.67
3:A:301:1RO:C13	3:A:301:1RO:C2	2.75	0.64
1:A:127:ASP:OD1	1:A:165[A]:THR:HG23	1.97	0.64
1:A:-1:GLY:HA3	1:A:68:ASP:OD2	1.97	0.64
2:B:183:HIS:HB2	2:B:317:GLN:HE22	1.63	0.64
1:A:161:HIS:O	1:A:162:GLU:O	2.17	0.62
1:C:71:HIS:CE1	2:D:304:PHE:HE2	2.17	0.62
1:A:129:LYS:NZ	1:A:165[A]:THR:HG21	2.13	0.62
1:C:13:GLY:HA2	3:C:301:1RO:H2	1.83	0.61
1:C:98:GLY:HA2	1:C:199:ARG:HD3	1.81	0.61
2:B:334[A]:MET:HE3	6:B:619:HOH:O	1.99	0.60
1:C:216:PHE:HB3	1:C:221:THR:HG22	1.82	0.60
1:C:60:HIS:HD2	1:C:62:ASN:H	1.48	0.59
1:C:227:TRP:O	1:C:230:VAL:CG2	2.50	0.58
1:C:119:HIS:HD2	6:D:607:HOH:O	1.86	0.58
2:B:344:ALA:HB1	2:B:348:LEU:HD22	1.85	0.58
1:A:162:GLU:HG2	6:A:408:HOH:O	2.02	0.58
2:B:219:VAL:HG22	2:B:232:LEU:HD11	1.85	0.56
1:A:14[A]:THR:HG21	1:A:148:LEU:HD13	1.88	0.56
1:C:161:HIS:HD2	6:C:439:HOH:O	1.88	0.56
3:C:301:1RO:C13	3:C:301:1RO:C2	2.82	0.55
1:A:94:SER:OG	1:A:295:HIS:HE1	1.89	0.55
1:A:287:GLN:HG2	6:A:515:HOH:O	2.05	0.55
1:A:223:ASP:H	1:A:226:VAL:HG12	1.72	0.55
1:A:71:HIS:HB2	1:A:76:LEU:CD1	2.36	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:71:HIS:CE1	2:D:304:PHE:CE2	2.96	0.53
1:A:295:HIS:HD2	1:A:297:ARG:HA	1.74	0.52
1:A:268:HIS:CE1	6:A:485:HOH:O	2.61	0.52
1:A:295:HIS:HD2	1:A:297:ARG:H	1.56	0.52
2:D:282:THR:HG21	2:D:286:TYR:HD2	1.72	0.52
2:B:233:HIS:HE1	6:B:619:HOH:O	1.93	0.52
1:A:295:HIS:CD2	1:A:297:ARG:HA	2.45	0.51
1:C:72:THR:HG1	1:C:73:GLU:C	2.13	0.51
2:B:346:PRO:O	2:B:349:LYS:HG2	2.10	0.51
6:C:420:HOH:O	2:D:296:HIS:HD2	1.93	0.51
1:A:181:SER:HB3	6:A:476:HOH:O	2.11	0.51
2:B:176:PRO:HA	2:B:179[A]:HIS:CG	2.46	0.50
1:A:13:GLY:HA2	3:A:301:1RO:H2	1.94	0.50
1:C:52:ILE:HD11	1:C:78:LEU:HD21	1.94	0.49
1:A:129:LYS:HZ2	1:A:165[A]:THR:HG21	1.78	0.48
1:C:277:ALA:O	1:C:281:LEU:HD22	2.13	0.48
2:D:282:THR:HG22	2:D:282:THR:O	2.13	0.48
2:D:374:GLU:HA	2:D:377:ILE:HD12	1.95	0.48
2:D:346:PRO:O	2:D:349:LYS:HG2	2.13	0.48
1:A:295:HIS:HD2	1:A:297:ARG:N	2.12	0.47
1:C:73:GLU:HB3	1:C:74:ASN:ND2	2.30	0.46
1:C:81:GLU:O	3:C:301:1RO:H9	2.15	0.46
1:C:119:HIS:HE1	1:C:185:ASP:OD2	1.98	0.46
2:B:207:THR:HG23	2:B:210:MET:H	1.78	0.46
1:A:60:HIS:CG	1:A:61:PRO:HD2	2.51	0.45
1:A:297:ARG:HD2	6:A:487:HOH:O	2.16	0.45
1:A:129:LYS:HZ3	1:A:165[A]:THR:HG21	1.80	0.45
1:C:202:LEU:HD12	1:C:203:PHE:CE2	2.52	0.45
1:A:94:SER:OG	1:A:295:HIS:CE1	2.70	0.45
3:A:301:1RO:N2	3:A:301:1RO:C23	2.79	0.44
2:B:285:THR:HG22	6:B:699:HOH:O	2.15	0.44
2:B:344:ALA:O	2:B:348:LEU:HB2	2.17	0.44
2:D:193:CYS:O	2:D:241:ARG:HD2	2.18	0.44
2:B:199:TYR:CE2	2:B:348:LEU:HD21	2.52	0.44
2:B:183:HIS:HB2	2:B:317:GLN:NE2	2.29	0.44
1:C:227:TRP:HB3	1:C:230:VAL:CG2	2.48	0.44
1:A:163:VAL:HA	6:A:440:HOH:O	2.18	0.44
1:C:221:THR:CG2	1:C:243:TRP:H	2.31	0.43
1:A:134:LEU:HD21	3:A:301:1RO:O1	2.17	0.43
2:D:399:LEU:HD23	2:D:426:PRO:HB2	2.00	0.43
3:C:301:1RO:N2	3:C:301:1RO:C23	2.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:71:HIS:CD2	1:A:76:LEU:HD13	2.54	0.43
2:D:233:HIS:HD2	6:D:603:HOH:O	2.00	0.43
1:A:295:HIS:HD2	1:A:297:ARG:CA	2.32	0.43
1:A:65:LYS:HB2	1:A:65:LYS:HE3	1.85	0.42
1:A:268:HIS:HD2	6:A:509:HOH:O	2.01	0.42
1:A:60:HIS:HE1	6:A:430:HOH:O	2.02	0.42
2:B:334[B]:MET:HE3	6:B:657:HOH:O	2.19	0.42
1:A:71:HIS:HA	1:A:72:THR:HA	1.86	0.42
2:B:233:HIS:HD2	6:B:602:HOH:O	2.02	0.42
1:C:252:VAL:CG2	1:C:255:LEU:HD12	2.45	0.42
2:D:395:HIS:HE1	2:D:427:PRO:O	2.03	0.42
1:C:181:SER:HB3	6:C:451:HOH:O	2.19	0.41
2:B:176:PRO:O	2:B:179[B]:HIS:HD2	2.02	0.41
1:A:14[A]:THR:CG2	1:A:148:LEU:HD13	2.50	0.41
2:D:373:PRO:HD2	2:D:376:LEU:HD12	2.03	0.41
1:A:52:ILE:CD1	1:A:78:LEU:HD21	2.46	0.41
1:A:17:VAL:HG23	1:A:34:LYS:HB3	2.03	0.41
1:A:37:LEU:HD13	2:B:296:HIS:NE2	2.35	0.41
2:D:378:ARG:HD2	2:D:378:ARG:HA	1.94	0.41
1:A:161:HIS:O	1:A:162:GLU:C	2.58	0.41
2:B:388:LYS:HB3	2:B:389:PRO:HD3	2.01	0.41
1:A:62:ASN:ND2	1:A:110:GLN:HB3	2.36	0.41
1:C:222:PRO:HD3	1:C:269:TYR:CZ	2.55	0.41
1:A:44:VAL:HA	1:A:45:PRO:HD3	1.96	0.41
2:D:203:GLN:HA	2:D:204:PRO:HD3	1.92	0.40
1:C:71:HIS:HB3	1:C:72:THR:H	1.18	0.40
2:D:345:ASP:HA	2:D:346:PRO:HA	1.92	0.40
2:D:202:LYS:O	2:D:204:PRO:HD3	2.22	0.40
2:B:345:ASP:HA	2:B:346:PRO:HA	1.88	0.40
2:D:183:HIS:CD2	2:D:379:LYS:HE3	2.56	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	297/300 (99%)	285 (96%)	9 (3%)	3 (1%)	19	11
1	C	297/300 (99%)	287 (97%)	9 (3%)	1 (0%)	46	41
2	B	257/258 (100%)	255 (99%)	2 (1%)	0	100	100
2	D	253/258 (98%)	247 (98%)	6 (2%)	0	100	100
All	All	1104/1116 (99%)	1074 (97%)	26 (2%)	4 (0%)	39	33

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	162	GLU
1	A	164	VAL
1	C	164	VAL
1	A	163	VAL

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	265/263 (101%)	256 (97%)	9 (3%)	44	41
1	C	264/263 (100%)	250 (95%)	14 (5%)	28	22
2	B	233/232 (100%)	228 (98%)	5 (2%)	61	63
2	D	229/232 (99%)	222 (97%)	7 (3%)	47	46
All	All	991/990 (100%)	956 (96%)	35 (4%)	42	40

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	55	LEU
1	A	72	THR
1	A	96	LEU
1	A	122	ARG

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Mol	Chain	Res	Type
1	A	148	LEU
1	A	150	ARG
1	A	161	HIS
1	A	162	GLU
1	A	163	VAL
2	B	196	LYS
2	B	232	LEU
2	B	285	THR
2	B	292	LEU
2	B	296	HIS
1	C	37	LEU
1	C	55	LEU
1	C	72	THR
1	C	73	GLU
1	C	101	LEU
1	C	103	LEU
1	C	122	ARG
1	C	150	ARG
1	C	202	LEU
1	C	230	VAL
1	C	278	LYS
1	C	281	LEU
1	C	284	PRO
1	C	287	GLN
2	D	179	HIS
2	D	196	LYS
2	D	232	LEU
2	D	250	ARG
2	D	292	LEU
2	D	296	HIS
2	D	328	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	60	HIS
1	A	295	HIS
2	B	233	HIS
2	B	254	GLN
2	B	395	HIS
2	B	425	ASN
1	C	60	HIS

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Mol	Chain	Res	Type
1	C	74	ASN
1	C	119	HIS
1	C	161	HIS
1	C	246	GLN
2	D	233	HIS
2	D	254	GLN
2	D	395	HIS

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	160	1	8,10,11	0.71	0	7,14,16	1.35	1 (14%)
1	TPO	C	160	1	8,10,11	0.68	0	7,14,16	1.16	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
1	TPO	A	160	1	-	0/8/11/13	0/0/0/0
1	TPO	C	160	1	-	0/8/11/13	0/0/0/0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	160	TPO	O3P-P-O2P	2.26	116.00	107.38

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	1RO	A	301	-	25,27,27	2.76	5 (20%)	26,37,37	2.85	9 (34%)
4	SGM	B	501	-	5,5,5	0.56	0	5,5,5	0.78	0
3	1RO	C	301	-	25,27,27	2.73	5 (20%)	26,37,37	2.71	8 (30%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	1RO	A	301	-	-	0/5/21/21	0/4/4/4
4	SGM	B	501	-	-	0/4/4/4	0/0/0/0
3	1RO	C	301	-	-	0/5/21/21	0/4/4/4

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	301	1RO	C13-N2	-2.78	1.32	1.37
3	C	301	1RO	C13-N2	-2.44	1.32	1.37
3	A	301	1RO	C15-N2	2.01	1.34	1.31
3	C	301	1RO	C15-N2	2.14	1.34	1.31
3	C	301	1RO	O1-C13	2.37	1.28	1.24
3	A	301	1RO	O1-C13	2.47	1.28	1.24
3	C	301	1RO	C3-C4	4.56	1.48	1.42
3	A	301	1RO	C3-C4	4.59	1.48	1.42
3	C	301	1RO	C11-C12	11.49	1.49	1.34
3	A	301	1RO	C11-C12	11.54	1.49	1.34

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	301	1RO	C1-C11-C12	-10.96	115.83	130.96
3	C	301	1RO	C1-C11-C12	-10.09	117.03	130.96
3	C	301	1RO	C22-C21-S2	-6.16	106.41	113.23
3	A	301	1RO	C22-C21-S2	-6.05	106.54	113.23
3	A	301	1RO	O1-C13-N2	-3.14	116.67	124.40
3	C	301	1RO	O1-C13-N2	-2.84	117.41	124.40
3	A	301	1RO	C18-N3-C15	-2.63	118.53	122.81
3	C	301	1RO	C18-N3-C15	-2.51	118.72	122.81
3	A	301	1RO	C3-C4-N1	-2.36	118.72	122.08
3	C	301	1RO	C3-C4-N1	-2.34	118.74	122.08
3	A	301	1RO	C11-C12-S1	-2.03	127.06	129.31
3	A	301	1RO	C5-C4-N1	2.41	122.52	118.52
3	A	301	1RO	C9-N1-C4	2.45	121.02	116.87
3	C	301	1RO	C9-N1-C4	2.49	121.10	116.87
3	C	301	1RO	C5-C4-N1	2.52	122.71	118.52
3	C	301	1RO	C18-C19-C23	2.65	134.16	128.63
3	A	301	1RO	C18-C19-C23	2.72	134.32	128.63

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	301	1RO	9	0
4	B	501	SGM	1	0
3	C	301	1RO	9	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	297/300 (99%)	0.43	15 (5%) 32 33	15, 24, 43, 86	0
1	C	296/300 (98%)	0.89	44 (14%) 3 3	22, 33, 51, 76	0
2	B	257/258 (99%)	0.84	35 (13%) 4 4	19, 34, 52, 76	0
2	D	255/258 (98%)	0.98	43 (16%) 2 3	18, 34, 62, 87	0
All	All	1105/1116 (99%)	0.78	137 (12%) 5 6	15, 31, 55, 87	0

All (137) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	176	PRO	10.1
2	D	175	VAL	9.6
1	A	72	THR	7.1
2	D	177	ASP	6.3
1	C	295	HIS	6.1
1	A	39	THR	6.1
2	B	432	LEU	5.5
1	C	186	ILE	5.3
2	D	323	GLN	5.2
2	B	176	PRO	5.1
1	A	38	ASP	5.1
2	B	323	GLN	4.8
2	D	378	ARG	4.7
1	C	128	LEU	4.5
2	D	280	TYR	4.5
2	B	284	ASP	4.5
2	D	381	GLY	4.4
1	C	225	VAL	4.4
1	C	287	GLN	4.4
1	C	189	LEU	4.3
1	C	72	THR	4.3

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Mol	Chain	Res	Type	RSRZ
2	B	280	TYR	4.2
1	C	162	GLU	4.1
1	C	97	THR	4.1
2	B	431	ASN	4.1
1	C	143	LEU	4.0
1	C	192	ILE	4.0
2	D	428	GLU	4.0
2	D	284	ASP	3.9
2	B	341	LEU	3.9
1	C	226	VAL	3.9
1	A	71	HIS	3.9
2	D	365	TYR	3.8
1	C	184	VAL	3.8
1	C	296	LEU	3.7
2	B	285	THR	3.7
2	D	423	LEU	3.7
2	D	429	THR	3.7
2	B	428	GLU	3.6
1	C	111	LEU	3.6
1	C	247	ASP	3.6
2	D	341	LEU	3.5
2	B	236	VAL	3.5
1	A	-2	PRO	3.4
2	D	374	GLU	3.4
1	A	36	ARG	3.4
2	B	324	PRO	3.3
2	D	419	HIS	3.3
2	D	385	GLU	3.3
2	B	283	ASP	3.3
1	A	178	LYS	3.3
2	B	177	ASP	3.2
1	A	73	GLU	3.2
1	C	248	PHE	3.2
1	C	179	TYR	3.2
2	D	325	ALA	3.1
2	D	324	PRO	3.1
1	C	258	ASP	3.1
1	C	101	LEU	3.0
2	D	283	ASP	3.0
1	C	191	CYS	3.0
2	D	388	LYS	3.0
1	A	161	HIS	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	288	ASP	3.0
2	B	385	GLU	2.9
2	B	198	GLY	2.9
2	B	403	GLN	2.8
2	D	416	SER	2.8
1	C	233	MET	2.8
2	D	424	LEU	2.8
1	C	187	TRP	2.8
2	D	232	LEU	2.8
1	C	36	ARG	2.8
2	D	355	ILE	2.7
1	A	74	ASN	2.7
1	C	252	VAL	2.7
2	B	289	LYS	2.7
1	A	287	GLN	2.7
1	C	102	PRO	2.7
2	B	260	ALA	2.6
1	C	232	SER	2.6
1	C	133	LEU	2.6
1	C	138	GLU	2.6
1	C	108	LEU	2.6
2	B	336	LEU	2.6
1	C	161	HIS	2.6
2	D	392	MET	2.5
1	C	115	LEU	2.5
2	B	356	ALA	2.5
1	C	273	LYS	2.5
2	D	328	LYS	2.5
2	D	367	VAL	2.5
2	B	197	VAL	2.4
2	D	235	ALA	2.4
2	B	359	ALA	2.4
2	B	201	LYS	2.4
2	B	232	LEU	2.4
2	B	311	VAL	2.4
2	B	369	GLY	2.4
2	D	420	GLY	2.4
2	D	326	ASN	2.4
1	C	293	VAL	2.4
2	B	287	THR	2.4
2	B	234	LEU	2.3
1	A	2	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	111	LEU	2.3
2	B	315	LEU	2.3
1	C	231	THR	2.3
2	D	285	THR	2.3
1	C	124	LEU	2.2
2	D	234	LEU	2.2
1	C	250	LYS	2.2
1	C	73	GLU	2.2
2	D	320	LEU	2.2
2	B	263	LEU	2.2
1	C	144	ALA	2.2
1	C	228	PRO	2.2
2	D	178	TYR	2.2
2	D	400	LYS	2.1
2	D	271	TYR	2.1
2	B	256	VAL	2.1
1	C	249	SER	2.1
2	D	359	ALA	2.1
2	D	231	THR	2.1
2	D	197	VAL	2.1
2	D	311	VAL	2.1
2	B	209	SER	2.1
2	B	388	LYS	2.1
2	D	377	ILE	2.1
1	A	179	TYR	2.1
2	B	293	ARG	2.0
2	D	315	LEU	2.0
1	C	253	PRO	2.0
2	B	196	LYS	2.0
2	D	425	ASN	2.0
1	C	223[A]	ASP	2.0
1	A	184	VAL	2.0

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
1	TPO	A	160	11/12	0.99	0.10	-	20,21,22,23	0
1	TPO	C	160	11/12	0.99	0.08	-	23,25,28,28	0

6.3 Carbohydrates [i](#)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
3	1RO	A	301	24/24	0.85	0.16	2.11	24,29,32,35	0
5	MG	D	501	1/1	0.84	0.25	1.88	29,29,29,29	0
3	1RO	C	301	24/24	0.87	0.18	1.60	29,32,36,38	0
4	SGM	B	501	6/6	0.92	0.20	1.41	41,42,46,54	0

6.5 Other polymers [i](#)

There are no such residues in this entry.