Full wwPDB X-ray Structure Validation Report (i)

Dec 8, 2023 – 05:35 am GMT

PDB ID	:	2WMB
Title	:	Structural and thermodynamic consequences of cyclization of peptide ligands for the recruitment site of cyclin A
Authors	:	Robertson, G.F.; Endicott, J.A.; Noble, M.E.M.; McDonnell, J.M.
Deposited on	:	2009-06-30
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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

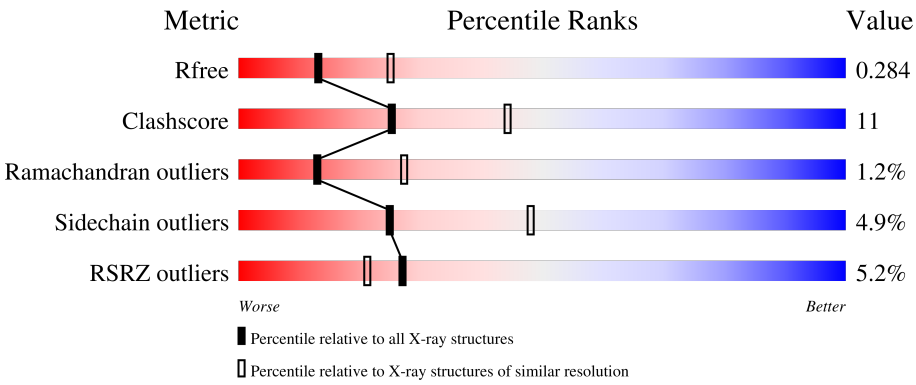
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance (i)

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))
R_{free}	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (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 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	303	3%, 72%, 23%, • • •
1	C	303	7%, 63%, 22%, •, 12%
2	B	259	2%, 75%, 23%, •
2	D	259	7%, 75%, 23%, •
3	I	5	20%, 80%, 20%

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
4	MG	B	1433	-	-	-	X

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 8855 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 CELL DIVISION PROTEIN KINASE 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	297	2388	1550	404	425	1	8	0	0	0
1	C	267	2146	1392	366	380	1	7	0	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	expression tag	UNP P24941
A	-3	PRO	-	expression tag	UNP P24941
A	-2	LEU	-	expression tag	UNP P24941
A	-1	GLY	-	expression tag	UNP P24941
A	0	SER	-	expression tag	UNP P24941
C	-4	GLY	-	expression tag	UNP P24941
C	-3	PRO	-	expression tag	UNP P24941
C	-2	LEU	-	expression tag	UNP P24941
C	-1	GLY	-	expression tag	UNP P24941
C	0	SER	-	expression tag	UNP P24941

- Molecule 2 is a protein called CYCLIN-A2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	258	2083	1350	339	383	11	0	0	0
2	D	258	2083	1350	339	383	11	0	0	0

- Molecule 3 is a protein called LINEAR RKLFD.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	I	5	47	31	9	7	0	0	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
4	B	1	1	1	0	0

- Molecule 5 is water.

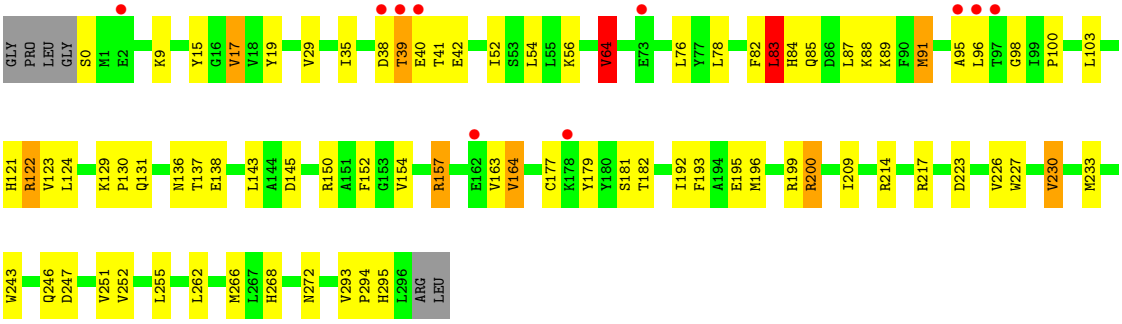
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	40	40	40	0	0
			Total	O		
5	B	33	33	33	0	0
			Total	O		
5	C	20	20	20	0	0
			Total	O		
5	D	14	14	14	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

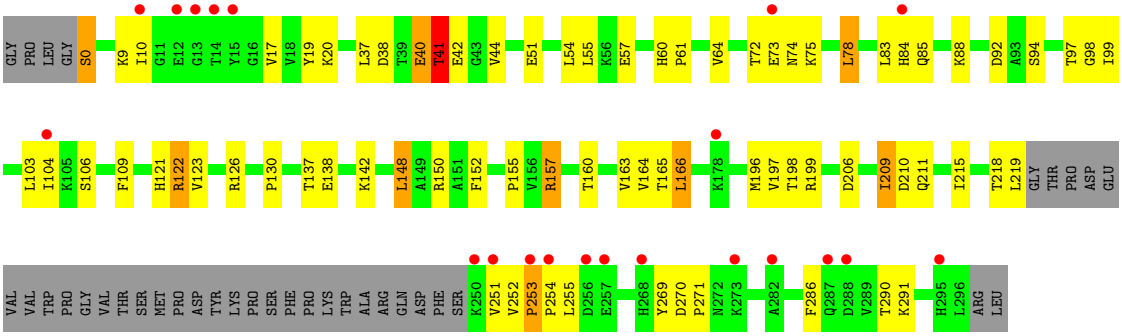
• Molecule 1: CELL DIVISION PROTEIN KINASE 2

Chain A:



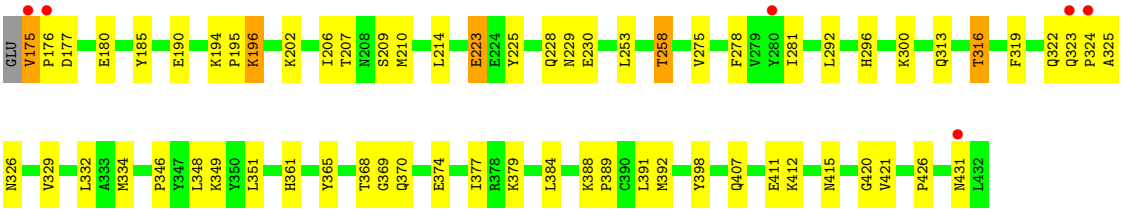
• Molecule 1: CELL DIVISION PROTEIN KINASE 2

Chain C:



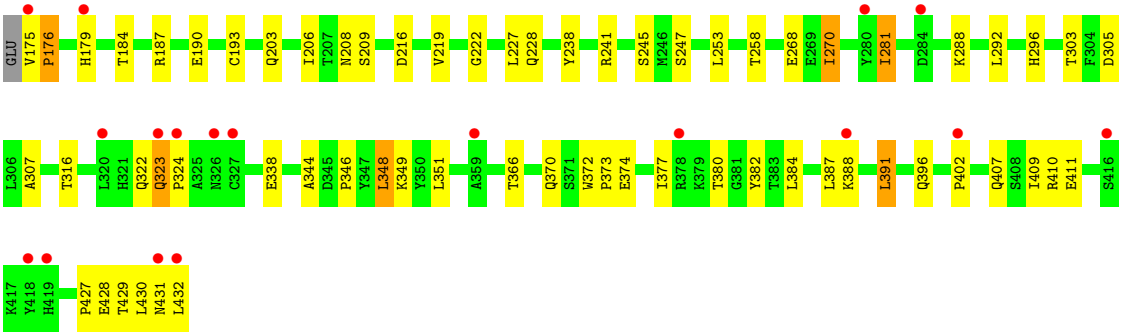
• Molecule 2: CYCLIN-A2

Chain B:



- Molecule 2: CYCLIN-A2

Chain D:



- Molecule 3: LINEAR RKLFD

Chain I:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	73.75Å 134.22Å 148.24Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	22.04 – 2.60 22.04 – 2.40	Depositor EDS
% Data completeness (in resolution range)	94.9 (22.04-2.60) 92.3 (22.04-2.40)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.13 (at 2.41Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.226 , 0.296 0.218 , 0.284	Depositor DCC
R_{free} test set	2708 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	49.4	Xtriage
Anisotropy	0.115	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 50.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	8855	wwPDB-VP
Average B, all atoms (Å^2)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.24% of the height of the origin peak. No significant pseudotranslation is detected.*

[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 (i)

5.1 Standard geometry (i)

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

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	0.85	0/2438	0.90	4/3308 (0.1%)
1	C	0.66	0/2183	0.78	3/2955 (0.1%)
2	B	0.84	2/2133 (0.1%)	0.83	0/2897
2	D	0.65	0/2133	0.74	0/2897
3	I	0.60	0/47	1.15	0/60
All	All	0.76	2/8934 (0.0%)	0.82	7/12117 (0.1%)

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	1
1	C	0	2
All	All	0	3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	229	ASN	CG-OD1	5.71	1.36	1.24
2	B	415	ASN	CG-OD1	5.21	1.35	1.24

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	78	LEU	CA-CB-CG	7.22	131.91	115.30
1	A	64	VAL	CB-CA-C	-6.09	99.84	111.40
1	A	83	LEU	CA-CB-CG	-5.91	101.71	115.30
1	A	230	VAL	CB-CA-C	-5.87	100.25	111.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	148	LEU	CA-CB-CG	5.37	127.66	115.30
1	C	78	LEU	CB-CG-CD2	5.11	119.68	111.00
1	A	247	ASP	N-CA-CB	5.05	119.69	110.60

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	246	GLN	Peptide
1	C	40	GLU	Peptide
1	C	41	THR	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2388	0	2430	64	2
1	C	2146	0	2206	57	0
2	B	2083	0	2107	42	2
2	D	2083	0	2107	40	0
3	I	47	0	49	0	0
4	B	1	0	0	0	0
5	A	40	0	0	2	0
5	B	33	0	0	2	0
5	C	20	0	0	5	0
5	D	14	0	0	0	0
All	All	8855	0	8899	188	2

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 11.

All (188) 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:C:41:THR:OG1	1:C:42:GLU:HA	1.19	1.31

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:LYS:HD2	1:A:131:GLN:HG3	1.23	1.17
1:C:84:HIS:HB2	5:C:2014:HOH:O	1.44	1.13
1:A:88:LYS:HD2	1:A:131:GLN:CG	1.95	0.96
1:C:41:THR:OG1	1:C:42:GLU:CA	2.14	0.96
2:D:270:ILE:H	2:D:270:ILE:HD12	1.32	0.91
2:B:176:PRO:HA	5:B:2001:HOH:O	1.72	0.89
1:A:177:CYS:HB2	1:A:233:MET:CE	2.06	0.86
1:C:253:PRO:HB2	1:C:254:PRO:HD3	1.59	0.84
1:A:88:LYS:CD	1:A:131:GLN:HG3	2.07	0.84
1:A:91:MET:HE2	1:A:195:GLU:HG2	1.62	0.80
1:C:40:GLU:OE1	5:C:2004:HOH:O	1.98	0.79
1:A:154:VAL:O	2:B:316:THR:HG22	1.83	0.79
1:A:272:ASN:OD1	2:B:175:VAL:HG22	1.83	0.78
1:A:91:MET:CE	1:A:195:GLU:HG2	2.14	0.77
1:A:177:CYS:HB2	1:A:233:MET:HE1	1.68	0.76
2:B:346:PRO:O	2:B:349:LYS:HG2	1.87	0.75
2:D:322:GLN:O	2:D:324:PRO:HA	1.88	0.73
2:B:368:THR:OG1	2:B:370:GLN:HG2	1.87	0.73
1:A:227:TRP:HB3	1:A:230:VAL:HG22	1.71	0.72
1:A:295:HIS:CG	1:A:295:HIS:O	2.42	0.72
2:D:270:ILE:H	2:D:270:ILE:CD1	2.02	0.72
1:A:177:CYS:SG	1:A:179:TYR:O	2.47	0.72
1:A:227:TRP:HB3	1:A:230:VAL:CG2	2.21	0.70
1:A:85:GLN:OE1	1:A:89:LYS:HD2	1.92	0.69
2:D:175:VAL:HB	2:D:176:PRO:HD3	1.72	0.69
2:D:176:PRO:HB2	2:D:179:HIS:HB2	1.75	0.68
2:B:374:GLU:HA	2:B:377:ILE:HD12	1.75	0.68
1:A:137:THR:O	1:A:293:VAL:HG13	1.94	0.68
2:D:208:ASN:OD1	2:D:344:ALA:HB3	1.93	0.67
2:B:176:PRO:CA	5:B:2001:HOH:O	2.35	0.67
1:A:91:MET:HE3	1:A:196:MET:HA	1.77	0.67
2:B:223:GLU:OE2	2:B:412:LYS:HE3	1.95	0.67
1:A:103:LEU:HD21	1:A:294:PRO:HB3	1.78	0.66
1:A:227:TRP:O	1:A:230:VAL:HG23	1.95	0.66
2:B:407:GLN:O	2:B:411:GLU:HG2	1.97	0.65
1:C:17:VAL:HG13	1:C:19:TYR:CE2	2.32	0.65
1:C:197:VAL:HG21	1:C:255:LEU:HD13	1.79	0.65
2:B:230:GLU:OE2	2:B:313:GLN:NE2	2.27	0.64
1:C:198:THR:HG22	1:C:253:PRO:HD2	1.82	0.62
2:D:222:GLY:HA2	2:D:227:LEU:HD12	1.82	0.61
1:C:218:THR:O	1:C:219:LEU:HD23	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:190:GLU:HG3	2:D:351:LEU:HD22	1.83	0.60
1:C:126:ARG:HB3	1:C:163:VAL:CG2	2.32	0.60
2:D:380:THR:HB	2:D:382:TYR:CD2	2.36	0.60
1:C:253:PRO:HB2	1:C:254:PRO:CD	2.31	0.60
1:A:163:VAL:HG13	1:A:164:VAL:HG23	1.83	0.59
2:B:361:HIS:HD2	2:B:391:LEU:HD21	1.68	0.58
2:D:346:PRO:HB2	2:D:349:LYS:HE2	1.86	0.58
2:D:184:THR:O	2:D:187:ARG:HB2	2.04	0.57
1:A:227:TRP:O	1:A:230:VAL:CG2	2.53	0.57
1:C:83:LEU:HD21	1:C:142:LYS:HD2	1.86	0.57
1:C:84:HIS:O	1:C:85:GLN:HB3	2.04	0.57
2:B:207:THR:HG23	2:B:210:MET:CE	2.34	0.57
1:C:51:GLU:O	1:C:55:LEU:HB2	2.04	0.57
2:D:203:GLN:HE22	2:D:247:SER:HA	1.68	0.56
1:A:42:GLU:HA	2:B:275:VAL:HG21	1.89	0.55
2:B:388:LYS:HB3	2:B:389:PRO:HD3	1.89	0.55
1:C:211:GLN:O	1:C:215:ILE:HG12	2.06	0.55
1:A:54:LEU:HD22	1:A:123:VAL:HG22	1.88	0.54
1:A:52:ILE:HD11	1:A:78:LEU:HD21	1.88	0.54
2:D:407:GLN:O	2:D:411:GLU:HG2	2.08	0.54
2:D:430:LEU:HD12	2:D:432:LEU:HD21	1.88	0.54
2:B:388:LYS:O	2:B:392:MET:HG2	2.08	0.54
1:C:38:ASP:OD2	1:C:41:THR:O	2.25	0.54
2:D:374:GLU:HA	2:D:377:ILE:HD12	1.89	0.54
1:A:39:THR:O	1:A:41:THR:N	2.40	0.53
1:A:227:TRP:CG	1:A:230:VAL:HG22	2.43	0.53
2:B:225:TYR:HE2	2:B:281:ILE:HG21	1.73	0.53
1:A:193:PHE:HD2	1:A:266:MET:HE3	1.74	0.53
1:C:57:GLU:O	5:C:2008:HOH:O	2.18	0.53
1:A:227:TRP:CB	1:A:230:VAL:HG22	2.37	0.53
1:A:84:HIS:CE1	1:A:137:THR:HG23	2.44	0.53
1:C:60:HIS:CG	1:C:61:PRO:HD2	2.43	0.52
2:D:322:GLN:C	2:D:324:PRO:HA	2.29	0.52
1:A:35:ILE:HB	1:A:76:LEU:HB3	1.91	0.52
1:C:10:ILE:HD11	1:C:20:LYS:HB2	1.91	0.52
1:A:82:PHE:C	1:A:82:PHE:CD2	2.84	0.51
1:A:64:VAL:HG22	1:A:143:LEU:O	2.11	0.51
2:D:366:THR:HG23	2:D:427:PRO:HD3	1.91	0.51
2:B:223:GLU:CD	2:B:412:LYS:HE3	2.31	0.50
1:A:122:ARG:HA	1:A:152:PHE:CE2	2.46	0.50
1:A:262:LEU:HG	1:A:266:MET:CE	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95:ALA:HA	1:A:199:ARG:NH1	2.28	0.49
2:B:207:THR:HG23	2:B:210:MET:HE3	1.93	0.49
2:B:332:LEU:HA	2:B:421:VAL:HG21	1.94	0.49
2:B:296:HIS:CE1	2:B:300:LYS:NZ	2.80	0.49
1:A:136:ASN:OD1	1:A:136:ASN:C	2.51	0.49
1:C:0:SER:N	5:C:2001:HOH:O	2.45	0.48
2:B:275:VAL:HG11	2:B:292:LEU:HD21	1.96	0.48
1:A:91:MET:HE1	1:A:195:GLU:HG2	1.94	0.48
1:A:154:VAL:O	2:B:316:THR:CG2	2.60	0.48
1:C:150:ARG:NH2	2:D:268:GLU:O	2.40	0.48
1:A:42:GLU:HA	2:B:275:VAL:CG2	2.43	0.48
2:B:319:PHE:O	2:B:322:GLN:HG2	2.14	0.48
1:C:72:THR:O	2:D:296:HIS:HE1	1.97	0.48
1:C:122:ARG:HD2	1:C:122:ARG:O	2.14	0.48
2:D:323:GLN:OE1	2:D:370:GLN:HG3	2.14	0.48
1:C:54:LEU:HD22	1:C:123:VAL:HG22	1.96	0.47
2:D:238:TYR:N	2:D:238:TYR:CD1	2.82	0.47
2:B:361:HIS:CD2	2:B:391:LEU:HD21	2.48	0.47
1:C:104:ILE:HG12	1:C:196:MET:HB3	1.95	0.47
1:A:82:PHE:CG	1:A:83:LEU:N	2.82	0.47
2:B:365:TYR:O	2:B:369:GLY:HA2	2.15	0.47
2:D:384:LEU:O	2:D:388:LYS:HB2	2.15	0.47
1:A:17:VAL:HG11	1:A:19:TYR:OH	2.15	0.47
1:C:88:LYS:HB2	1:C:130:PRO:HB2	1.96	0.47
1:A:100:PRO:O	1:A:103:LEU:N	2.49	0.46
1:C:106:SER:O	1:C:109:PHE:HB3	2.16	0.46
1:A:223:ASP:H	1:A:226:VAL:HG12	1.79	0.46
1:C:290:THR:HG22	1:C:291:LYS:H	1.79	0.46
1:A:38:ASP:HB2	5:A:2009:HOH:O	2.16	0.46
1:A:129:LYS:HA	1:A:192:ILE:HD11	1.97	0.46
1:A:251:VAL:HG12	1:A:252:VAL:HG23	1.97	0.46
1:C:72:THR:HG22	1:C:73:GLU:N	2.31	0.46
1:C:253:PRO:CB	1:C:254:PRO:HD3	2.35	0.46
2:B:326:ASN:HB3	2:B:329:VAL:CG2	2.46	0.46
2:B:322:GLN:HG3	2:B:325:ALA:HA	1.98	0.46
2:B:326:ASN:HB3	2:B:329:VAL:HG23	1.97	0.45
1:A:121:HIS:HD2	2:B:185:TYR:CE1	2.35	0.45
1:A:295:HIS:O	1:A:295:HIS:ND1	2.49	0.45
2:D:344:ALA:HB1	2:D:348:LEU:HD22	1.97	0.45
1:C:122:ARG:HA	1:C:152:PHE:CE2	2.51	0.45
1:C:137:THR:HG23	5:C:2014:HOH:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:303:THR:OG1	2:D:305:ASP:OD2	2.32	0.45
1:A:293:VAL:HG12	1:A:294:PRO:O	2.16	0.45
1:A:157:ARG:CZ	2:B:228:GLN:HG3	2.47	0.45
1:A:262:LEU:HG	1:A:266:MET:HE1	1.98	0.45
2:B:323:GLN:HA	2:B:324:PRO:HA	1.68	0.45
1:C:41:THR:HB	2:D:292:LEU:HD11	1.99	0.45
2:B:230:GLU:HA	2:B:230:GLU:OE1	2.17	0.44
1:C:9:LYS:HD3	1:C:17:VAL:HG21	1.98	0.44
1:C:138:GLU:N	1:C:138:GLU:OE1	2.50	0.44
1:C:126:ARG:HB3	1:C:163:VAL:HG21	2.00	0.44
1:C:72:THR:HG22	1:C:74:ASN:H	1.83	0.44
1:C:219:LEU:HD12	1:C:269:TYR:CE2	2.52	0.44
2:D:216:ASP:O	2:D:219:VAL:HB	2.17	0.44
1:C:270:ASP:HA	1:C:271:PRO:HD2	1.78	0.44
1:A:129:LYS:HD2	1:A:131:GLN:OE1	2.17	0.44
1:C:155:PRO:HD2	2:D:316:THR:HB	2.00	0.44
2:B:258:THR:HG22	2:B:278:PHE:HB3	1.99	0.44
1:C:37:LEU:HD22	1:C:44:VAL:HG22	2.00	0.43
1:C:165:THR:O	1:C:166:LEU:C	2.56	0.43
2:B:214:LEU:HD22	2:B:253:LEU:HG	2.00	0.43
1:A:15:TYR:CG	1:A:35:ILE:HG12	2.53	0.43
1:C:92:ASP:C	1:C:94:SER:H	2.21	0.43
1:C:99:ILE:HG23	1:C:103:LEU:HD23	2.00	0.43
1:A:87:LEU:HB3	1:A:130:PRO:O	2.18	0.43
2:B:190:GLU:HG3	2:B:351:LEU:HD22	2.00	0.43
2:B:379:LYS:HZ2	2:B:379:LYS:HG3	1.66	0.43
2:D:338:GLU:HG2	2:D:409:ILE:HD13	2.01	0.43
1:A:98:GLY:HA2	1:A:199:ARG:NE	2.34	0.43
1:A:84:HIS:ND1	1:A:137:THR:HG23	2.34	0.43
1:A:124:LEU:HG	1:A:152:PHE:CD2	2.53	0.43
1:C:157:ARG:NH2	2:D:228:GLN:HG3	2.33	0.43
2:D:203:GLN:NE2	2:D:247:SER:HA	2.32	0.42
1:C:98:GLY:HA2	1:C:199:ARG:HE	1.83	0.42
1:A:29:VAL:O	1:A:82:PHE:HB3	2.20	0.42
1:A:181:SER:OG	1:A:182:THR:N	2.51	0.42
1:C:98:GLY:HA2	1:C:199:ARG:NE	2.34	0.42
1:A:230:VAL:O	1:A:233:MET:HG3	2.19	0.41
2:B:196:LYS:HE3	2:B:196:LYS:HB3	1.85	0.41
2:B:334:MET:HE2	2:B:334:MET:HB3	1.92	0.41
1:A:214:ARG:HG2	5:A:2029:HOH:O	2.19	0.41
1:C:57:GLU:OE2	2:D:307:ALA:HB3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:387:LEU:O	2:D:391:LEU:HD12	2.20	0.41
1:C:17:VAL:CG1	1:C:19:TYR:CE2	3.02	0.41
1:C:121:HIS:O	1:C:122:ARG:HG3	2.19	0.41
1:C:41:THR:HG22	2:D:288:LYS:NZ	2.35	0.41
1:C:103:LEU:O	1:C:104:ILE:C	2.57	0.41
2:D:206:ILE:HD12	2:D:253:LEU:HD13	2.02	0.41
2:D:372:TRP:HA	2:D:373:PRO:HD3	1.87	0.41
1:A:88:LYS:HD2	1:A:131:GLN:HE21	1.84	0.41
1:C:109:PHE:HB2	1:C:286:PHE:CE1	2.55	0.41
1:A:9:LYS:HD2	1:A:17:VAL:CG1	2.51	0.41
1:C:72:THR:HB	1:C:75:LYS:H	1.86	0.41
1:C:209:ILE:HG22	1:C:210:ASP:N	2.36	0.41
2:D:407:GLN:HE22	2:D:410:ARG:HD2	1.86	0.41
1:C:41:THR:CG2	2:D:288:LYS:NZ	2.84	0.41
2:D:281:ILE:H	2:D:281:ILE:HG13	1.71	0.41
1:A:217:ARG:HG3	1:A:243:TRP:CE2	2.56	0.40
1:A:98:GLY:HA2	1:A:199:ARG:HE	1.85	0.40
2:B:196:LYS:NZ	2:B:202:LYS:HD2	2.36	0.40
1:C:60:HIS:ND1	1:C:61:PRO:HD2	2.36	0.40
2:D:193:CYS:O	2:D:241:ARG:HD2	2.22	0.40
2:D:388:LYS:HE2	2:D:432:LEU:HD22	2.03	0.40
2:B:194:LYS:HA	2:B:195:PRO:HD3	1.89	0.40
2:B:398:TYR:CE2	2:B:426:PRO:HA	2.57	0.40

All (2) 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:200:ARG:NH2	2:B:180:GLU:OE2[4_456]	2.10	0.10
1:A:96:LEU:O	2:B:374:GLU:OE1[4_456]	2.17	0.03

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	294/303 (97%)	274 (93%)	16 (5%)	4 (1%)	11	22
1	C	262/303 (86%)	233 (89%)	25 (10%)	4 (2%)	10	21
2	B	256/259 (99%)	243 (95%)	12 (5%)	1 (0%)	34	57
2	D	256/259 (99%)	230 (90%)	22 (9%)	4 (2%)	9	19
3	I	3/5 (60%)	2 (67%)	1 (33%)	0	100	100
All	All	1071/1129 (95%)	982 (92%)	76 (7%)	13 (1%)	13	27

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	39	THR
1	A	40	GLU
2	D	323	GLN
1	C	164	VAL
1	C	253	PRO
1	A	164	VAL
1	C	166	LEU
1	C	209	ILE
2	D	431	ASN
1	A	145	ASP
2	D	402	PRO
2	B	420	GLY
2	D	176	PRO

5.3.2 Protein sidechains (i)

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	261/265 (98%)	247 (95%)	14 (5%)	22	44
1	C	234/265 (88%)	223 (95%)	11 (5%)	26	50
2	B	232/233 (100%)	221 (95%)	11 (5%)	26	50
2	D	232/233 (100%)	222 (96%)	10 (4%)	29	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	I	5/5 (100%)	4 (80%)	1 (20%)	1 2
All	All	964/1001 (96%)	917 (95%)	47 (5%)	25 48

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	0	SER
1	A	17	VAL
1	A	56	LYS
1	A	64	VAL
1	A	83	LEU
1	A	91	MET
1	A	122	ARG
1	A	138	GLU
1	A	150	ARG
1	A	157	ARG
1	A	200	ARG
1	A	209	ILE
1	A	255	LEU
1	A	268	HIS
2	B	175	VAL
2	B	177	ASP
2	B	196	LYS
2	B	206	ILE
2	B	209	SER
2	B	223	GLU
2	B	258	THR
2	B	316	THR
2	B	348	LEU
2	B	384	LEU
2	B	431	ASN
1	C	0	SER
1	C	41	THR
1	C	64	VAL
1	C	78	LEU
1	C	97	THR
1	C	122	ARG
1	C	148	LEU
1	C	157	ARG
1	C	206	ASP
1	C	251	VAL
1	C	252	VAL

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Mol	Chain	Res	Type
2	D	209	SER
2	D	245	SER
2	D	258	THR
2	D	270	ILE
2	D	281	ILE
2	D	348	LEU
2	D	391	LEU
2	D	396	GLN
2	D	428	GLU
2	D	429	THR
3	I	34	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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	C	160	1	8,10,11	1.03	1 (12%)	10,14,16	1.14	1 (10%)
1	TPO	A	160	1	8,10,11	0.74	0	10,14,16	1.13	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	C	160	1	-	1/9/11/13	-
1	TPO	A	160	1	-	1/9/11/13	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	160	TPO	P-OG1	2.52	1.64	1.59

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	160	TPO	O-C-CA	-2.01	119.50	124.78

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	160	TPO	O-C-CA-CB
1	C	160	TPO	O-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 (i)

6.1 Protein, DNA and RNA chains (i)

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	296/303 (97%)	-0.30	10 (3%) 45 38	20, 32, 64, 78	0
1	C	266/303 (87%)	0.09	21 (7%) 12 9	25, 53, 77, 97	0
2	B	258/259 (99%)	-0.29	6 (2%) 60 54	21, 34, 51, 67	0
2	D	258/259 (99%)	0.18	18 (6%) 16 12	25, 54, 88, 98	0
3	I	5/5 (100%)	0.25	1 (20%) 1 0	53, 56, 62, 70	0
All	All	1083/1129 (95%)	-0.09	56 (5%) 27 21	20, 43, 79, 98	0

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	175	VAL	7.8
1	A	40	GLU	5.6
1	A	96	LEU	4.2
1	C	273	LYS	4.1
2	D	175	VAL	4.0
1	C	257	GLU	4.0
2	D	432	LEU	3.8
2	D	323	GLN	3.8
1	C	12	GLU	3.7
2	D	324	PRO	3.7
1	C	287	GLN	3.6
1	C	13	GLY	3.5
1	C	84	HIS	3.4
2	D	284	ASP	3.3
2	D	416	SER	3.3
1	C	254	PRO	3.2
1	C	295	HIS	3.2
2	D	378	ARG	3.2
2	D	327	CYS	3.1
1	C	15	TYR	3.1

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Mol	Chain	Res	Type	RSRZ
2	D	359	ALA	3.0
1	A	162	GLU	2.9
2	D	431	ASN	2.9
1	A	39	THR	2.8
1	C	250	LYS	2.8
2	B	323	GLN	2.8
1	C	253	PRO	2.8
1	A	38	ASP	2.8
1	C	256	ASP	2.8
2	D	280	TYR	2.8
1	C	282	ALA	2.7
2	B	176	PRO	2.6
2	D	326	ASN	2.6
2	D	402	PRO	2.6
1	C	178	LYS	2.6
1	C	104	ILE	2.6
1	A	97	THR	2.5
2	B	280	TYR	2.4
3	I	34	ASP	2.4
1	C	251	VAL	2.4
2	D	418	TYR	2.3
1	A	178	LYS	2.3
2	B	431	ASN	2.3
2	B	324	PRO	2.2
2	D	419	HIS	2.2
1	C	14	THR	2.2
2	D	388	LYS	2.1
1	C	73	GLU	2.1
1	C	10	ILE	2.1
1	A	95	ALA	2.1
2	D	320	LEU	2.1
1	A	73	GLU	2.1
1	C	288	ASP	2.0
1	C	268	HIS	2.0
2	D	179	HIS	2.0
1	A	2	GLU	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. 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	C	160	11/12	0.95	0.13	52,57,59,60	0
1	TPO	A	160	11/12	0.98	0.10	29,34,38,39	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	MG	B	1433	1/1	0.34	0.41	91,91,91,91	0

6.5 Other polymers (i)

There are no such residues in this entry.