Full wwPDB X-ray Structure Validation Report (i)

Aug 16, 2023 – 05:02 PM EDT

PDB ID	:	2A1F
Title	:	Crystal Structure of Uridylate kinase
Authors	:	Gorman, J.; Shapiro, L.; Burley, S.K.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on	:	2005-06-20
Resolution	:	2.10 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 (1)) were used in the production of this report:

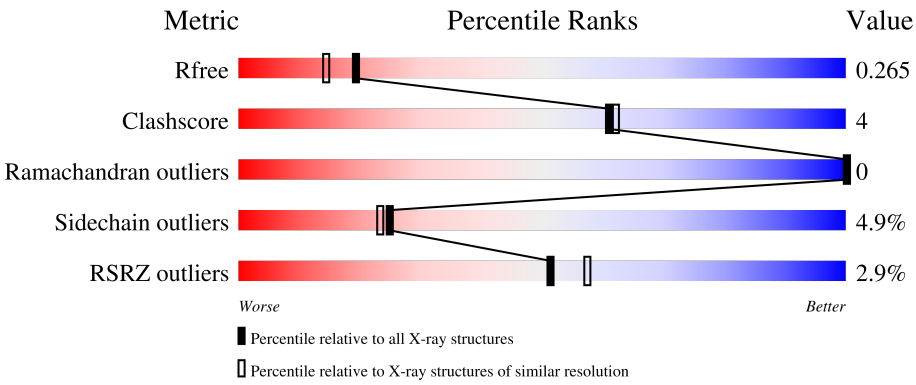
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	247	3% 82% 11% • 6%
1	B	247	3% 85% 8% 6%
1	C	247	2% 84% 11% • •
1	D	247	3% 83% 12% •
1	E	247	3% 84% 11% • 5%

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Mol	Chain	Length	Quality of chain
1	F	247	3% 79% 14% • 5%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 11567 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 Uridylate kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	232	1755	1108	301	330	16	0	0	0
1	B	232	1755	1108	301	330	16	0	0	0
1	C	237	1807	1138	318	335	16	0	0	0
1	D	236	1797	1132	315	334	16	0	0	0
1	E	235	1787	1126	312	333	16	0	0	0
1	F	234	1777	1120	309	332	16	0	0	0

There are 66 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	cloning artifact	UNP P43890
A	0	SER	-	cloning artifact	UNP P43890
A	1	LEU	-	cloning artifact	UNP P43890
A	238	GLU	-	cloning artifact	UNP P43890
A	239	GLY	-	cloning artifact	UNP P43890
A	240	HIS	-	expression tag	UNP P43890
A	241	HIS	-	expression tag	UNP P43890
A	242	HIS	-	expression tag	UNP P43890
A	243	HIS	-	expression tag	UNP P43890
A	244	HIS	-	expression tag	UNP P43890
A	245	HIS	-	expression tag	UNP P43890
B	-1	MET	-	cloning artifact	UNP P43890
B	0	SER	-	cloning artifact	UNP P43890
B	1	LEU	-	cloning artifact	UNP P43890
B	238	GLU	-	cloning artifact	UNP P43890
B	239	GLY	-	cloning artifact	UNP P43890
B	240	HIS	-	expression tag	UNP P43890

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Chain	Residue	Modelled	Actual	Comment	Reference
B	241	HIS	-	expression tag	UNP P43890
B	242	HIS	-	expression tag	UNP P43890
B	243	HIS	-	expression tag	UNP P43890
B	244	HIS	-	expression tag	UNP P43890
B	245	HIS	-	expression tag	UNP P43890
C	-1	MET	-	cloning artifact	UNP P43890
C	0	SER	-	cloning artifact	UNP P43890
C	1	LEU	-	cloning artifact	UNP P43890
C	238	GLU	-	cloning artifact	UNP P43890
C	239	GLY	-	cloning artifact	UNP P43890
C	240	HIS	-	expression tag	UNP P43890
C	241	HIS	-	expression tag	UNP P43890
C	242	HIS	-	expression tag	UNP P43890
C	243	HIS	-	expression tag	UNP P43890
C	244	HIS	-	expression tag	UNP P43890
C	245	HIS	-	expression tag	UNP P43890
D	-1	MET	-	cloning artifact	UNP P43890
D	0	SER	-	cloning artifact	UNP P43890
D	1	LEU	-	cloning artifact	UNP P43890
D	238	GLU	-	cloning artifact	UNP P43890
D	239	GLY	-	cloning artifact	UNP P43890
D	240	HIS	-	expression tag	UNP P43890
D	241	HIS	-	expression tag	UNP P43890
D	242	HIS	-	expression tag	UNP P43890
D	243	HIS	-	expression tag	UNP P43890
D	244	HIS	-	expression tag	UNP P43890
D	245	HIS	-	expression tag	UNP P43890
E	-1	MET	-	cloning artifact	UNP P43890
E	0	SER	-	cloning artifact	UNP P43890
E	1	LEU	-	cloning artifact	UNP P43890
E	238	GLU	-	cloning artifact	UNP P43890
E	239	GLY	-	cloning artifact	UNP P43890
E	240	HIS	-	expression tag	UNP P43890
E	241	HIS	-	expression tag	UNP P43890
E	242	HIS	-	expression tag	UNP P43890
E	243	HIS	-	expression tag	UNP P43890
E	244	HIS	-	expression tag	UNP P43890
E	245	HIS	-	expression tag	UNP P43890
F	-1	MET	-	cloning artifact	UNP P43890
F	0	SER	-	cloning artifact	UNP P43890
F	1	LEU	-	cloning artifact	UNP P43890
F	238	GLU	-	cloning artifact	UNP P43890

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Chain	Residue	Modelled	Actual	Comment	Reference
F	239	GLY	-	cloning artifact	UNP P43890
F	240	HIS	-	expression tag	UNP P43890
F	241	HIS	-	expression tag	UNP P43890
F	242	HIS	-	expression tag	UNP P43890
F	243	HIS	-	expression tag	UNP P43890
F	244	HIS	-	expression tag	UNP P43890
F	245	HIS	-	expression tag	UNP P43890

- Molecule 2 is water.

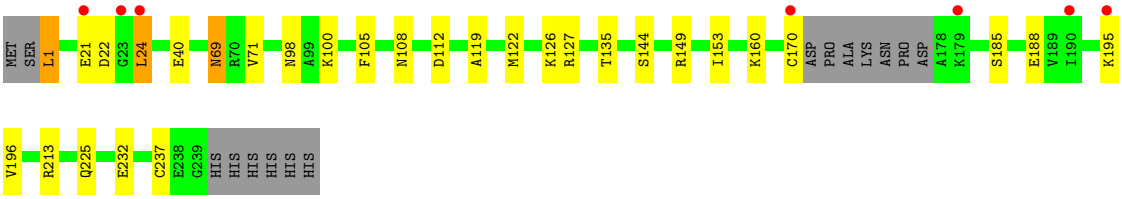
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	154	154	154	0	0
			Total	O		
2	B	145	145	145	0	0
			Total	O		
2	C	129	129	129	0	0
			Total	O		
2	D	167	167	167	0	0
			Total	O		
2	E	156	156	156	0	0
			Total	O		
2	F	138	138	138	0	0

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.

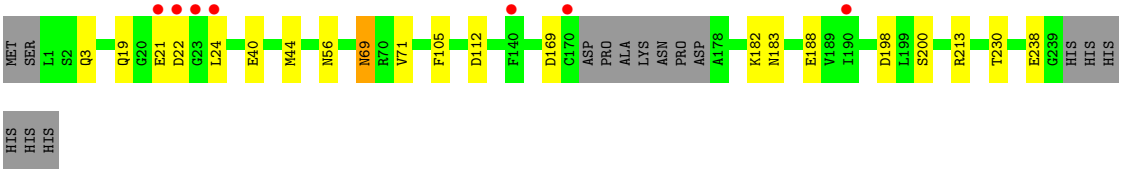
• Molecule 1: Uridylate kinase

Chain A:



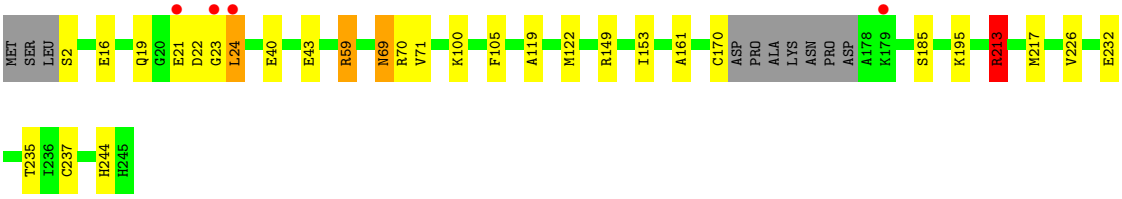
• Molecule 1: Uridylate kinase

Chain B:



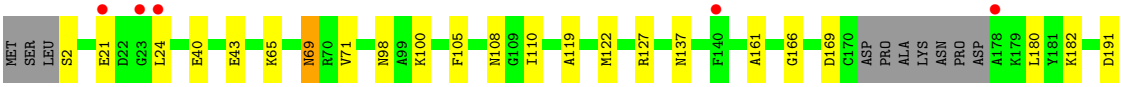
• Molecule 1: Uridylate kinase

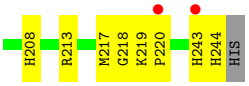
Chain C:



• Molecule 1: Uridylate kinase

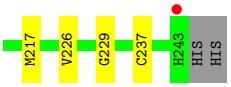
Chain D:





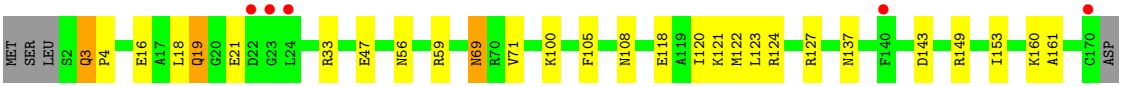
• Molecule 1: Uridylate kinase

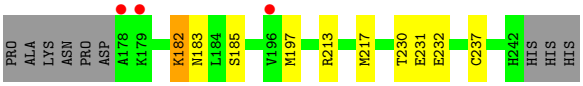
Chain E:



• Molecule 1: Uridylate kinase

Chain F:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	77.37Å 79.89Å 79.90Å 94.85° 96.68° 96.88°	Depositor
Resolution (Å)	20.00 – 2.10 19.85 – 2.10	Depositor EDS
% Data completeness (in resolution range)	96.5 (20.00-2.10) 95.7 (19.85-2.10)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.79 (at 2.09Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.210 , 0.263 0.216 , 0.265	Depositor DCC
R_{free} test set	5265 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å^2)	24.6	Xtriage
Anisotropy	0.224	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 41.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	0.038 for k,l,h 0.038 for l,h,k 0.037 for -k,-h,-l 0.038 for -l,-k,-h 0.438 for -h,-l,-k	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	11567	wwPDB-VP
Average B, all atoms (Å^2)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.33% 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)

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	0.57	0/1775	0.73	2/2386 (0.1%)
1	B	0.58	0/1775	0.73	2/2386 (0.1%)
1	C	0.57	0/1833	0.68	2/2465 (0.1%)
1	D	0.58	0/1822	0.72	3/2450 (0.1%)
1	E	0.58	0/1811	0.76	4/2435 (0.2%)
1	F	0.58	0/1800	0.74	3/2420 (0.1%)
All	All	0.58	0/10816	0.73	16/14542 (0.1%)

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	213	ARG	NE-CZ-NH2	-11.46	114.57	120.30
1	F	213	ARG	NE-CZ-NH2	-11.26	114.67	120.30
1	A	213	ARG	NE-CZ-NH2	-10.11	115.25	120.30
1	C	213	ARG	NE-CZ-NH2	-9.68	115.46	120.30
1	D	213	ARG	NE-CZ-NH2	-9.37	115.62	120.30
1	B	213	ARG	NE-CZ-NH2	-9.35	115.62	120.30
1	A	213	ARG	NE-CZ-NH1	6.65	123.62	120.30
1	B	213	ARG	NE-CZ-NH1	6.54	123.57	120.30
1	E	213	ARG	NE-CZ-NH1	6.39	123.49	120.30
1	F	213	ARG	NE-CZ-NH1	5.92	123.26	120.30
1	E	213	ARG	CG-CD-NE	-5.71	99.82	111.80
1	D	213	ARG	CG-CD-NE	-5.58	100.08	111.80
1	D	213	ARG	NE-CZ-NH1	5.50	123.05	120.30
1	E	149	ARG	NE-CZ-NH1	5.32	122.96	120.30
1	C	213	ARG	NE-CZ-NH1	5.22	122.91	120.30
1	F	213	ARG	CG-CD-NE	-5.15	100.98	111.80

There are no chirality outliers.

There are no planarity outliers.

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	1755	0	1806	16	0
1	B	1755	0	1806	10	0
1	C	1807	0	1834	17	0
1	D	1797	0	1827	19	0
1	E	1787	0	1820	15	0
1	F	1777	0	1813	23	0
2	A	154	0	0	4	0
2	B	145	0	0	1	0
2	C	129	0	0	2	0
2	D	167	0	0	6	0
2	E	156	0	0	3	0
2	F	138	0	0	5	0
All	All	11567	0	10906	97	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 4.

All (97) 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:19:GLN:HE21	1:C:24:LEU:HA	1.41	0.86
1:E:182:LYS:HD3	2:E:377:HOH:O	1.90	0.71
1:A:108:ASN:ND2	2:A:383:HOH:O	2.27	0.67
1:F:108:ASN:ND2	2:F:367:HOH:O	2.29	0.65
1:D:182:LYS:HD3	2:D:412:HOH:O	1.97	0.65
1:B:69:ASN:HD22	1:B:71:VAL:H	1.45	0.63
1:F:3:GLN:HG2	1:F:4:PRO:HD2	1.79	0.63
1:E:183:ASN:HB3	2:E:280:HOH:O	2.01	0.60
1:B:69:ASN:ND2	1:B:71:VAL:H	1.99	0.60
1:A:69:ASN:HD22	1:A:71:VAL:H	1.50	0.58
1:D:119:ALA:HA	1:D:122:MET:HE2	1.86	0.58
1:D:243:HIS:O	1:D:244:HIS:HB2	2.03	0.58
1:F:182:LYS:HZ1	1:F:231:GLU:CD	2.07	0.57
1:A:69:ASN:ND2	1:A:71:VAL:H	2.03	0.57
1:D:218:GLY:O	1:D:220:PRO:HD3	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:18:LEU:HD22	2:F:365:HOH:O	2.04	0.57
1:A:149:ARG:O	1:A:153:ILE:HG13	2.05	0.56
1:D:69:ASN:HD22	1:D:71:VAL:H	1.54	0.56
1:F:19:GLN:HE21	1:F:56:ASN:HA	1.71	0.56
1:E:161:ALA:HB1	1:E:217:MET:HB2	1.88	0.55
1:F:118:GLU:HA	1:F:121:LYS:HD2	1.88	0.55
1:A:1:LEU:N	2:A:381:HOH:O	2.40	0.54
1:D:119:ALA:HA	1:D:122:MET:CE	2.37	0.54
1:A:100:LYS:NZ	1:A:127:ARG:HE	2.05	0.54
1:D:208:HIS:HE1	2:D:349:HOH:O	1.90	0.54
1:D:161:ALA:HB1	1:D:217:MET:HB2	1.90	0.53
1:C:19:GLN:NE2	1:C:24:LEU:HA	2.19	0.53
1:E:98:ASN:ND2	1:E:127:ARG:HG2	2.23	0.53
1:C:69:ASN:HD22	1:C:70:ARG:N	2.07	0.52
1:F:19:GLN:NE2	2:F:317:HOH:O	2.41	0.52
1:F:127:ARG:NH2	2:F:332:HOH:O	2.43	0.52
1:D:108:ASN:ND2	2:D:401:HOH:O	2.35	0.52
1:E:40:GLU:O	1:E:44:MET:HG3	2.11	0.51
1:F:69:ASN:HD22	1:F:71:VAL:H	1.59	0.51
1:B:3:GLN:HG2	2:B:270:HOH:O	2.11	0.51
1:A:24:LEU:N	2:A:393:HOH:O	2.44	0.50
1:B:182:LYS:HG2	1:B:183:ASN:ND2	2.27	0.50
1:F:149:ARG:O	1:F:153:ILE:HG13	2.13	0.49
1:A:135:THR:HB	1:F:137:ASN:ND2	2.28	0.49
1:C:213:ARG:HD3	1:C:235:THR:OG1	2.13	0.48
1:F:69:ASN:ND2	1:F:71:VAL:H	2.11	0.48
1:C:100:LYS:NZ	2:C:308:HOH:O	2.46	0.48
1:C:161:ALA:HB1	1:C:217:MET:HB2	1.95	0.48
1:E:2:SER:HA	2:E:270:HOH:O	2.12	0.48
1:F:16:GLU:OE2	1:F:59:ARG:NH2	2.46	0.48
1:E:213:ARG:NH2	1:E:229:GLY:O	2.40	0.48
1:E:119:ALA:HA	1:E:122:MET:HE2	1.96	0.47
1:F:143:ASP:OD2	2:F:383:HOH:O	2.20	0.47
1:E:185:SER:HA	1:E:237:CYS:O	2.14	0.47
1:B:40:GLU:O	1:B:44:MET:HG3	2.14	0.47
1:B:19:GLN:HE21	1:B:56:ASN:HA	1.79	0.47
1:B:69:ASN:HD22	1:B:71:VAL:N	2.11	0.47
1:B:198:ASP:OD1	1:B:200:SER:OG	2.31	0.47
1:C:185:SER:HA	1:C:237:CYS:O	2.15	0.47
1:F:47:GLU:HG2	1:F:123:LEU:O	2.15	0.46
1:D:40:GLU:HA	1:D:43:GLU:HG2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:120:ILE:HG22	1:F:124:ARG:HE	1.81	0.46
1:D:166:GLY:HA3	1:D:180:LEU:HD11	1.98	0.46
1:D:219:LYS:O	1:D:220:PRO:C	2.55	0.46
1:E:69:ASN:HD22	1:E:71:VAL:H	1.63	0.45
1:C:69:ASN:HD22	1:C:71:VAL:H	1.64	0.45
1:A:69:ASN:HD22	1:A:71:VAL:N	2.13	0.45
1:E:117:SER:O	1:E:121:LYS:HG3	2.17	0.45
1:A:119:ALA:HA	1:A:122:MET:HE2	2.00	0.44
1:C:2:SER:N	2:C:333:HOH:O	2.49	0.44
1:F:118:GLU:O	1:F:122:MET:HG3	2.17	0.44
1:E:213:ARG:NH2	1:E:226:VAL:O	2.51	0.44
1:D:69:ASN:ND2	1:D:71:VAL:H	2.16	0.44
1:C:16:GLU:OE2	1:C:59:ARG:NH2	2.51	0.43
1:C:149:ARG:O	1:C:153:ILE:HG13	2.19	0.43
1:A:126:LYS:HE3	2:A:264:HOH:O	2.18	0.43
1:C:105:PHE:CZ	1:D:110:ILE:HD11	2.54	0.42
1:C:40:GLU:HA	1:C:43:GLU:HG2	2.02	0.42
1:C:119:ALA:HA	1:C:122:MET:HE2	2.00	0.42
1:F:185:SER:HA	1:F:237:CYS:O	2.19	0.42
1:F:161:ALA:HB1	1:F:217:MET:HB2	2.00	0.42
1:A:225:GLN:HB3	1:A:232:GLU:HG3	2.01	0.42
1:A:135:THR:HB	1:F:137:ASN:HD21	1.84	0.41
1:A:185:SER:HA	1:A:237:CYS:O	2.19	0.41
1:D:243:HIS:O	1:D:244:HIS:CB	2.68	0.41
1:C:19:GLN:NE2	1:C:23:GLY:O	2.54	0.41
1:E:190:ILE:CD1	1:E:206:ARG:NH1	2.83	0.41
1:A:69:ASN:HD22	1:A:69:ASN:C	2.23	0.41
1:E:69:ASN:ND2	1:E:71:VAL:H	2.18	0.41
1:F:230:THR:HG22	1:F:230:THR:O	2.21	0.41
1:C:213:ARG:NH2	1:C:226:VAL:O	2.54	0.41
2:D:405:HOH:O	1:E:200:SER:HB3	2.21	0.41
1:B:69:ASN:HD22	1:B:69:ASN:C	2.23	0.40
1:D:24:LEU:HB3	2:D:276:HOH:O	2.20	0.40
1:D:137:ASN:ND2	2:D:369:HOH:O	2.54	0.40
1:F:143:ASP:OD1	1:F:160:LYS:HE2	2.21	0.40
1:D:98:ASN:ND2	1:D:127:ARG:HG2	2.37	0.40
1:D:100:LYS:HZ1	1:D:127:ARG:NE	2.19	0.40
1:C:69:ASN:ND2	1:C:71:VAL:H	2.19	0.40
1:A:160:LYS:HE2	1:A:196:VAL:O	2.22	0.40
1:B:19:GLN:HG3	1:B:56:ASN:HB3	2.03	0.40
1:F:69:ASN:HD22	1:F:71:VAL:N	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	228/247 (92%)	226 (99%)	2 (1%)	0	100	100
1	B	228/247 (92%)	223 (98%)	5 (2%)	0	100	100
1	C	233/247 (94%)	229 (98%)	4 (2%)	0	100	100
1	D	232/247 (94%)	226 (97%)	6 (3%)	0	100	100
1	E	231/247 (94%)	227 (98%)	4 (2%)	0	100	100
1	F	230/247 (93%)	227 (99%)	3 (1%)	0	100	100
All	All	1382/1482 (93%)	1358 (98%)	24 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	187/201 (93%)	174 (93%)	13 (7%)	15	12
1	B	187/201 (93%)	177 (95%)	10 (5%)	22	20
1	C	192/201 (96%)	182 (95%)	10 (5%)	23	21
1	D	191/201 (95%)	184 (96%)	7 (4%)	34	35
1	E	190/201 (94%)	185 (97%)	5 (3%)	46	50
1	F	189/201 (94%)	178 (94%)	11 (6%)	20	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1136/1206 (94%)	1080 (95%)	56 (5%)	25 23

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	LEU
1	A	21	GLU
1	A	22	ASP
1	A	24	LEU
1	A	40	GLU
1	A	69	ASN
1	A	98	ASN
1	A	105	PHE
1	A	112	ASP
1	A	144	SER
1	A	170	CYS
1	A	188	GLU
1	A	195	LYS
1	B	21	GLU
1	B	22	ASP
1	B	24	LEU
1	B	69	ASN
1	B	105	PHE
1	B	112	ASP
1	B	169	ASP
1	B	188	GLU
1	B	230	THR
1	B	238	GLU
1	C	21	GLU
1	C	22	ASP
1	C	24	LEU
1	C	59	ARG
1	C	69	ASN
1	C	170	CYS
1	C	195	LYS
1	C	213	ARG
1	C	232	GLU
1	C	244	HIS
1	D	2	SER
1	D	21	GLU
1	D	65	LYS
1	D	69	ASN

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Mol	Chain	Res	Type
1	D	105	PHE
1	D	169	ASP
1	D	191	ASP
1	E	21	GLU
1	E	69	ASN
1	E	105	PHE
1	E	170	CYS
1	E	195	LYS
1	F	3	GLN
1	F	19	GLN
1	F	21	GLU
1	F	33	ARG
1	F	69	ASN
1	F	100	LYS
1	F	105	PHE
1	F	182	LYS
1	F	183	ASN
1	F	197	MET
1	F	232	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	GLN
1	A	69	ASN
1	A	108	ASN
1	A	183	ASN
1	A	208	HIS
1	B	69	ASN
1	B	108	ASN
1	B	183	ASN
1	C	69	ASN
1	C	108	ASN
1	C	137	ASN
1	C	243	HIS
1	D	19	GLN
1	D	69	ASN
1	D	108	ASN
1	D	137	ASN
1	D	183	ASN
1	D	208	HIS
1	D	243	HIS

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Mol	Chain	Res	Type
1	E	19	GLN
1	E	69	ASN
1	E	98	ASN
1	E	108	ASN
1	E	137	ASN
1	E	208	HIS
1	F	3	GLN
1	F	19	GLN
1	F	69	ASN
1	F	108	ASN
1	F	137	ASN
1	F	208	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides 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 (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	232/247 (93%)	0.07	7 (3%)	50	56	13, 25, 43, 51	1 (0%)
1	B	232/247 (93%)	0.04	7 (3%)	50	56	13, 25, 43, 48	1 (0%)
1	C	237/247 (95%)	-0.03	4 (1%)	70	74	12, 26, 45, 53	1 (0%)
1	D	236/247 (95%)	-0.01	7 (2%)	50	56	13, 25, 42, 51	1 (0%)
1	E	235/247 (95%)	0.10	8 (3%)	45	51	12, 25, 42, 51	1 (0%)
1	F	234/247 (94%)	0.10	8 (3%)	45	51	13, 26, 42, 53	1 (0%)
All	All	1406/1482 (94%)	0.04	41 (2%)	51	57	12, 25, 43, 53	6 (0%)

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	23	GLY	5.3
1	D	23	GLY	4.8
1	E	23	GLY	4.6
1	A	170	CYS	4.4
1	E	178	ALA	4.3
1	B	24	LEU	4.2
1	F	170	CYS	3.9
1	E	170	CYS	3.6
1	A	24	LEU	3.3
1	C	24	LEU	3.3
1	A	23	GLY	3.3
1	C	23	GLY	3.3
1	E	243	HIS	3.2
1	D	140	PHE	3.1
1	F	22	ASP	3.0
1	E	21	GLU	3.0
1	D	178	ALA	3.0
1	F	24	LEU	3.0
1	B	170	CYS	2.8

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Mol	Chain	Res	Type	RSRZ
1	E	22	ASP	2.7
1	A	179	LYS	2.7
1	D	220	PRO	2.7
1	F	140	PHE	2.7
1	E	2	SER	2.6
1	F	178	ALA	2.5
1	B	21	GLU	2.5
1	D	21	GLU	2.4
1	B	140	PHE	2.4
1	F	179	LYS	2.3
1	F	23	GLY	2.2
1	E	59	ARG	2.2
1	A	21	GLU	2.2
1	C	179	LYS	2.2
1	D	243	HIS	2.2
1	F	196	VAL	2.1
1	A	190	ILE	2.1
1	B	22	ASP	2.1
1	A	195	LYS	2.1
1	C	21	GLU	2.1
1	D	24	LEU	2.0
1	B	190	ILE	2.0

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

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

6.3 Carbohydrates (i)

There are no monosaccharides 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.