Full wwPDB X-ray Structure Validation Report (i)

Sep 16, 2023 – 08:13 PM EDT

PDB ID	:	1O24
Title	:	Crystal structure of Thymidylate Synthase Complementing Protein (TM0449) from Thermotoga maritima at 2.0 A resolution
Authors	:	Mathews, I.I.; Deacon, A.M.; Canaves, J.M.; McMullan, D.; Lesley, S.A.; Agarwalla, S.; Kuhn, P.; Joint Center for Structural Genomics (JCSG)
Deposited on	:	2003-02-18
Resolution	:	2.00 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:

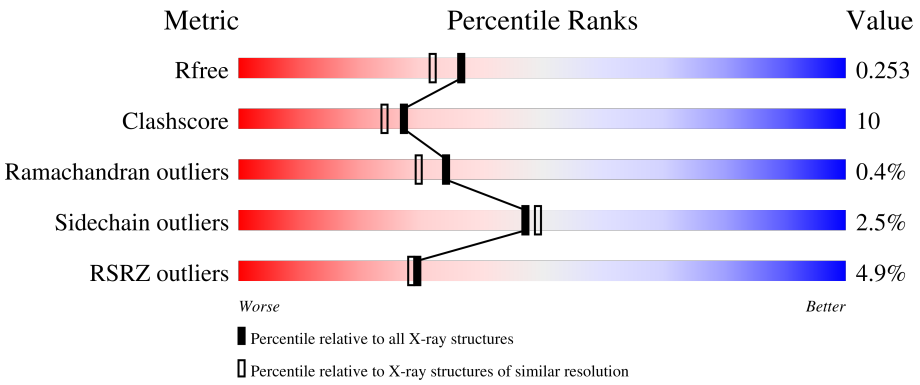
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (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 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	232	4% 71% 17% • 10%
1	B	232	3% 73% 17% • 8%
1	C	232	6% 77% 17% • 5%
1	D	232	5% 69% 22% 8%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 7543 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 Thymidylate synthase thyX.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	208	1743	1136	299	302	6	0	0	0
			Total	C	N	O	S			
1	B	213	1775	1155	306	309	5	0	0	0
			Total	C	N	O	S			
1	C	220	1841	1197	314	324	6	0	0	0
			Total	C	N	O	S			
1	D	214	1776	1156	301	313	6	0	0	0

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	expression tag	UNP Q9WYT0
A	-10	GLY	-	expression tag	UNP Q9WYT0
A	-9	SER	-	expression tag	UNP Q9WYT0
A	-8	ASP	-	expression tag	UNP Q9WYT0
A	-7	LYS	-	expression tag	UNP Q9WYT0
A	-6	ILE	-	expression tag	UNP Q9WYT0
A	-5	HIS	-	expression tag	UNP Q9WYT0
A	-4	HIS	-	expression tag	UNP Q9WYT0
A	-3	HIS	-	expression tag	UNP Q9WYT0
A	-2	HIS	-	expression tag	UNP Q9WYT0
A	-1	HIS	-	expression tag	UNP Q9WYT0
A	0	HIS	-	expression tag	UNP Q9WYT0
B	-11	MET	-	expression tag	UNP Q9WYT0
B	-10	GLY	-	expression tag	UNP Q9WYT0
B	-9	SER	-	expression tag	UNP Q9WYT0
B	-8	ASP	-	expression tag	UNP Q9WYT0
B	-7	LYS	-	expression tag	UNP Q9WYT0
B	-6	ILE	-	expression tag	UNP Q9WYT0
B	-5	HIS	-	expression tag	UNP Q9WYT0
B	-4	HIS	-	expression tag	UNP Q9WYT0
B	-3	HIS	-	expression tag	UNP Q9WYT0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	HIS	-	expression tag	UNP Q9WYT0
B	-1	HIS	-	expression tag	UNP Q9WYT0
B	0	HIS	-	expression tag	UNP Q9WYT0
C	-11	MET	-	expression tag	UNP Q9WYT0
C	-10	GLY	-	expression tag	UNP Q9WYT0
C	-9	SER	-	expression tag	UNP Q9WYT0
C	-8	ASP	-	expression tag	UNP Q9WYT0
C	-7	LYS	-	expression tag	UNP Q9WYT0
C	-6	ILE	-	expression tag	UNP Q9WYT0
C	-5	HIS	-	expression tag	UNP Q9WYT0
C	-4	HIS	-	expression tag	UNP Q9WYT0
C	-3	HIS	-	expression tag	UNP Q9WYT0
C	-2	HIS	-	expression tag	UNP Q9WYT0
C	-1	HIS	-	expression tag	UNP Q9WYT0
C	0	HIS	-	expression tag	UNP Q9WYT0
D	-11	MET	-	expression tag	UNP Q9WYT0
D	-10	GLY	-	expression tag	UNP Q9WYT0
D	-9	SER	-	expression tag	UNP Q9WYT0
D	-8	ASP	-	expression tag	UNP Q9WYT0
D	-7	LYS	-	expression tag	UNP Q9WYT0
D	-6	ILE	-	expression tag	UNP Q9WYT0
D	-5	HIS	-	expression tag	UNP Q9WYT0
D	-4	HIS	-	expression tag	UNP Q9WYT0
D	-3	HIS	-	expression tag	UNP Q9WYT0
D	-2	HIS	-	expression tag	UNP Q9WYT0
D	-1	HIS	-	expression tag	UNP Q9WYT0
D	0	HIS	-	expression tag	UNP Q9WYT0

- Molecule 2 is water.

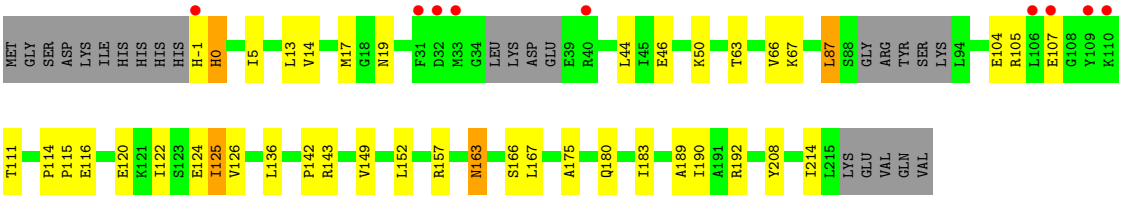
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	96	96	96	0	0
			Total	O		
2	B	107	107	107	0	0
			Total	O		
2	C	115	115	115	0	0
			Total	O		
2	D	90	90	90	0	0

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.

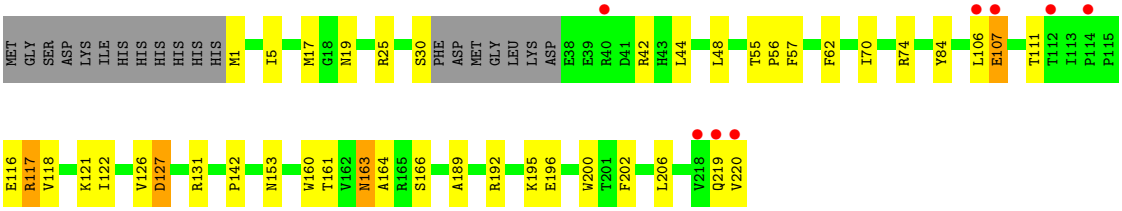
• Molecule 1: Thymidylate synthase thyX

Chain A:



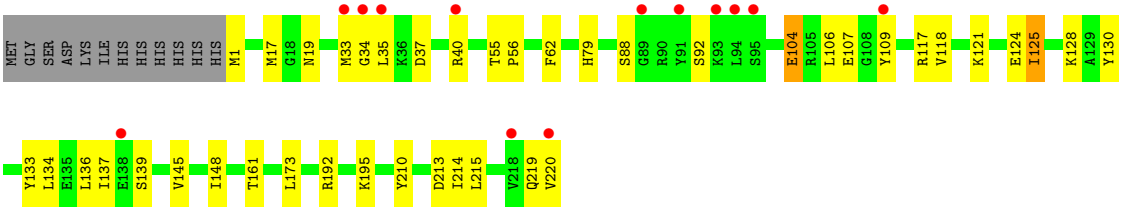
• Molecule 1: Thymidylate synthase thyX

Chain B:



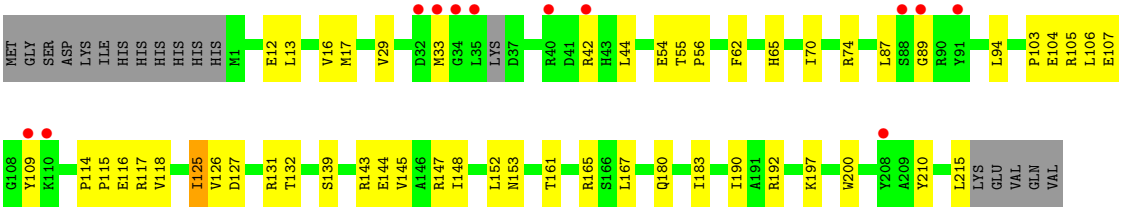
• Molecule 1: Thymidylate synthase thyX

Chain C:



• Molecule 1: Thymidylate synthase thyX

Chain D:


MET
GLY
SER
ASP
LYS
ILE
HIS
HIS
HIS
HIS
HIS
HIS
M1
E12
L13
V16
M17
V29
D32
M33
G34
L35
LYS
D37
R40
D41
R42
H43
L44
E54
T55
P56
F62
H65
I70
R74
L87
S88
G89
R90
Y91
L94
P103
E104
R105
L106
E107
G108
Y109
K110
P114
P115
E116
R117
V118
I125
V126
D127
R131
T132
S139
R143
E144
V145
A146
R147
I148
L152
M153
T161
R165
S166
L167
Q180
I183
I190
A191
R192
K197
W200
Y208
A209
Y210
L215
LYS
GLU
VAL
GLN
VAL

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	54.48Å 116.64Å 142.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00 46.63 – 2.00	Depositor EDS
% Data completeness (in resolution range)	95.6 (20.00-2.00) 96.2 (46.63-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$< I/\sigma(I) >$ [1]	2.47 (at 2.00Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.207 , 0.252 0.208 , 0.253	Depositor DCC
R_{free} test set	3016 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å^2)	31.1	Xtriage
Anisotropy	0.354	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 50.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	7543	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.88% 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	0.34	0/1791	0.58	0/2422
1	B	0.34	0/1822	0.59	0/2462
1	C	0.35	0/1890	0.59	0/2554
1	D	0.34	0/1824	0.56	0/2467
All	All	0.34	0/7327	0.58	0/9905

There are no bond length outliers.

There are no bond angle outliers.

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	1743	0	1729	37	0
1	B	1775	0	1775	41	0
1	C	1841	0	1839	36	0
1	D	1776	0	1752	41	0
2	A	96	0	0	4	0
2	B	107	0	0	2	0
2	C	115	0	0	4	0
2	D	90	0	0	2	0
All	All	7543	0	7095	144	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 10.

All (144) 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:17:MET:HB2	1:D:17:MET:HB2	1.48	0.93
1:C:106:LEU:HD21	1:C:118:VAL:HG11	1.52	0.92
1:A:17:MET:HB2	1:B:17:MET:HB2	1.52	0.89
1:C:219:GLN:HG3	1:C:220:VAL:HG12	1.64	0.79
1:B:42:ARG:HG3	1:B:42:ARG:HH11	1.49	0.78
1:A:122:ILE:HA	1:A:125:ILE:HD11	1.68	0.74
1:A:163:ASN:ND2	1:A:166:SER:H	1.89	0.71
1:D:192:ARG:HH11	1:D:192:ARG:HG3	1.60	0.67
1:B:163:ASN:ND2	1:B:166:SER:H	1.92	0.67
1:B:106:LEU:CD1	1:B:118:VAL:HB	2.25	0.67
1:A:122:ILE:O	1:A:125:ILE:HD12	1.97	0.65
1:A:125:ILE:HG12	1:D:132:THR:HG21	1.80	0.64
1:A:163:ASN:C	1:A:163:ASN:HD22	2.00	0.64
1:B:42:ARG:HH12	1:B:200:TRP:HA	1.62	0.64
1:A:19:ASN:HB2	2:A:475:HOH:O	1.99	0.63
1:C:192:ARG:HG3	1:C:220:VAL:HG22	1.82	0.62
1:A:167:LEU:HD11	1:A:190:ILE:CG2	2.31	0.61
1:C:195:LYS:HD3	1:C:220:VAL:HG23	1.82	0.61
1:C:125:ILE:HD13	1:C:125:ILE:O	2.01	0.60
1:A:50:LYS:HG2	1:A:208:TYR:CD2	2.37	0.60
1:C:19:ASN:HB2	2:C:477:HOH:O	2.02	0.60
1:D:89:GLY:N	1:D:94:LEU:HD21	2.17	0.59
1:A:46:GLU:O	1:A:50:LYS:HG3	2.02	0.59
1:B:163:ASN:HD22	1:B:163:ASN:C	2.06	0.59
1:B:42:ARG:HG3	1:B:42:ARG:NH1	2.18	0.59
1:B:118:VAL:HG13	1:C:136:LEU:HD22	1.84	0.58
1:D:167:LEU:HD11	1:D:190:ILE:CG2	2.33	0.58
1:A:180:GLN:O	1:A:183:ILE:HG22	2.04	0.58
1:A:167:LEU:HD11	1:A:190:ILE:HG21	1.86	0.57
1:D:180:GLN:O	1:D:183:ILE:HG22	2.04	0.57
1:D:104:GLU:HA	1:D:107:GLU:HG2	1.87	0.57
1:B:116:GLU:H	1:B:116:GLU:CD	2.09	0.56
1:B:127:ASP:O	1:B:131:ARG:HD3	2.04	0.56
1:A:142:PRO:HG3	1:D:109:TYR:CE2	2.40	0.56
1:C:124:GLU:HG2	1:C:128:LYS:HZ2	1.71	0.56
1:D:210:TYR:CE2	1:D:215:LEU:HB2	2.40	0.56
1:A:163:ASN:HD21	1:A:166:SER:H	1.54	0.56
1:A:152:LEU:HD23	1:D:152:LEU:HD23	1.88	0.55
1:A:104:GLU:O	1:A:107:GLU:HB2	2.07	0.55
1:C:106:LEU:CD2	1:C:118:VAL:HG11	2.31	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:192:ARG:HG2	1:B:220:VAL:HG11	1.88	0.55
1:B:192:ARG:HG2	1:B:220:VAL:CG1	2.37	0.55
1:C:121:LYS:HE2	2:C:490:HOH:O	2.06	0.55
1:B:195:LYS:HD3	1:B:220:VAL:HG13	1.88	0.54
1:C:106:LEU:HD22	1:C:118:VAL:HG21	1.89	0.54
1:D:167:LEU:HD11	1:D:190:ILE:HG21	1.90	0.54
1:A:111:THR:HA	1:D:139:SER:O	2.09	0.53
1:B:42:ARG:NH1	2:B:508:HOH:O	2.42	0.52
1:B:106:LEU:HD13	1:B:118:VAL:HB	1.90	0.52
1:D:145:VAL:O	1:D:148:ILE:HG12	2.10	0.52
1:A:87:LEU:HD11	1:A:157:ARG:NH2	2.25	0.52
1:B:106:LEU:HD11	1:B:118:VAL:HB	1.91	0.52
1:A:125:ILE:HD12	1:A:126:VAL:H	1.74	0.52
1:B:111:THR:HA	1:C:139:SER:O	2.10	0.52
1:A:143:ARG:HD3	2:A:341:HOH:O	2.10	0.52
1:D:210:TYR:CZ	1:D:215:LEU:HB2	2.45	0.51
1:C:210:TYR:CE2	1:C:215:LEU:HB2	2.46	0.51
1:C:192:ARG:NH1	1:C:220:VAL:HG13	2.26	0.51
1:A:120:GLU:O	1:A:124:GLU:HG3	2.12	0.50
1:D:29:VAL:HG12	1:D:29:VAL:O	2.12	0.50
1:B:192:ARG:C	1:B:192:ARG:HD3	2.32	0.49
1:C:213:ASP:OD1	1:C:214:ILE:HG23	2.12	0.49
1:D:13:LEU:HD21	1:D:16:VAL:CG2	2.43	0.48
1:B:44:LEU:HD11	1:B:48:LEU:HD11	1.95	0.48
1:C:1:MET:N	2:C:463:HOH:O	2.45	0.48
1:B:192:ARG:HD3	1:B:192:ARG:O	2.13	0.48
1:B:117:ARG:HD2	1:B:121:LYS:HE2	1.95	0.47
1:A:149:VAL:HB	1:D:125:ILE:HG21	1.95	0.47
1:C:220:VAL:HA	2:C:503:HOH:O	2.13	0.47
1:B:42:ARG:NH1	1:B:200:TRP:CD1	2.83	0.47
1:D:54:GLU:HG3	1:D:165:ARG:NE	2.30	0.47
1:A:122:ILE:O	1:A:125:ILE:CD1	2.62	0.47
1:B:44:LEU:C	1:B:44:LEU:HD13	2.35	0.47
1:C:106:LEU:H	1:C:106:LEU:HD12	1.80	0.47
1:C:192:ARG:HH12	1:C:220:VAL:HG13	1.80	0.47
1:D:74:ARG:HD3	2:D:315:HOH:O	2.15	0.47
1:B:106:LEU:O	1:B:107:GLU:C	2.53	0.46
1:B:70:ILE:O	1:B:74:ARG:HG3	2.16	0.46
1:D:126:VAL:HG21	1:D:153:ASN:HD21	1.80	0.46
1:B:25:ARG:HG3	1:B:30:SER:O	2.15	0.46
1:B:55:THR:OG1	1:B:56:PRO:HD3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:106:LEU:O	1:C:109:TYR:HD1	1.99	0.46
1:C:124:GLU:HG2	1:C:128:LYS:NZ	2.30	0.46
1:D:12:GLU:CG	1:D:65:HIS:HB3	2.46	0.46
1:B:84:TYR:CE2	1:B:160:TRP:CD1	3.03	0.46
1:B:163:ASN:HD21	1:B:166:SER:H	1.62	0.46
1:D:13:LEU:HD11	1:D:16:VAL:CG2	2.45	0.46
1:D:13:LEU:HD21	1:D:16:VAL:HG23	1.98	0.45
1:C:79:HIS:HE1	1:C:173:LEU:HD12	1.81	0.45
1:C:213:ASP:OD1	1:C:214:ILE:N	2.49	0.45
1:D:192:ARG:HG3	1:D:192:ARG:NH1	2.28	0.45
1:D:106:LEU:HD11	1:D:118:VAL:HG11	1.98	0.45
1:D:125:ILE:HD13	1:D:125:ILE:HA	1.86	0.45
1:A:67:LYS:HA	1:A:157:ARG:HG2	1.99	0.45
1:C:104:GLU:O	1:C:107:GLU:HB3	2.16	0.45
1:D:55:THR:N	1:D:56:PRO:CD	2.80	0.45
1:C:192:ARG:HG3	1:C:220:VAL:CG2	2.47	0.45
1:D:103:PRO:HB3	1:D:116:GLU:HG3	1.99	0.45
1:C:88:SER:O	1:C:92:SER:HB2	2.17	0.45
1:C:33:MET:C	1:C:35:LEU:H	2.20	0.44
1:D:70:ILE:O	1:D:74:ARG:HG3	2.17	0.44
1:C:130:TYR:CE2	1:C:134:LEU:HD11	2.52	0.44
1:A:175:ALA:HA	1:A:214:ILE:HD11	1.99	0.44
1:B:192:ARG:HA	1:B:220:VAL:HG12	2.00	0.44
1:C:37:ASP:OD2	1:C:40:ARG:HG2	2.18	0.44
1:C:145:VAL:O	1:C:148:ILE:HG12	2.18	0.44
1:B:202:PHE:CE2	1:B:206:LEU:HD11	2.53	0.43
1:D:62:PHE:O	1:D:161:THR:HA	2.18	0.43
1:A:125:ILE:HD12	1:A:126:VAL:N	2.33	0.43
1:B:122:ILE:O	1:B:126:VAL:HG23	2.19	0.43
1:B:19:ASN:HB2	2:B:504:HOH:O	2.18	0.43
1:D:42:ARG:NH1	1:D:200:TRP:CD1	2.79	0.43
1:D:127:ASP:O	1:D:131:ARG:HD3	2.19	0.43
1:D:144:GLU:HG2	2:D:583:HOH:O	2.18	0.42
1:A:0:HIS:CE1	2:A:393:HOH:O	2.73	0.42
1:B:57:PHE:O	1:B:164:ALA:HB3	2.20	0.42
1:C:133:TYR:O	1:C:137:ILE:HG12	2.20	0.42
1:D:143:ARG:O	1:D:147:ARG:HG2	2.20	0.42
1:A:116:GLU:H	1:A:116:GLU:CD	2.23	0.42
1:A:136:LEU:HD22	1:D:118:VAL:HG13	2.02	0.41
1:D:114:PRO:HA	1:D:115:PRO:HD3	1.97	0.41
1:A:50:LYS:HG2	1:A:208:TYR:CG	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:50:LYS:NZ	2:A:335:HOH:O	2.53	0.41
1:A:14:VAL:HB	1:A:63:THR:HG22	2.02	0.41
1:A:114:PRO:HA	1:A:115:PRO:HD3	1.97	0.41
1:C:55:THR:OG1	1:C:56:PRO:HD3	2.21	0.41
1:C:62:PHE:O	1:C:161:THR:HA	2.20	0.41
1:B:117:ARG:HH11	1:B:121:LYS:HG3	1.85	0.41
1:A:5:ILE:HD11	1:A:189:ALA:HB2	2.03	0.41
1:A:66:VAL:O	1:A:157:ARG:HA	2.21	0.41
1:D:13:LEU:CD2	1:D:197:LYS:HE3	2.51	0.41
1:C:117:ARG:O	1:C:121:LYS:HG2	2.20	0.41
1:D:12:GLU:HG2	1:D:65:HIS:HB3	2.02	0.41
1:D:89:GLY:CA	1:D:94:LEU:HD21	2.51	0.41
1:B:62:PHE:O	1:B:161:THR:HA	2.21	0.41
1:B:126:VAL:HG21	1:B:153:ASN:HD21	1.86	0.41
1:B:5:ILE:HD11	1:B:189:ALA:HB2	2.03	0.41
1:D:42:ARG:NH1	1:D:200:TRP:CE2	2.89	0.41
1:A:0:HIS:HB2	1:A:13:LEU:O	2.21	0.40
1:D:55:THR:OG1	1:D:56:PRO:HD3	2.22	0.40
1:A:87:LEU:HD12	1:A:157:ARG:HB2	2.04	0.40
1:B:42:ARG:NH1	1:B:200:TRP:CG	2.90	0.40
1:B:1:MET:SD	1:B:196:GLU:OE1	2.79	0.40
1:B:142:PRO:HG2	1:C:109:TYR:CE2	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	202/232 (87%)	194 (96%)	7 (4%)	1 (0%)	29 23
1	B	209/232 (90%)	203 (97%)	6 (3%)	0	100 100
1	C	218/232 (94%)	208 (95%)	9 (4%)	1 (0%)	29 23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	210/232 (90%)	202 (96%)	7 (3%)	1 (0%)	29	23
All	All	839/928 (90%)	807 (96%)	29 (4%)	3 (0%)	34	30

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	0	HIS
1	D	33	MET
1	C	34	GLY

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	185/207 (89%)	178 (96%)	7 (4%)	33	31
1	B	188/207 (91%)	183 (97%)	5 (3%)	44	46
1	C	196/207 (95%)	194 (99%)	2 (1%)	76	81
1	D	187/207 (90%)	182 (97%)	5 (3%)	44	46
All	All	756/828 (91%)	737 (98%)	19 (2%)	47	49

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	-1	HIS
1	A	44	LEU
1	A	87	LEU
1	A	105	ARG
1	A	125	ILE
1	A	163	ASN
1	A	192	ARG
1	B	107	GLU
1	B	117	ARG
1	B	127	ASP
1	B	163	ASN

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Mol	Chain	Res	Type
1	B	219	GLN
1	C	104	GLU
1	C	125	ILE
1	D	44	LEU
1	D	87	LEU
1	D	105	ARG
1	D	117	ARG
1	D	125	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	163	ASN
1	B	163	ASN
1	B	169	ASN
1	B	219	GLN
1	D	75	GLN

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	208/232 (89%)	0.13	9 (4%)	35	34	20, 33, 55, 68	0
1	B	213/232 (91%)	0.03	8 (3%)	40	39	21, 33, 62, 72	0
1	C	220/232 (94%)	0.13	13 (5%)	22	21	20, 31, 60, 67	0
1	D	214/232 (92%)	0.21	12 (5%)	24	23	21, 35, 62, 76	0
All	All	855/928 (92%)	0.12	42 (4%)	29	28	20, 33, 61, 76	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	33	MET	5.3
1	D	40	ARG	4.7
1	C	91	TYR	4.5
1	C	220	VAL	4.3
1	D	34	GLY	4.1
1	D	32	ASP	3.9
1	D	35	LEU	3.7
1	C	34	GLY	3.6
1	C	138	GLU	3.5
1	A	32	ASP	3.3
1	D	89	GLY	3.1
1	D	109	TYR	3.1
1	B	220	VAL	3.0
1	B	219	GLN	3.0
1	A	31	PHE	3.0
1	A	110	LYS	3.0
1	A	106	LEU	2.9
1	A	40	ARG	2.9
1	C	94	LEU	2.9
1	C	33	MET	2.8
1	C	89	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	109	TYR	2.6
1	A	107	GLU	2.4
1	A	109	TYR	2.3
1	D	42	ARG	2.3
1	A	-1	HIS	2.3
1	B	106	LEU	2.3
1	B	218	VAL	2.3
1	C	218	VAL	2.3
1	A	33	MET	2.2
1	D	88	SER	2.2
1	C	35	LEU	2.2
1	D	91	TYR	2.2
1	D	110	LYS	2.2
1	B	107	GLU	2.1
1	C	95	SER	2.1
1	B	112	THR	2.1
1	B	114	PRO	2.1
1	D	208	TYR	2.1
1	C	40	ARG	2.0
1	B	40	ARG	2.0
1	C	93	LYS	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.