Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 08:53 AM GMT

PDB ID	:	3GAF
Title	:	2.2A Crystal Structure of 7-Alpha-Hydroxysteroid Dehydrogenase from Brucella Melitensis
Authors	:	Seattle Structural Genomics Center for Infectious Disease; Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on	:	2009-02-17
Resolution	:	2.20 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

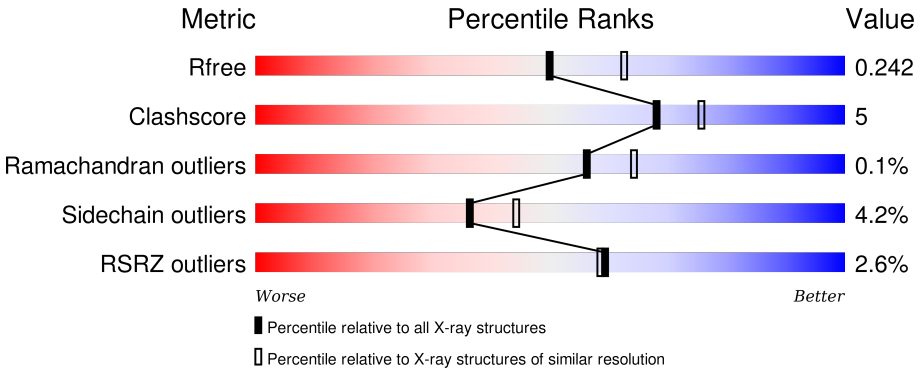
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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.



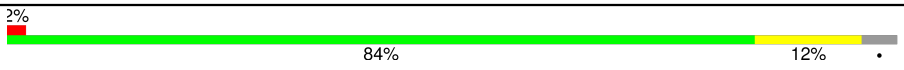
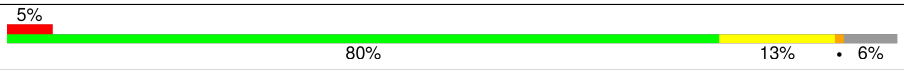
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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 <=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	256	86% 11% •
1	B	256	81% 14% 5%
1	C	256	4% 88% 6% 5%
1	D	256	2% 87% 9% •
1	E	256	2% 81% 13% 5%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	256	
1	G	256	
1	H	256	

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 14131 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 7-ALPHA-HYDROXYSTEROID DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	249	Total	C	N	O	S	0	0	0
			1763	1108	315	331	9			
1	B	243	Total	C	N	O	S	0	0	0
			1717	1078	306	324	9			
1	C	243	Total	C	N	O	S	0	0	0
			1706	1069	306	322	9			
1	D	245	Total	C	N	O	S	0	0	0
			1713	1076	308	320	9			
1	E	243	Total	C	N	O	S	0	0	0
			1716	1078	306	323	9			
1	F	246	Total	C	N	O	S	0	0	0
			1737	1090	310	328	9			
1	G	246	Total	C	N	O	S	0	0	0
			1733	1088	310	326	9			
1	H	241	Total	C	N	O	S	0	0	0
			1679	1054	300	316	9			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	EXPRESSION TAG	UNP Q8YIN7
B	0	SER	-	EXPRESSION TAG	UNP Q8YIN7
C	0	SER	-	EXPRESSION TAG	UNP Q8YIN7
D	0	SER	-	EXPRESSION TAG	UNP Q8YIN7
E	0	SER	-	EXPRESSION TAG	UNP Q8YIN7
F	0	SER	-	EXPRESSION TAG	UNP Q8YIN7
G	0	SER	-	EXPRESSION TAG	UNP Q8YIN7
H	0	SER	-	EXPRESSION TAG	UNP Q8YIN7

- Molecule 2 is water.

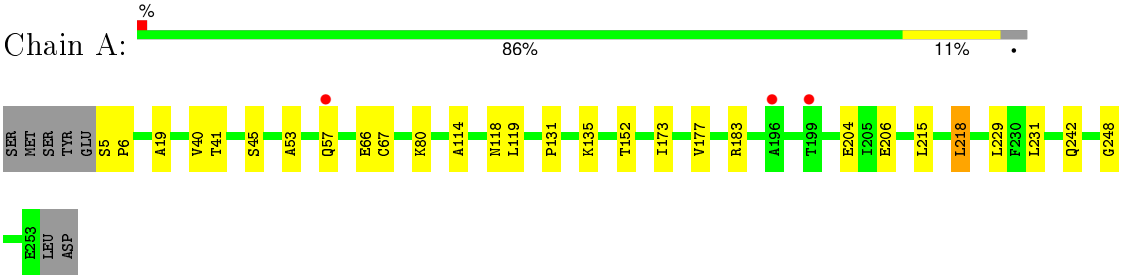
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	73	Total O 73 73	0	0
2	B	55	Total O 55 55	0	0
2	C	51	Total O 51 51	0	0
2	D	47	Total O 47 47	0	0
2	E	45	Total O 45 45	0	0
2	F	32	Total O 32 32	0	0
2	G	36	Total O 36 36	0	0
2	H	28	Total O 28 28	0	0

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.

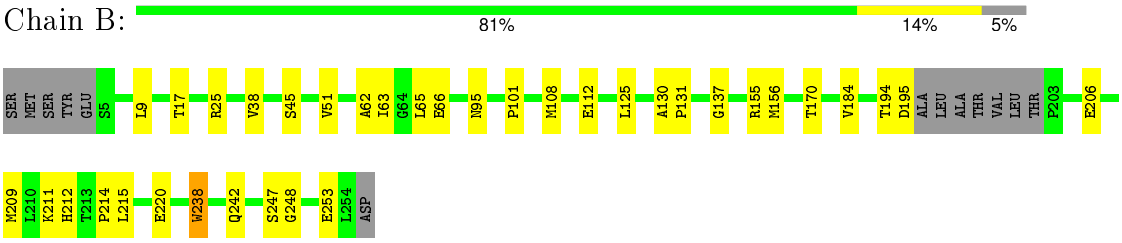
- Molecule 1: 7-ALPHA-HYDROXYSTEROID DEHYDROGENASE

Chain A:



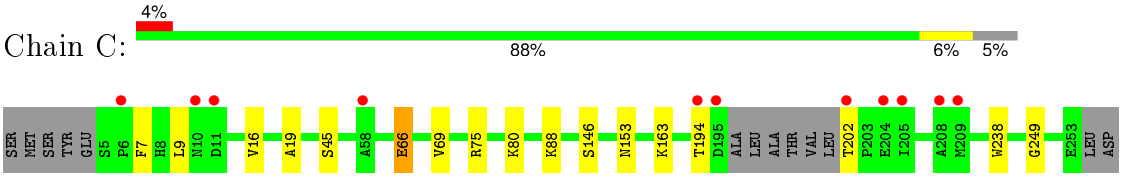
- Molecule 1: 7-ALPHA-HYDROXYSTEROID DEHYDROGENASE

Chain B:



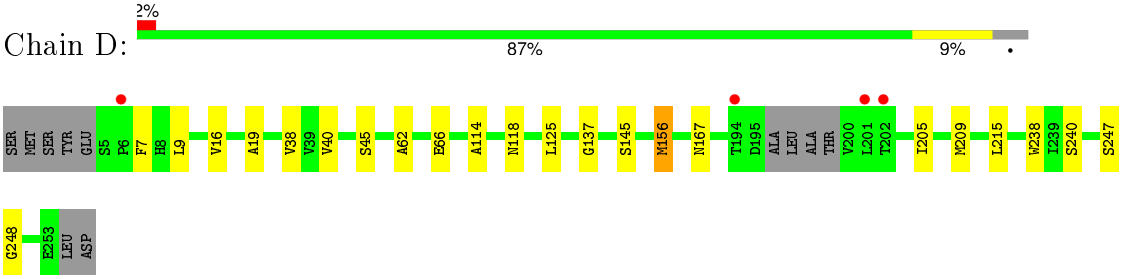
- Molecule 1: 7-ALPHA-HYDROXYSTEROID DEHYDROGENASE

Chain C:



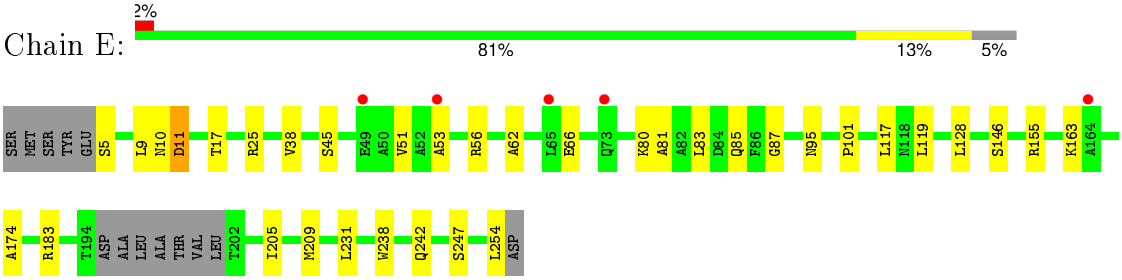
- Molecule 1: 7-ALPHA-HYDROXYSTEROID DEHYDROGENASE

Chain D:



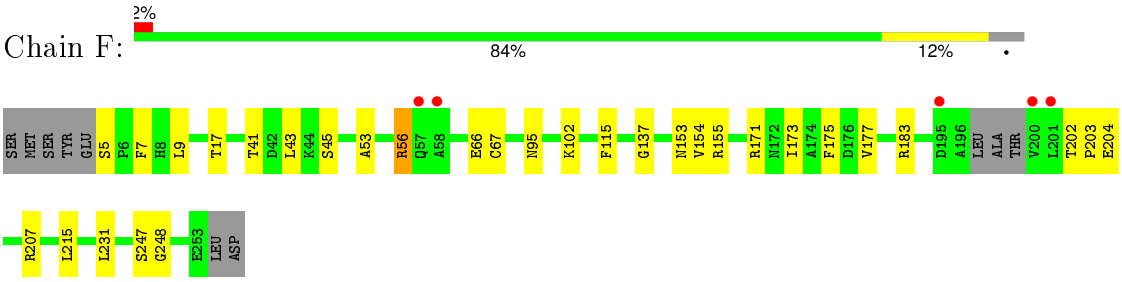
- Molecule 1: 7-ALPHA-HYDROXYSTEROID DEHYDROGENASE

Chain E:



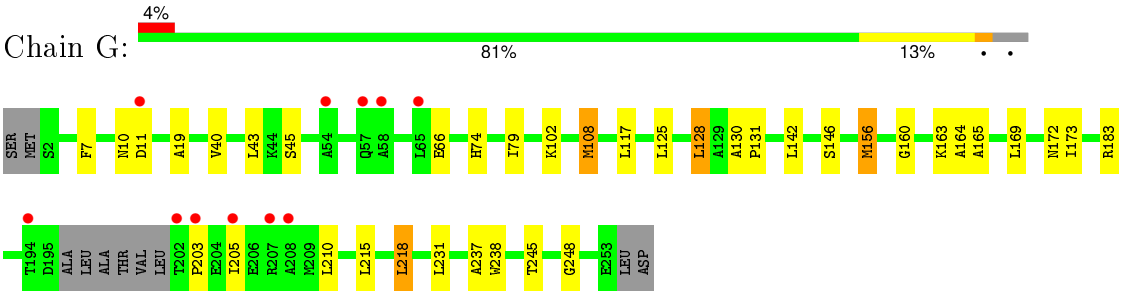
• Molecule 1: 7-ALPHA-HYDROXYSTEROID DEHYDROGENASE

Chain F:



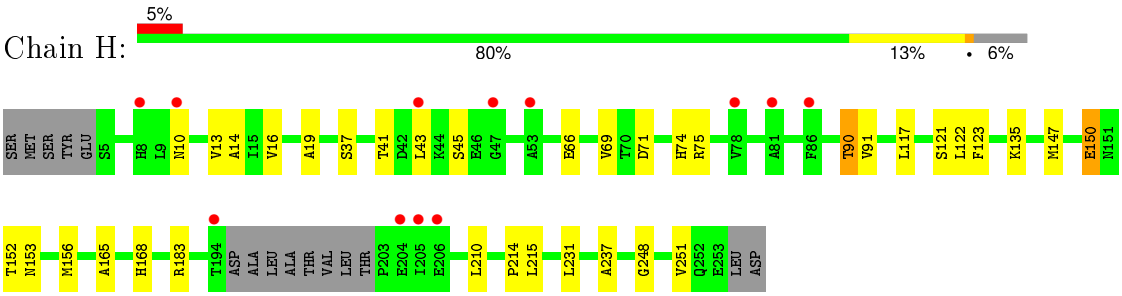
• Molecule 1: 7-ALPHA-HYDROXYSTEROID DEHYDROGENASE

Chain G:



• Molecule 1: 7-ALPHA-HYDROXYSTEROID DEHYDROGENASE

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	75.32Å 134.78Å 105.27Å 90.00° 109.52° 90.00°	Depositor
Resolution (Å)	48.51 – 2.20 48.49 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.1 (48.51-2.20) 99.1 (48.49-2.20)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.17 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.196 , 0.244 0.195 , 0.242	Depositor DCC
R_{free} test set	4955 reflections (5.26%)	DCC
Wilson B-factor (Å^2)	39.5	Xtriage
Anisotropy	0.086	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 43.9	EDS
Estimated twinning fraction	0.021 for h,-k,-h-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Outliers	0 of 99158 reflections	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	14131	wwPDB-VP
Average B, all atoms (Å^2)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.62% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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	0.67	0/1792	0.68	0/2435
1	B	0.64	0/1745	0.67	1/2368 (0.0%)
1	C	0.59	0/1734	0.64	0/2357
1	D	0.59	0/1741	0.63	0/2365
1	E	0.58	0/1744	0.65	0/2368
1	F	0.58	0/1765	0.63	0/2399
1	G	0.56	0/1762	0.64	0/2395
1	H	0.50	0/1707	0.61	1/2321 (0.0%)
All	All	0.59	0/13990	0.64	2/19008 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	125	LEU	CA-CB-CG	5.39	127.69	115.30
1	H	122	LEU	CA-CB-CG	5.37	127.65	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1763	0	1753	23	0
1	B	1717	0	1694	19	0
1	C	1706	0	1668	7	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1713	0	1678	13	0
1	E	1716	0	1696	17	0
1	F	1737	0	1712	20	0
1	G	1733	0	1697	25	0
1	H	1679	0	1631	24	0
2	A	73	0	0	1	0
2	B	55	0	0	2	0
2	C	51	0	0	0	0
2	D	47	0	0	1	0
2	E	45	0	0	2	0
2	F	32	0	0	2	0
2	G	36	0	0	0	0
2	H	28	0	0	3	0
All	All	14131	0	13529	127	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 5.

All (127) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:41:THR:HG23	1:A:67:CYS:HB3	1.55	0.89
1:F:41:THR:HG23	1:F:67:CYS:HB3	1.62	0.82
1:F:137:GLY:HA3	2:F:259:HOH:O	1.82	0.77
1:A:45:SER:HB3	1:A:66:GLU:HB2	1.69	0.72
1:H:183:ARG:NH2	1:H:231:LEU:O	2.17	0.72
1:F:45:SER:HB3	1:F:66:GLU:HB2	1.72	0.72
1:G:108:MET:HE2	1:G:108:MET:HA	1.75	0.69
1:H:13:VAL:H	1:H:90:THR:HG22	1.58	0.68
1:E:146:SER:HB3	1:E:163:LYS:HG3	1.76	0.68
1:C:45:SER:HB3	1:C:66:GLU:HB2	1.76	0.68
1:D:156:MET:HG2	2:E:269:HOH:O	1.94	0.67
1:G:183:ARG:NH2	1:G:231:LEU:O	2.28	0.67
1:A:5:SER:CB	1:A:6:PRO:CD	2.73	0.66
1:H:90:THR:HG23	1:H:91:VAL:HG23	1.76	0.66
1:B:137:GLY:HA3	2:B:256:HOH:O	1.97	0.65
1:G:172:ASN:ND2	1:H:153:ASN:H	1.96	0.63
1:E:10:ASN:O	1:E:11:ASP:HB2	1.99	0.62
1:A:5:SER:HB2	1:A:6:PRO:HD2	1.81	0.62
1:H:45:SER:HB3	1:H:66:GLU:HB2	1.82	0.62
1:H:156:MET:HG2	2:H:259:HOH:O	2.00	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:205:ILE:O	1:D:209:MET:HG3	2.01	0.60
1:A:53:ALA:O	1:A:57:GLN:HG2	2.01	0.60
1:F:183:ARG:NH2	1:F:231:LEU:O	2.36	0.59
1:G:45:SER:HB3	1:G:66:GLU:HB2	1.86	0.58
1:H:71:ASP:HB3	1:H:74:HIS:HB2	1.85	0.57
1:G:210:LEU:HD21	1:G:218:LEU:HD13	1.85	0.57
1:B:63:ILE:HD12	1:B:65:LEU:HD21	1.87	0.56
1:H:13:VAL:H	1:H:90:THR:CG2	2.20	0.55
1:A:183:ARG:NH2	1:A:231:LEU:O	2.38	0.55
1:G:172:ASN:HD22	1:H:153:ASN:H	1.54	0.55
1:A:131:PRO:O	1:A:135:LYS:HG2	2.06	0.55
1:A:5:SER:HB3	1:A:6:PRO:CD	2.38	0.54
1:E:45:SER:HB3	1:E:66:GLU:HB2	1.89	0.54
1:D:45:SER:HB3	1:D:66:GLU:HB2	1.89	0.54
1:A:41:THR:HG22	2:A:327:HOH:O	2.08	0.54
1:B:130:ALA:HB3	1:B:131:PRO:HD3	1.89	0.54
1:D:137:GLY:HA2	2:D:273:HOH:O	2.08	0.52
1:H:183:ARG:HD2	1:H:237:ALA:O	2.09	0.52
1:B:45:SER:HB3	1:B:66:GLU:HB2	1.91	0.52
1:G:10:ASN:O	1:G:11:ASP:CB	2.57	0.51
1:G:146:SER:HB3	1:G:163:LYS:HG3	1.91	0.51
1:C:238:TRP:CZ3	1:D:247:SER:HA	2.46	0.51
1:E:242:GLN:NE2	2:E:337:HOH:O	2.17	0.51
1:F:41:THR:CG2	1:F:67:CYS:HB3	2.38	0.51
1:B:242:GLN:OE1	2:B:284:HOH:O	2.20	0.51
1:A:215:LEU:HD12	1:A:248:GLY:HA2	1.92	0.50
1:D:16:VAL:HG12	1:D:19:ALA:HB2	1.93	0.50
1:G:183:ARG:HD2	1:G:237:ALA:O	2.12	0.50
1:A:41:THR:CG2	1:A:67:CYS:HB3	2.36	0.50
1:G:215:LEU:HD12	1:G:248:GLY:HA2	1.94	0.50
1:A:5:SER:CB	1:A:6:PRO:HD2	2.42	0.49
1:D:19:ALA:HB3	1:D:40:VAL:HG13	1.93	0.49
1:E:38:VAL:O	1:E:62:ALA:HA	2.12	0.49
1:B:17:THR:O	1:B:95:ASN:HB3	2.13	0.49
1:G:130:ALA:HB3	1:G:131:PRO:HD3	1.95	0.49
1:E:183:ARG:NH2	1:E:231:LEU:O	2.45	0.48
1:H:156:MET:CG	2:H:259:HOH:O	2.58	0.48
1:B:238:TRP:CZ3	1:E:247:SER:HA	2.48	0.48
1:E:83:LEU:O	1:E:87:GLY:HA2	2.14	0.47
1:A:5:SER:HB3	1:A:6:PRO:HD3	1.96	0.47
1:B:214:PRO:HB3	1:E:174:ALA:O	2.14	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:152:THR:CG2	1:F:171:ARG:HB3	2.43	0.47
1:G:19:ALA:HB3	1:G:40:VAL:HG13	1.97	0.47
1:B:211:LYS:HE2	1:B:212:HIS:NE2	2.30	0.47
1:B:25:ARG:HG3	1:B:51:VAL:HG22	1.96	0.47
1:B:156:MET:HE3	1:F:207:ARG:HH21	1.78	0.47
1:C:146:SER:HB3	1:C:163:LYS:HG3	1.95	0.47
1:G:108:MET:HE1	1:H:123:PHE:CE2	2.49	0.47
1:C:7:PHE:CD1	1:D:7:PHE:CD1	3.03	0.47
1:B:215:LEU:HD12	1:B:248:GLY:HA2	1.97	0.47
1:G:10:ASN:O	1:G:11:ASP:HB3	2.15	0.46
1:A:5:SER:HB2	1:A:6:PRO:CD	2.41	0.46
1:D:38:VAL:O	1:D:62:ALA:HA	2.15	0.46
1:H:215:LEU:HD12	1:H:248:GLY:HA2	1.98	0.46
1:C:69:VAL:O	1:C:75:ARG:HD3	2.16	0.46
1:C:249:GLY:HA2	1:D:240:SER:O	2.16	0.46
1:E:17:THR:O	1:E:95:ASN:HB3	2.16	0.46
1:A:152:THR:HG21	1:F:171:ARG:HB3	1.98	0.45
1:E:25:ARG:HG3	1:E:51:VAL:CG2	2.46	0.45
1:G:210:LEU:HD21	1:G:218:LEU:CD1	2.47	0.45
1:B:38:VAL:O	1:B:62:ALA:HA	2.17	0.45
1:H:14:ALA:HA	1:H:91:VAL:O	2.17	0.45
1:G:66:GLU:OE1	1:G:74:HIS:HE1	1.99	0.45
1:A:119:LEU:HD21	1:F:115:PHE:CZ	2.53	0.44
1:E:25:ARG:HG3	1:E:51:VAL:HG22	1.99	0.44
1:A:206:GLU:HG3	1:A:218:LEU:HD22	1.98	0.44
1:D:215:LEU:HD12	1:D:248:GLY:HA2	1.99	0.44
1:F:247:SER:OG	2:F:260:HOH:O	2.21	0.44
1:G:165:ALA:HB2	1:H:165:ALA:HB2	1.99	0.44
1:G:108:MET:HA	1:G:108:MET:CE	2.44	0.44
1:F:154:VAL:HG22	1:F:155:ARG:HG3	1.98	0.43
1:B:108:MET:O	1:B:112:GLU:HG3	2.18	0.43
1:H:69:VAL:O	1:H:75:ARG:NH1	2.46	0.43
1:D:145:SER:OG	1:D:167:ASN:ND2	2.52	0.43
1:A:242:GLN:NE2	1:G:245:THR:HB	2.34	0.43
1:E:101:PRO:HA	1:E:155:ARG:O	2.18	0.43
1:B:101:PRO:HA	1:B:155:ARG:O	2.19	0.43
1:A:173:ILE:O	1:A:177:VAL:HG22	2.17	0.43
1:B:170:THR:HG23	1:B:184:VAL:HG12	1.99	0.43
1:C:16:VAL:HG12	1:C:19:ALA:HB2	2.00	0.43
1:G:156:MET:HG3	1:G:160:GLY:H	1.84	0.42
1:F:202:THR:HB	1:F:203:PRO:CD	2.50	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:215:LEU:HD12	1:F:248:GLY:HA2	1.99	0.42
1:G:164:ALA:HB2	1:H:168:HIS:CD2	2.54	0.42
1:H:13:VAL:N	1:H:90:THR:HG22	2.30	0.42
1:G:79:ILE:HG13	1:G:128:LEU:HB3	2.02	0.42
1:H:150:GLU:OE2	2:H:275:HOH:O	2.22	0.42
1:E:53:ALA:HA	1:E:56:ARG:NH1	2.35	0.42
1:F:175:PHE:CD2	1:H:214:PRO:HG3	2.55	0.41
1:G:169:LEU:O	1:G:173:ILE:HG12	2.20	0.41
1:H:147:MET:HE2	1:H:251:VAL:HG12	2.02	0.41
1:F:53:ALA:HA	1:F:56:ARG:NH1	2.34	0.41
1:B:156:MET:HE3	1:F:207:ARG:HE	1.84	0.41
1:A:229:LEU:HD23	1:G:7:PHE:CE2	2.54	0.41
1:G:172:ASN:ND2	1:H:152:THR:HA	2.35	0.41
1:F:173:ILE:O	1:F:177:VAL:HG22	2.21	0.41
1:E:81:ALA:O	1:E:85:GLN:HB2	2.20	0.41
1:E:205:ILE:O	1:E:209:MET:HG3	2.21	0.41
1:F:17:THR:O	1:F:95:ASN:HB3	2.20	0.41
1:B:247:SER:HA	1:E:238:TRP:CZ3	2.55	0.41
1:A:114:ALA:O	1:A:118:ASN:HB2	2.21	0.41
1:D:114:ALA:O	1:D:118:ASN:HB2	2.21	0.40
1:H:16:VAL:HG12	1:H:19:ALA:HB2	2.03	0.40
1:F:5:SER:HB3	1:F:7:PHE:H	1.87	0.40
1:H:117:LEU:O	1:H:121:SER:OG	2.34	0.40
1:A:19:ALA:HB3	1:A:40:VAL:HG13	2.04	0.40
1:B:156:MET:CE	1:F:207:ARG:HE	2.34	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	247/256 (96%)	242 (98%)	5 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	239/256 (93%)	233 (98%)	6 (2%)	0	100	100
1	C	239/256 (93%)	234 (98%)	5 (2%)	0	100	100
1	D	241/256 (94%)	233 (97%)	8 (3%)	0	100	100
1	E	239/256 (93%)	231 (97%)	8 (3%)	0	100	100
1	F	242/256 (94%)	231 (96%)	11 (4%)	0	100	100
1	G	242/256 (94%)	233 (96%)	8 (3%)	1 (0%)	39	42
1	H	237/256 (93%)	229 (97%)	8 (3%)	0	100	100
All	All	1926/2048 (94%)	1866 (97%)	59 (3%)	1 (0%)	56	64

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	203	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	170/184 (92%)	167 (98%)	3 (2%)	66	79
1	B	165/184 (90%)	157 (95%)	8 (5%)	31	37
1	C	162/184 (88%)	155 (96%)	7 (4%)	35	43
1	D	161/184 (88%)	157 (98%)	4 (2%)	55	67
1	E	165/184 (90%)	157 (95%)	8 (5%)	31	37
1	F	167/184 (91%)	161 (96%)	6 (4%)	42	52
1	G	165/184 (90%)	154 (93%)	11 (7%)	20	21
1	H	157/184 (85%)	149 (95%)	8 (5%)	29	34
All	All	1312/1472 (89%)	1257 (96%)	55 (4%)	36	44

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	80	LYS
1	A	204	GLU
1	A	218	LEU
1	B	9	LEU
1	B	194	THR
1	B	195	ASP
1	B	206	GLU
1	B	209	MET
1	B	220	GLU
1	B	238	TRP
1	B	253	GLU
1	C	9	LEU
1	C	66	GLU
1	C	80	LYS
1	C	88	LYS
1	C	153	ASN
1	C	194	THR
1	C	202	THR
1	D	9	LEU
1	D	125	LEU
1	D	156	MET
1	D	238	TRP
1	E	5	SER
1	E	9	LEU
1	E	11	ASP
1	E	80	LYS
1	E	117	LEU
1	E	119	LEU
1	E	128	LEU
1	E	254	LEU
1	F	9	LEU
1	F	43	LEU
1	F	56	ARG
1	F	102	LYS
1	F	153	ASN
1	F	204	GLU
1	G	43	LEU
1	G	102	LYS
1	G	108	MET
1	G	117	LEU
1	G	125	LEU
1	G	128	LEU
1	G	142	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	G	156	MET
1	G	205	ILE
1	G	218	LEU
1	G	238	TRP
1	H	10	ASN
1	H	37	SER
1	H	41	THR
1	H	43	LEU
1	H	90	THR
1	H	135	LYS
1	H	150	GLU
1	H	210	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	242	GLN
1	B	132	HIS
1	B	242	GLN
1	D	167	ASN
1	F	57	GLN
1	F	94	ASN
1	G	172	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

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, 95^{th} 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	249/256 (97%)	-0.12	3 (1%) 81 80	22, 36, 54, 69	0
1	B	243/256 (94%)	-0.10	0 100 100	23, 38, 55, 69	0
1	C	243/256 (94%)	-0.00	11 (4%) 37 36	26, 42, 60, 89	0
1	D	245/256 (95%)	-0.10	4 (1%) 74 73	26, 42, 64, 89	0
1	E	243/256 (94%)	0.10	5 (2%) 67 65	25, 41, 60, 65	0
1	F	246/256 (96%)	0.08	5 (2%) 68 67	26, 45, 66, 79	0
1	G	246/256 (96%)	0.09	11 (4%) 37 36	28, 47, 69, 89	0
1	H	241/256 (94%)	0.30	12 (4%) 32 32	33, 52, 75, 83	0
All	All	1956/2048 (95%)	0.03	51 (2%) 59 58	22, 42, 69, 89	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	208	ALA	5.7
1	C	202	THR	4.2
1	C	195	ASP	4.1
1	A	199	THR	3.9
1	A	196	ALA	3.9
1	H	53	ALA	3.9
1	G	205	ILE	3.6
1	D	201	LEU	3.6
1	H	43	LEU	3.4
1	F	57	GLN	3.3
1	G	202	THR	3.2
1	C	209	MET	3.2
1	D	194	THR	2.8
1	C	58	ALA	2.8
1	D	6	PRO	2.7
1	C	194	THR	2.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	H	205	ILE	2.7
1	F	200	VAL	2.7
1	G	203	PRO	2.7
1	E	49	GLU	2.6
1	G	57	GLN	2.6
1	G	207	ARG	2.6
1	F	58	ALA	2.5
1	C	11	ASP	2.5
1	C	6	PRO	2.5
1	A	57	GLN	2.5
1	F	201	LEU	2.4
1	H	206	GLU	2.4
1	H	8	HIS	2.4
1	E	65	LEU	2.4
1	C	204	GLU	2.4
1	H	81	ALA	2.4
1	H	78	VAL	2.3
1	E	164	ALA	2.3
1	G	58	ALA	2.3
1	G	11	ASP	2.3
1	H	10	ASN	2.2
1	C	10	ASN	2.2
1	D	202	THR	2.2
1	F	195	ASP	2.2
1	H	204	GLU	2.2
1	G	65	LEU	2.2
1	G	194	THR	2.2
1	E	53	ALA	2.2
1	E	73	GLN	2.1
1	G	54	ALA	2.1
1	H	86	PHE	2.1
1	G	208	ALA	2.1
1	H	47	GLY	2.1
1	H	194	THR	2.0
1	C	205	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

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.