Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 03:21 am BST

PDB ID	:	3OMZ
Title	:	Crystal structure of MICA-specific human gamma delta T cell receptor
Authors	:	Xu, B.; Holmes, M.A.; Strong, R.K.
Deposited on	:	2010-08-27
Resolution	:	3.04 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 ⓘ symbol.

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

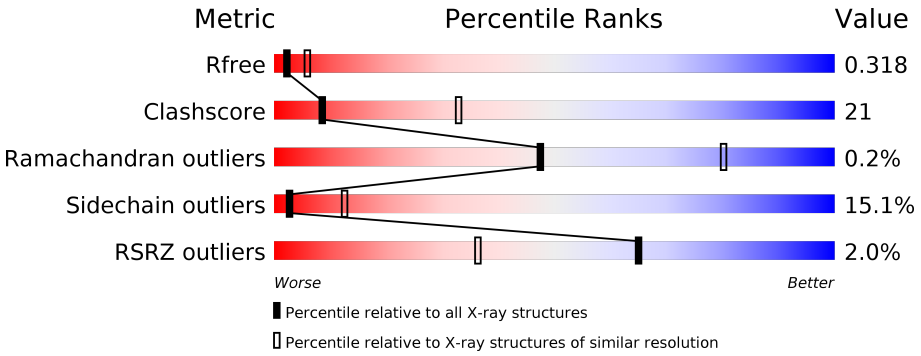
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 3.04 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	2752 (3.08-3.00)
Clashscore	141614	3096 (3.08-3.00)
Ramachandran outliers	138981	2986 (3.08-3.00)
Sidechain outliers	138945	2988 (3.08-3.00)
RSRZ outliers	127900	2636 (3.08-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria 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	259	51% 28% 17%
1	C	259	53% 21% 7% 19%
1	E	259	3% 49% 15% 34%
1	G	259	2% 31% 9% 60%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 4999 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 human Vdelta1 gamma delta T cell receptor delta1A/B-3.

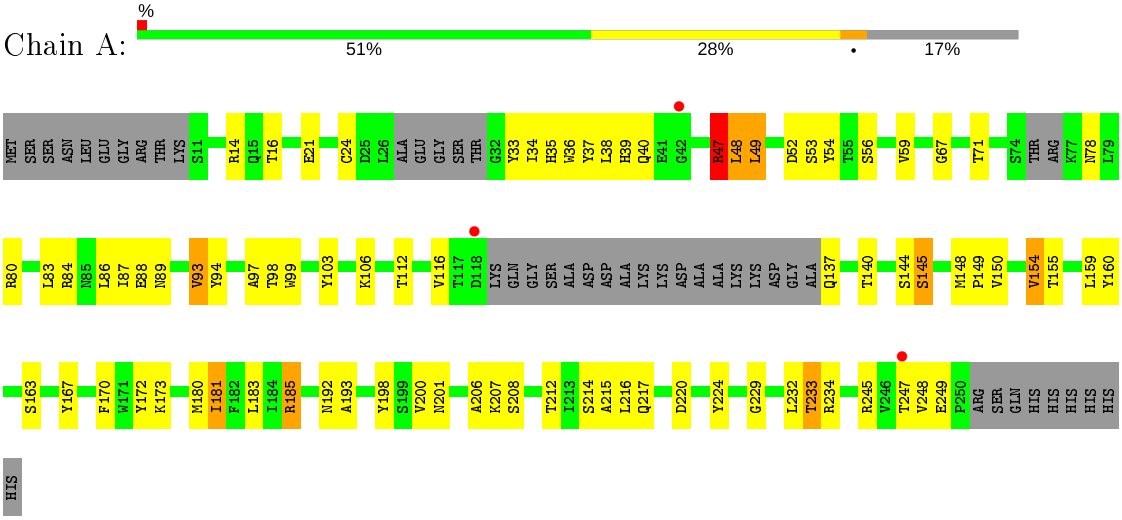
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	215	Total	C	N	O	S	0	0	0
			1594	1030	266	291	7			
1	C	209	Total	C	N	O	S	0	0	0
			1554	999	260	288	7			
1	E	172	Total	C	N	O	S	0	0	0
			1152	736	197	213	6			
1	G	103	Total	C	N	O	S	0	0	0
			699	447	115	134	3			

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 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.

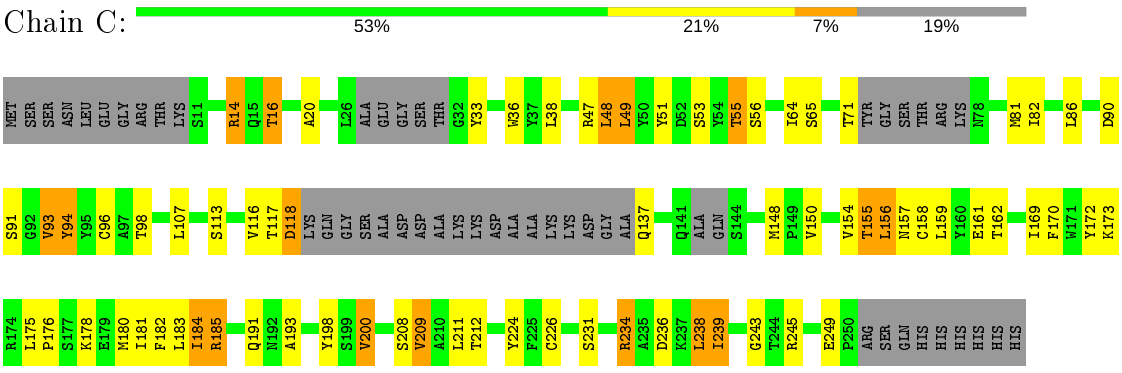
- Molecule 1: human Vdelta1 gamma delta T cell receptor delta1A/B-3

Chain A:



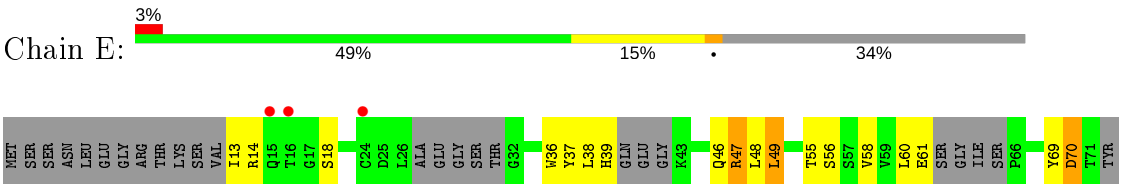
- Molecule 1: human Vdelta1 gamma delta T cell receptor delta1A/B-3

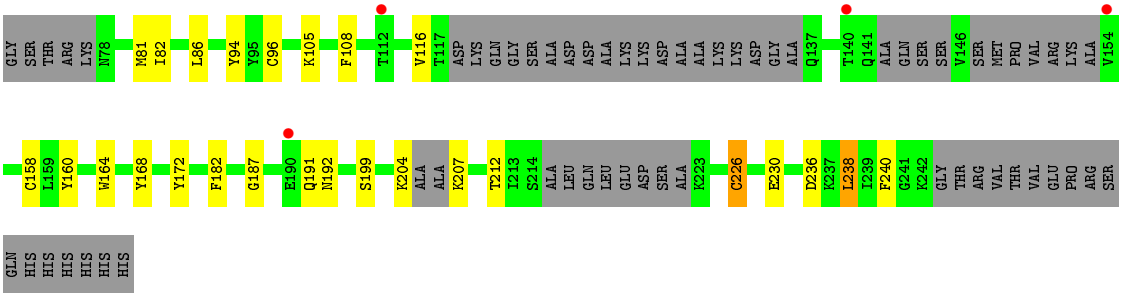
Chain C:



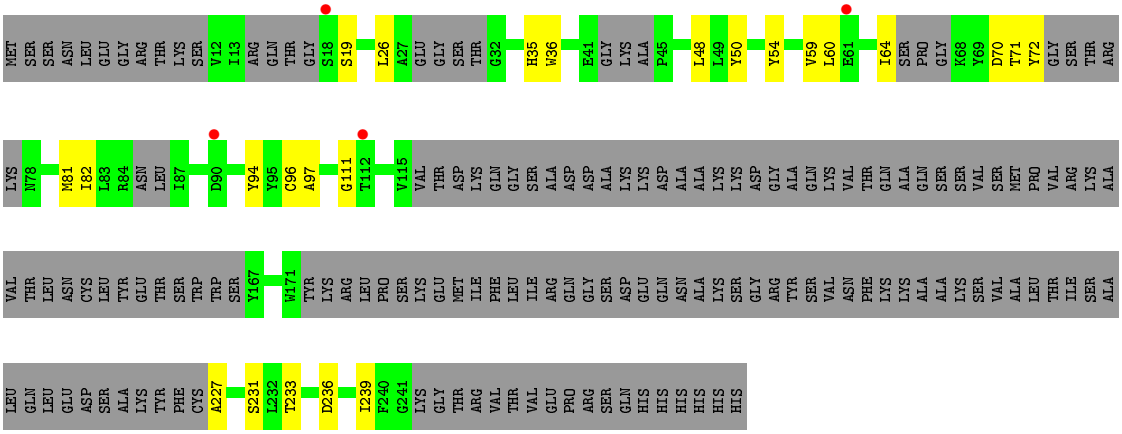
- Molecule 1: human Vdelta1 gamma delta T cell receptor delta1A/B-3

Chain E:





- Molecule 1: human Vdelta1 gamma delta T cell receptor delta1A/B-3



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α, β, γ	112.37Å 112.37Å 108.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.83 – 3.04 32.82 – 3.04	Depositor EDS
% Data completeness (in resolution range)	99.8 (32.83-3.04) 99.8 (32.82-3.04)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$< I/\sigma(I) >$ [1]	3.89 (at 3.06Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.265 , 0.308 0.273 , 0.318	Depositor DCC
R_{free} test set	1324 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å^2)	94.7	Xtriage
Anisotropy	0.036	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.26 , 75.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.008 for -h,-l,-k 0.000 for -h,l,k 0.000 for l,-k,h 0.007 for -l,-k,-h 0.028 for h,-k,-l	Xtriage
F_o,F_c correlation	0.88	EDS
Total number of atoms	4999	wwPDB-VP
Average B, all atoms (Å^2)	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.04% 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

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	0/1629	0.76	1/2213 (0.0%)
1	C	0.79	1/1587 (0.1%)	0.85	2/2156 (0.1%)
1	E	0.46	0/1174	0.58	0/1598
1	G	0.37	0/711	0.55	0/965
All	All	0.63	1/5101 (0.0%)	0.73	3/6932 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	94	TYR	CD1-CE1	-5.92	1.30	1.39

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	47	ARG	NE-CZ-NH1	5.36	122.98	120.30
1	C	245	ARG	NE-CZ-NH1	5.17	122.89	120.30
1	C	184	ILE	CG1-CB-CG2	-5.13	100.10	111.40

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	1594	0	1437	72	0
1	C	1554	0	1397	65	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	1152	0	799	39	0
1	G	699	0	468	15	0
All	All	4999	0	4101	188	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 21.

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:A:160:TYR:CE1	1:A:207:LYS:HG2	1.91	1.05
1:A:47:ARG:HH11	1:A:47:ARG:HG2	1.30	0.96
1:A:185:ARG:HH21	1:A:185:ARG:HG2	1.32	0.94
1:C:148:MET:HG3	1:C:154:VAL:HG22	1.50	0.92
1:C:169:ILE:HG21	1:C:209:VAL:HG11	1.55	0.88
1:C:49:LEU:HD22	1:C:49:LEU:C	2.00	0.81
1:E:48:LEU:HD23	1:E:69:TYR:CZ	2.15	0.81
1:E:38:LEU:HB2	1:E:48:LEU:HD11	1.63	0.80
1:A:170:PHE:CE2	1:A:185:ARG:CD	2.66	0.78
1:C:16:THR:HG22	1:C:117:THR:O	1.83	0.78
1:A:170:PHE:CE2	1:A:185:ARG:HD3	2.21	0.76
1:C:48:LEU:HB3	1:C:49:LEU:HD12	1.66	0.75
1:C:49:LEU:HD22	1:C:49:LEU:O	1.86	0.75
1:A:183:LEU:HD22	1:A:198:TYR:CZ	2.23	0.74
1:A:159:LEU:HD21	1:C:157:ASN:HD22	1.53	0.73
1:E:38:LEU:CB	1:E:48:LEU:HD11	2.19	0.72
1:A:185:ARG:HH21	1:A:185:ARG:CG	2.03	0.72
1:A:33:TYR:O	1:A:98:THR:HG22	1.90	0.71
1:A:170:PHE:CE2	1:A:185:ARG:HD2	2.26	0.71
1:A:160:TYR:CZ	1:A:207:LYS:HG2	2.25	0.71
1:C:86:LEU:HD13	1:C:116:VAL:HG22	1.73	0.71
1:C:49:LEU:N	1:C:49:LEU:HD13	2.07	0.69
1:A:181:ILE:N	1:A:181:ILE:HD13	2.07	0.69
1:G:36:TRP:CG	1:G:81:MET:CE	2.77	0.68
1:A:33:TYR:CE2	1:A:234:ARG:HD2	2.29	0.67
1:E:199:SER:CB	1:E:212:THR:HG23	2.25	0.67
1:A:172:TYR:HB3	1:A:180:MET:HE3	1.77	0.67
1:C:86:LEU:HD13	1:C:116:VAL:CG2	2.24	0.66
1:A:185:ARG:NH2	1:A:185:ARG:HG2	2.06	0.66
1:C:148:MET:HG3	1:C:154:VAL:CG2	2.25	0.65
1:A:49:LEU:CD2	1:A:49:LEU:C	2.66	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:55:THR:HG23	1:C:55:THR:O	1.97	0.64
1:A:170:PHE:HE2	1:A:185:ARG:HD3	1.63	0.64
1:C:49:LEU:N	1:C:49:LEU:CD1	2.62	0.63
1:C:162:THR:O	1:C:162:THR:HG23	1.97	0.63
1:A:192:ASN:ND2	1:A:201:ASN:HA	2.14	0.62
1:E:38:LEU:HD13	1:E:94:TYR:CE1	2.34	0.62
1:E:238:LEU:HD13	1:E:240:PHE:HE2	1.63	0.62
1:E:37:TYR:OH	1:E:238:LEU:HD12	2.00	0.62
1:G:71:THR:HG22	1:G:81:MET:HG3	1.82	0.61
1:E:14:ARG:O	1:E:116:VAL:HA	2.00	0.61
1:E:38:LEU:HD13	1:E:94:TYR:CZ	2.36	0.61
1:A:52:ASP:C	1:A:52:ASP:OD1	2.38	0.61
1:C:193:ALA:HB3	1:C:200:VAL:HG13	1.82	0.61
1:A:49:LEU:HD22	1:A:49:LEU:C	2.21	0.61
1:E:70:ASP:O	1:E:81:MET:HA	2.01	0.61
1:C:239:ILE:N	1:C:239:ILE:HD13	2.16	0.60
1:E:105:LYS:HD3	1:E:182:PHE:CD2	2.35	0.60
1:E:38:LEU:HD12	1:E:39:HIS:H	1.68	0.59
1:E:49:LEU:CD2	1:E:49:LEU:C	2.71	0.58
1:C:191:GLN:NE2	1:C:191:GLN:HA	2.18	0.58
1:A:148:MET:HG3	1:A:154:VAL:HG22	1.84	0.58
1:A:144:SER:O	1:A:145:SER:C	2.42	0.58
1:A:193:ALA:HB3	1:A:200:VAL:HB	1.85	0.57
1:C:184:ILE:CG2	1:C:185:ARG:N	2.66	0.57
1:C:155:THR:HA	1:C:211:LEU:O	2.05	0.57
1:A:150:VAL:HG22	1:A:248:VAL:HG12	1.87	0.56
1:C:36:TRP:HB2	1:C:49:LEU:HD11	1.86	0.56
1:C:38:LEU:HD13	1:C:94:TYR:CZ	2.40	0.56
1:C:49:LEU:CD2	1:C:49:LEU:C	2.70	0.56
1:C:14:ARG:O	1:C:116:VAL:HA	2.06	0.55
1:C:183:LEU:HD22	1:C:198:TYR:CZ	2.41	0.55
1:A:40:GLN:NE2	1:A:89:ASN:O	2.38	0.55
1:A:150:VAL:HG13	1:A:217:GLN:HA	1.89	0.55
1:G:36:TRP:CD2	1:G:81:MET:CE	2.88	0.55
1:A:47:ARG:NH1	1:A:47:ARG:HG2	2.10	0.55
1:A:172:TYR:CB	1:A:180:MET:HE3	2.37	0.54
1:A:183:LEU:HD22	1:A:198:TYR:CE1	2.43	0.54
1:E:48:LEU:CD2	1:E:69:TYR:CZ	2.90	0.53
1:C:172:TYR:HB3	1:C:180:MET:HE3	1.90	0.53
1:E:204:LYS:O	1:E:207:LYS:N	2.41	0.53
1:C:172:TYR:CB	1:C:180:MET:HE3	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:149:PRO:HA	1:A:249:GLU:O	2.09	0.53
1:E:18:SER:O	1:E:86:LEU:HD12	2.09	0.53
1:E:36:TRP:CD2	1:E:81:MET:HE2	2.44	0.53
1:A:155:THR:CB	1:A:212:THR:HG22	2.40	0.52
1:E:37:TYR:HA	1:E:46:GLN:O	2.10	0.52
1:C:181:ILE:HD13	1:C:181:ILE:N	2.25	0.52
1:G:36:TRP:CD2	1:G:81:MET:HE1	2.46	0.51
1:A:233:THR:O	1:A:234:ARG:C	2.49	0.51
1:E:238:LEU:HD13	1:E:240:PHE:CE2	2.43	0.51
1:A:170:PHE:CZ	1:A:185:ARG:HD2	2.46	0.51
1:C:64:ILE:HG22	1:C:65:SER:N	2.26	0.51
1:C:154:VAL:O	1:C:212:THR:HA	2.11	0.51
1:C:170:PHE:CE2	1:C:185:ARG:HD3	2.46	0.51
1:A:173:LYS:HB2	1:A:183:LEU:HD11	1.94	0.50
1:C:156:LEU:N	1:C:156:LEU:HD13	2.26	0.50
1:C:91:SER:HB3	1:C:116:VAL:H	1.77	0.50
1:E:55:THR:O	1:E:56:SER:HB2	2.11	0.50
1:C:33:TYR:CE2	1:C:234:ARG:HG3	2.46	0.49
1:C:155:THR:HA	1:C:212:THR:HA	1.93	0.49
1:C:48:LEU:CB	1:C:49:LEU:HD12	2.37	0.49
1:A:38:LEU:HD13	1:A:94:TYR:CZ	2.47	0.49
1:A:34:ILE:N	1:A:34:ILE:HD12	2.28	0.49
1:A:137:GLN:HE22	1:A:163:SER:CB	2.25	0.49
1:C:118:ASP:OD1	1:C:118:ASP:N	2.44	0.49
1:A:172:TYR:CB	1:A:180:MET:CE	2.91	0.48
1:C:51:TYR:CE1	1:C:53:SER:HA	2.47	0.48
1:A:88:GLU:HA	1:A:116:VAL:HB	1.96	0.48
1:A:33:TYR:C	1:A:34:ILE:HD12	2.34	0.48
1:A:35:HIS:O	1:A:97:ALA:N	2.46	0.48
1:C:93:VAL:HA	1:C:113:SER:HA	1.95	0.48
1:C:36:TRP:HB2	1:C:49:LEU:CD1	2.44	0.48
1:E:48:LEU:HD23	1:E:69:TYR:CE2	2.47	0.48
1:C:249:GLU:HA	1:C:249:GLU:OE1	2.14	0.48
1:A:159:LEU:CD2	1:C:157:ASN:HD22	2.25	0.47
1:A:37:TYR:OH	1:A:106:LYS:NZ	2.40	0.47
1:E:49:LEU:C	1:E:49:LEU:HD22	2.35	0.47
1:G:94:TYR:O	1:G:111:GLY:HA2	2.15	0.47
1:A:206:ALA:O	1:A:207:LYS:C	2.52	0.47
1:A:38:LEU:HB2	1:A:48:LEU:HD21	1.96	0.47
1:E:36:TRP:CG	1:E:81:MET:CE	2.97	0.47
1:A:21:GLU:OE1	1:A:80:ARG:HD2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:36:TRP:CD2	1:E:81:MET:CE	2.98	0.47
1:A:99:TRP:CE2	1:A:106:LYS:HD2	2.50	0.47
1:A:52:ASP:OD1	1:A:54:TYR:N	2.47	0.47
1:C:184:ILE:HG22	1:C:185:ARG:N	2.29	0.47
1:E:49:LEU:O	1:E:49:LEU:HD22	2.15	0.47
1:A:93:VAL:HG22	1:A:93:VAL:O	2.15	0.46
1:A:160:TYR:CD1	1:A:207:LYS:HG2	2.47	0.46
1:A:183:LEU:CD2	1:A:198:TYR:CZ	2.94	0.46
1:C:173:LYS:HE3	1:C:175:LEU:HD21	1.97	0.46
1:A:172:TYR:HB2	1:A:180:MET:CE	2.46	0.46
1:G:36:TRP:CD2	1:G:81:MET:HE3	2.52	0.45
1:E:168:TYR:HD1	1:E:187:GLY:HA2	1.81	0.45
1:C:86:LEU:HB3	1:C:116:VAL:HG21	1.99	0.45
1:E:172:TYR:CD1	1:E:182:PHE:HA	2.52	0.45
1:E:108:PHE:CD1	1:E:108:PHE:N	2.85	0.45
1:C:93:VAL:HG22	1:C:93:VAL:O	2.16	0.45
1:C:38:LEU:HD13	1:C:94:TYR:CE1	2.52	0.45
1:E:164:TRP:CH2	1:E:230:GLU:HB2	2.52	0.45
1:A:217:GLN:O	1:A:248:VAL:HG21	2.16	0.44
1:G:35:HIS:O	1:G:96:CYS:HA	2.16	0.44
1:C:137:GLN:HA	1:C:161:GLU:O	2.18	0.44
1:E:49:LEU:HB2	1:E:60:LEU:HD23	2.00	0.44
1:G:36:TRP:CG	1:G:81:MET:HE1	2.51	0.44
1:A:180:MET:C	1:A:181:ILE:HD13	2.38	0.44
1:A:215:ALA:O	1:A:216:LEU:C	2.56	0.44
1:A:93:VAL:HA	1:A:112:THR:O	2.17	0.43
1:G:60:LEU:HD22	1:G:64:ILE:CB	2.48	0.43
1:E:191:GLN:O	1:E:192:ASN:C	2.56	0.43
1:C:180:MET:C	1:C:181:ILE:HD13	2.38	0.43
1:G:227:ALA:HB1	1:G:239:ILE:O	2.18	0.43
1:A:103:TYR:HB3	1:A:232:LEU:HB3	2.01	0.43
1:E:160:TYR:CZ	1:E:207:LYS:HA	2.53	0.43
1:E:49:LEU:CB	1:E:60:LEU:HD23	2.49	0.42
1:G:26:LEU:HD12	1:G:96:CYS:SG	2.59	0.42
1:A:67:GLY:O	1:A:84:ARG:HG3	2.18	0.42
1:C:162:THR:CG2	1:C:162:THR:O	2.65	0.42
1:C:48:LEU:O	1:C:49:LEU:HB3	2.19	0.42
1:C:36:TRP:CE3	1:C:81:MET:HE2	2.54	0.42
1:C:180:MET:HE3	1:C:180:MET:HB3	1.83	0.42
1:A:86:LEU:HB3	1:A:116:VAL:CG1	2.50	0.42
1:G:50:TYR:CE1	1:G:59:VAL:HB	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:20:ALA:O	1:C:82:ILE:HA	2.19	0.42
1:C:86:LEU:HA	1:C:90:ASP:OD2	2.20	0.42
1:E:47:ARG:NH1	1:E:61:GLU:OE2	2.53	0.42
1:G:70:ASP:HB3	1:G:72:TYR:CE2	2.55	0.42
1:A:78:ASN:O	1:A:80:ARG:HG3	2.20	0.42
1:C:155:THR:HG22	1:C:212:THR:HG23	2.02	0.42
1:C:224:TYR:CD2	1:C:224:TYR:N	2.87	0.41
1:A:160:TYR:CZ	1:A:207:LYS:CG	2.99	0.41
1:A:224:TYR:CD2	1:A:224:TYR:N	2.88	0.41
1:G:35:HIS:N	1:G:97:ALA:O	2.44	0.41
1:E:70:ASP:HB2	1:E:82:ILE:HB	2.02	0.41
1:A:24:CYS:HB2	1:A:36:TRP:CH2	2.55	0.41
1:A:53:SER:O	1:A:54:TYR:C	2.58	0.41
1:C:33:TYR:CE2	1:C:234:ARG:NE	2.89	0.41
1:G:70:ASP:O	1:G:82:ILE:N	2.53	0.41
1:A:167:TYR:HB2	1:A:229:GLY:O	2.21	0.41
1:C:191:GLN:HE21	1:C:191:GLN:HA	1.84	0.41
1:C:238:LEU:HD12	1:C:238:LEU:HA	1.75	0.41
1:A:159:LEU:HD21	1:C:157:ASN:ND2	2.28	0.41
1:A:154:VAL:O	1:A:212:THR:HA	2.20	0.41
1:A:49:LEU:HB2	1:A:59:VAL:O	2.21	0.40
1:A:39:HIS:O	1:A:93:VAL:HG13	2.21	0.40
1:C:172:TYR:CD1	1:C:182:PHE:HA	2.56	0.40
1:A:150:VAL:HG23	1:A:249:GLU:O	2.22	0.40
1:A:87:ILE:O	1:A:89:ASN:N	2.54	0.40
1:C:224:TYR:O	1:C:243:GLY:HA2	2.21	0.40
1:C:36:TRP:CZ3	1:C:96:CYS:HB3	2.56	0.40
1:E:13:ILE:O	1:E:14:ARG:HG3	2.21	0.40
1:E:226:CYS:SG	1:E:226:CYS:O	2.79	0.40
1:E:238:LEU:O	1:E:238:LEU:HD12	2.22	0.40
1:E:36:TRP:CZ3	1:E:96:CYS:HB3	2.56	0.40
1:C:16:THR:CG2	1:C:118:ASP:HA	2.52	0.40
1:C:176:PRO:C	1:C:178:LYS:H	2.25	0.40
1:A:220:ASP:O	1:A:224:TYR:OH	2.25	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	207/259 (80%)	186 (90%)	21 (10%)	0	100 100
1	C	199/259 (77%)	179 (90%)	20 (10%)	0	100 100
1	E	153/259 (59%)	139 (91%)	14 (9%)	0	100 100
1	G	85/259 (33%)	77 (91%)	7 (8%)	1 (1%)	13 44
All	All	644/1036 (62%)	581 (90%)	62 (10%)	1 (0%)	47 80

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	54	TYR

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	143/222 (64%)	124 (87%)	19 (13%)	4 16
1	C	141/222 (64%)	114 (81%)	27 (19%)	1 7
1	E	67/222 (30%)	59 (88%)	8 (12%)	5 20
1	G	41/222 (18%)	36 (88%)	5 (12%)	5 19
All	All	392/888 (44%)	333 (85%)	59 (15%)	3 12

All (59) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	ARG
1	A	16	THR
1	A	47	ARG
1	A	48	LEU
1	A	49	LEU
1	A	56	SER
1	A	71	THR
1	A	83	LEU
1	A	93	VAL
1	A	140	THR
1	A	145	SER
1	A	154	VAL
1	A	181	ILE
1	A	185	ARG
1	A	208	SER
1	A	214	SER
1	A	233	THR
1	A	245	ARG
1	A	247	THR
1	C	14	ARG
1	C	16	THR
1	C	47	ARG
1	C	48	LEU
1	C	49	LEU
1	C	55	THR
1	C	56	SER
1	C	71	THR
1	C	93	VAL
1	C	98	THR
1	C	107	LEU
1	C	118	ASP
1	C	150	VAL
1	C	155	THR
1	C	156	LEU
1	C	158	CYS
1	C	159	LEU
1	C	185	ARG
1	C	200	VAL
1	C	208	SER
1	C	209	VAL
1	C	226	CYS
1	C	231	SER
1	C	234	ARG

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Mol	Chain	Res	Type
1	C	236	ASP
1	C	238	LEU
1	C	239	ILE
1	E	47	ARG
1	E	49	LEU
1	E	58	VAL
1	E	70	ASP
1	E	158	CYS
1	E	226	CYS
1	E	236	ASP
1	E	238	LEU
1	G	19	SER
1	G	48	LEU
1	G	231	SER
1	G	233	THR
1	G	236	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	192	ASN
1	C	157	ASN
1	C	191	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 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	215/259 (83%)	-0.45	3 (1%) 75 49	50, 73, 115, 152	0
1	C	209/259 (80%)	-0.45	0 100 100	44, 68, 100, 119	0
1	E	172/259 (66%)	0.01	7 (4%) 37 15	73, 121, 165, 189	0
1	G	103/259 (39%)	0.01	4 (3%) 39 16	95, 119, 146, 176	0
All	All	699/1036 (67%)	-0.27	14 (2%) 65 36	44, 87, 153, 189	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	190	GLU	4.9
1	E	112	THR	4.1
1	G	18	SER	3.2
1	G	112	THR	2.8
1	G	61	GLU	2.7
1	A	247	THR	2.5
1	E	24	CYS	2.5
1	E	140	THR	2.4
1	E	15	GLN	2.4
1	G	90	ASP	2.4
1	E	154	VAL	2.3
1	A	118	ASP	2.1
1	A	42	GLY	2.1
1	E	16	THR	2.1

6.2 Non-standard residues in protein, DNA, RNA chains

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.