



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 11:18 AM GMT

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 wwPDB X-ray Structure Validation Summary 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) 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

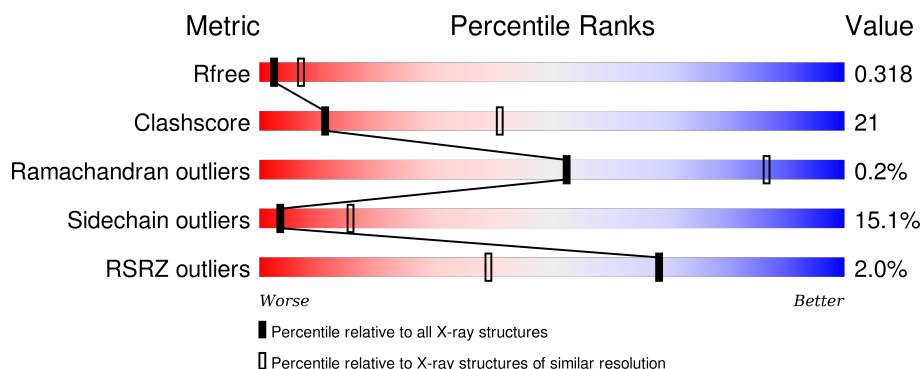
1 Overall quality at a glance ⓘ

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}	91344	1995 (3.08-3.00)
Clashscore	102246	2351 (3.08-3.00)
Ramachandran outliers	100387	2272 (3.08-3.00)
Sidechain outliers	100360	2275 (3.08-3.00)
RSRZ outliers	91569	2013 (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. 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 $\leq 5\%$. 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	<div> <div>3%</div> <div>51% 28% • 17%</div> </div>
1	C	259	<div> <div>53% 21% 7% 19%</div> </div>
1	E	259	<div> <div>3%</div> <div>49% 15% • 34%</div> </div>
1	G	259	<div> <div>2%</div> <div>31% 9% 60%</div> </div>

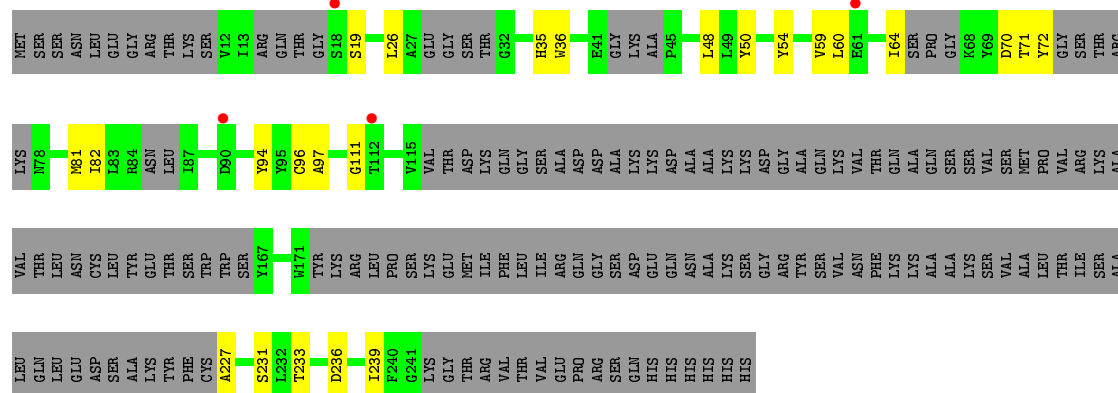
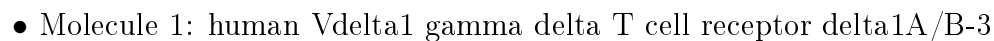
2 Entry composition

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			



4 Data and refinement statistics

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
$\langle I/\sigma(I) \rangle$ 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	1318 reflections (5.36%)	DCC
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 , 76.0	EDS
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
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 25978 reflections	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 $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0.67	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(°)	Ideal(°)
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 [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	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.

The worst 5 of 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

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	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%)	16	53
All	All	644/1036 (62%)	581 (90%)	62 (10%)	1 (0%)	52	87

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%)	5	20
1	C	141/222 (64%)	114 (81%)	27 (19%)	2	9
1	E	67/222 (30%)	59 (88%)	8 (12%)	6	25
1	G	41/222 (18%)	36 (88%)	5 (12%)	6	24
All	All	392/888 (44%)	333 (85%)	59 (15%)	3	15

5 of 59 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	71	THR
1	C	156	LEU
1	G	19	SER
1	C	93	VAL
1	C	107	LEU

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 ⓘ

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 [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	215/259 (83%)	-0.44	3 (1%) 78 51	50, 73, 115, 152	0
1	C	209/259 (80%)	-0.44	0 100 100	44, 68, 100, 119	0
1	E	172/259 (66%)	0.03	7 (4%) 41 17	73, 121, 165, 189	0
1	G	103/259 (39%)	0.03	4 (3%) 43 18	95, 119, 146, 176	0
All	All	699/1036 (67%)	-0.26	14 (2%) 68 39	44, 87, 153, 189	0

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	190	GLU	4.9
1	E	112	THR	4.2
1	G	18	SER	3.3
1	G	112	THR	2.9
1	E	24	CYS	2.7

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 carbohydrates 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.