



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 12, 2020 – 02:02 AM EST

PDB ID : 4GUM
Title : Crystal structure of locked-trimer of human MIF
Authors : Fan, C.; Lolis, E.
Deposited on : 2012-08-29
Resolution : 2.33 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.14.6
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) : 2.14.6

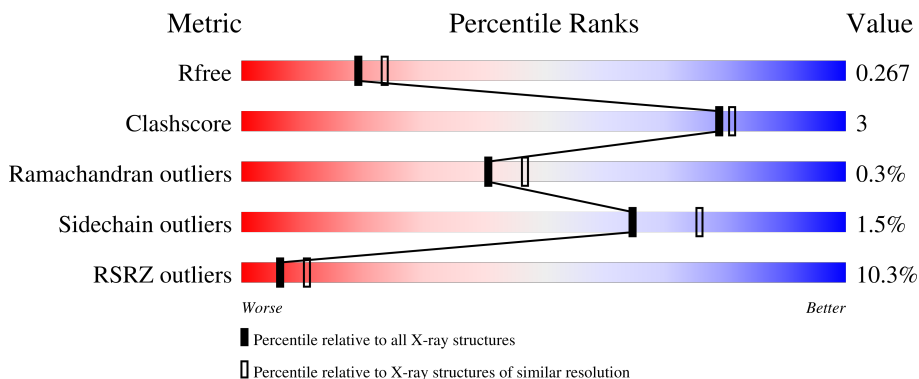
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.33 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.



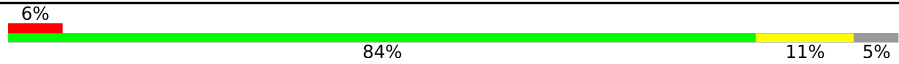

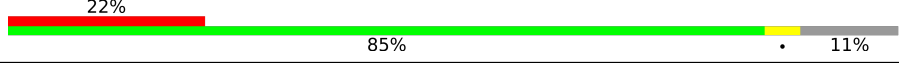
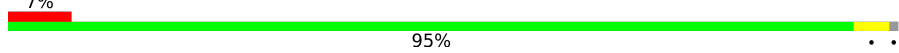
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2096 (2.36-2.32)
Clashscore	141614	2193 (2.36-2.32)
Ramachandran outliers	138981	2159 (2.36-2.32)
Sidechain outliers	138945	2160 (2.36-2.32)
RSRZ outliers	127900	2067 (2.36-2.32)

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 $\leq 5\%$. 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	114	96%
1	B	114	8%
1	C	114	6%
1	D	114	4%
1	E	114	5%

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Mol	Chain	Length	Quality of chain
1	F	114	
1	G	114	
1	H	114	
1	I	114	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7524 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 Macrophage migration inhibitory factor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	114	Total 857	C 541	N 149	O 160	S 7	1	0	0
1	B	114	Total 854	C 543	N 149	O 155	S 7	1	0	0
1	C	112	Total 847	C 535	N 147	O 158	S 7	1	0	0
1	D	110	Total 834	C 528	N 145	O 154	S 7	1	0	0
1	E	111	Total 828	C 526	N 142	O 153	S 7	1	0	0
1	F	108	Total 793	C 501	N 138	O 147	S 7	1	0	0
1	G	110	Total 808	C 511	N 142	O 149	S 6	1	0	0
1	H	101	Total 728	C 458	N 130	O 134	S 6	2	0	0
1	I	113	Total 838	C 530	N 146	O 155	S 7	0	0	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	110	CYS	ASN	engineered mutation	UNP P14174
B	110	CYS	ASN	engineered mutation	UNP P14174
C	110	CYS	ASN	engineered mutation	UNP P14174
D	110	CYS	ASN	engineered mutation	UNP P14174
E	110	CYS	ASN	engineered mutation	UNP P14174
F	110	CYS	ASN	engineered mutation	UNP P14174
G	110	CYS	ASN	engineered mutation	UNP P14174
H	110	CYS	ASN	engineered mutation	UNP P14174
I	110	CYS	ASN	engineered mutation	UNP P14174

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	I	1	Total Cl 1 1	0	0
2	A	1	Total Cl 1 1	0	0
2	D	3	Total Cl 3 3	0	0
2	C	2	Total Cl 2 2	0	0
2	E	1	Total Cl 1 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	25	Total O 25 25	0	0
3	B	14	Total O 14 14	0	0
3	C	22	Total O 22 22	0	0
3	D	21	Total O 21 21	0	0
3	E	15	Total O 15 15	0	0
3	F	13	Total O 13 13	0	0
3	G	2	Total O 2 2	0	0
3	H	3	Total O 3 3	0	0
3	I	14	Total O 14 14	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: Macrophage migration inhibitory factor

Chain A:  96%




- Molecule 1: Macrophage migration inhibitory factor

Chain B:  89% 8% 11%




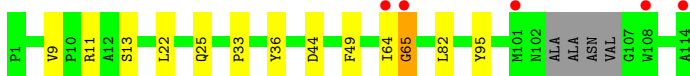
- Molecule 1: Macrophage migration inhibitory factor

Chain C:  85% 6% 12%




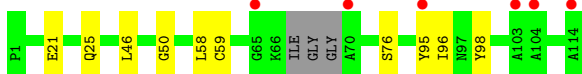
- Molecule 1: Macrophage migration inhibitory factor

Chain D:  85% 4% 11%

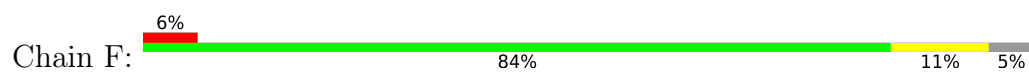


- Molecule 1: Macrophage migration inhibitory factor

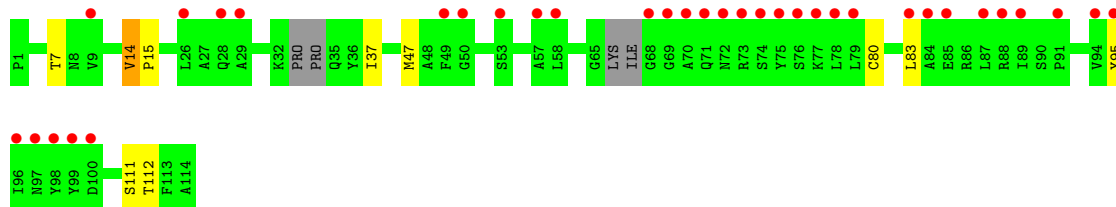
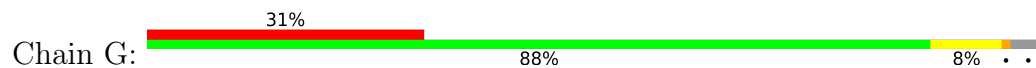
Chain E:  89% 5% 9%



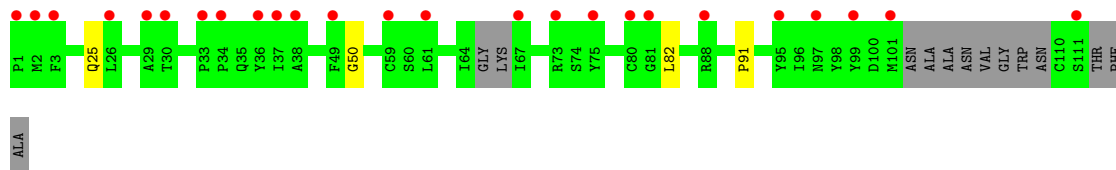
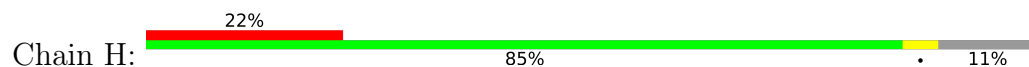
- Molecule 1: Macrophage migration inhibitory factor



- Molecule 1: Macrophage migration inhibitory factor



- Molecule 1: Macrophage migration inhibitory factor



- Molecule 1: Macrophage migration inhibitory factor



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	50.31Å 100.38Å 199.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.79 – 2.33 48.79 – 2.33	Depositor EDS
% Data completeness (in resolution range)	98.5 (48.79-2.33) 98.5 (48.79-2.33)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.01 (at 2.34Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.222 , 0.272 0.215 , 0.267	Depositor DCC
R_{free} test set	2185 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	51.7	Xtrriage
Anisotropy	0.100	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 48.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7524	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 29.67 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.4886e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CL

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	0.24	0/877	0.40	0/1194
1	B	0.23	0/874	0.41	0/1189
1	C	0.22	0/866	0.40	0/1177
1	D	0.23	0/853	0.40	0/1157
1	E	0.22	0/847	0.41	0/1155
1	F	0.22	0/808	0.38	0/1096
1	G	0.22	0/824	0.41	0/1120
1	H	0.22	0/742	0.39	0/1009
1	I	0.23	0/858	0.40	0/1167
All	All	0.23	0/7549	0.40	0/10264

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	857	0	835	3	0
1	B	854	0	845	8	0
1	C	847	0	830	8	0
1	D	834	0	815	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	828	0	796	7	0
1	F	793	0	770	7	0
1	G	808	0	769	3	0
1	H	728	0	688	3	0
1	I	838	0	801	4	0
2	A	1	0	0	0	0
2	C	2	0	0	0	0
2	D	3	0	0	0	0
2	E	1	0	0	0	0
2	I	1	0	0	0	0
3	A	25	0	0	0	0
3	B	14	0	0	0	0
3	C	22	0	0	0	0
3	D	21	0	0	0	0
3	E	15	0	0	0	0
3	F	13	0	0	0	0
3	G	2	0	0	0	0
3	H	3	0	0	0	0
3	I	14	0	0	0	0
All	All	7524	0	7149	41	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 3.

All (41) 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:25:GLN:HG3	1:C:82:LEU:HD22	1.78	0.65
1:H:25:GLN:HG3	1:H:82:LEU:HD22	1.78	0.65
1:D:25:GLN:HG3	1:D:82:LEU:HD22	1.80	0.64
1:B:1:PRO:HD2	1:B:37:ILE:HG12	1.83	0.59
1:A:25:GLN:HG3	1:A:82:LEU:HD22	1.85	0.59
1:F:25:GLN:HG3	1:F:82:LEU:HD22	1.84	0.58
1:I:25:GLN:HG3	1:I:82:LEU:HD22	1.88	0.56
1:A:41:VAL:HB	1:C:46:LEU:HB2	1.86	0.56
1:E:58:LEU:HD23	1:E:95:TYR:HB2	1.89	0.53
1:E:76:SER:OG	1:E:98:TYR:OH	2.27	0.53
1:E:46:LEU:HD21	1:F:11:ARG:HE	1.73	0.52
1:B:25:GLN:HG3	1:B:82:LEU:HD22	1.92	0.51
1:D:49:PHE:HZ	1:D:95:TYR:CE1	2.29	0.50
1:E:76:SER:HG	1:E:98:TYR:HH	1.58	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:50:GLY:HA2	1:C:34:PRO:O	2.12	0.49
1:B:32:LYS:HB3	1:B:36:TYR:HE1	1.77	0.48
1:B:58:LEU:HD23	1:B:95:TYR:HB2	1.96	0.47
1:C:104:ALA:HA	1:C:105:ASN:HA	1.61	0.46
1:B:32:LYS:HB3	1:B:36:TYR:CE1	2.51	0.46
1:F:9:VAL:HG13	1:F:13:SER:HB3	1.98	0.46
1:C:24:GLN:O	1:C:28:GLN:HG2	2.16	0.46
1:E:50:GLY:HA2	1:F:34:PRO:O	2.16	0.45
1:H:50:GLY:HA2	1:I:34:PRO:O	2.16	0.45
1:C:1:PRO:HD2	1:C:37:ILE:HD13	1.98	0.45
1:H:91:PRO:O	1:I:110:CYS:HB2	2.18	0.43
1:D:33:PRO:HD2	1:D:36:TYR:HD2	1.84	0.43
1:B:80:CYS:HB3	1:C:110:CYS:HB3	1.87	0.42
1:D:22:LEU:HD23	1:D:22:LEU:HA	1.94	0.42
1:F:64:ILE:HD13	1:F:101:MET:HB2	2.02	0.42
1:D:11:ARG:HB2	1:D:44:ASP:OD2	2.19	0.42
1:F:33:PRO:HA	1:F:34:PRO:HD3	1.95	0.42
1:G:7:THR:HA	1:G:47:MET:HE1	2.02	0.42
1:G:14:VAL:HA	1:G:15:PRO:HD3	1.89	0.42
1:B:64:ILE:HG23	1:B:103:ALA:HB2	2.02	0.41
1:E:59:CYS:HB2	1:E:96:ILE:HG12	2.02	0.41
1:D:64:ILE:HA	1:D:65:GLY:HA2	1.75	0.41
1:E:21:GLU:O	1:E:25:GLN:HG2	2.20	0.41
1:F:14:VAL:HA	1:F:15:PRO:HD3	1.93	0.41
1:A:111:SER:HB3	1:C:92:ASP:HB3	2.02	0.41
1:D:9:VAL:HG13	1:D:13:SER:OG	2.21	0.40
1:G:111:SER:HA	1:I:91:PRO:HB2	2.02	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	112/114 (98%)	111 (99%)	1 (1%)	0	100	100
1	B	112/114 (98%)	108 (96%)	4 (4%)	0	100	100
1	C	108/114 (95%)	106 (98%)	1 (1%)	1 (1%)	17	17
1	D	106/114 (93%)	102 (96%)	3 (3%)	1 (1%)	17	17
1	E	107/114 (94%)	105 (98%)	2 (2%)	0	100	100
1	F	102/114 (90%)	98 (96%)	4 (4%)	0	100	100
1	G	104/114 (91%)	97 (93%)	6 (6%)	1 (1%)	15	14
1	H	95/114 (83%)	92 (97%)	3 (3%)	0	100	100
1	I	111/114 (97%)	106 (96%)	5 (4%)	0	100	100
All	All	957/1026 (93%)	925 (97%)	29 (3%)	3 (0%)	41	47

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	65	GLY
1	G	37	ILE
1	C	106	VAL

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	92/94 (98%)	91 (99%)	1 (1%)	73	83
1	B	91/94 (97%)	89 (98%)	2 (2%)	52	63
1	C	92/94 (98%)	89 (97%)	3 (3%)	38	46
1	D	90/94 (96%)	90 (100%)	0	100	100
1	E	87/94 (93%)	87 (100%)	0	100	100
1	F	83/94 (88%)	82 (99%)	1 (1%)	71	82
1	G	82/94 (87%)	77 (94%)	5 (6%)	18	21
1	H	74/94 (79%)	74 (100%)	0	100	100
1	I	87/94 (93%)	87 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	778/846 (92%)	766 (98%)	12 (2%)	65	76

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	112	THR
1	B	36	TYR
1	B	78	LEU
1	C	35	GLN
1	C	106	VAL
1	C	112	THR
1	F	49	PHE
1	G	14	VAL
1	G	80	CYS
1	G	83	LEU
1	G	95	TYR
1	G	112	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	72	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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

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, 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	114/114 (100%)	0.26	0 100 100	30, 43, 70, 92	1 (0%)
1	B	114/114 (100%)	0.48	9 (7%) 12 19	35, 59, 123, 154	1 (0%)
1	C	112/114 (98%)	0.35	7 (6%) 20 28	33, 50, 93, 132	1 (0%)
1	D	110/114 (96%)	0.23	5 (4%) 33 44	32, 45, 105, 124	1 (0%)
1	E	111/114 (97%)	0.29	6 (5%) 25 36	33, 51, 86, 115	1 (0%)
1	F	108/114 (94%)	0.32	7 (6%) 18 26	37, 61, 104, 120	1 (0%)
1	G	110/114 (96%)	1.75	35 (31%) 0 0	45, 99, 161, 187	1 (0%)
1	H	101/114 (88%)	1.02	25 (24%) 0 1	39, 76, 120, 142	1 (0%)
1	I	113/114 (99%)	0.33	8 (7%) 16 23	34, 49, 102, 128	0
All	All	993/1026 (96%)	0.55	102 (10%) 6 11	30, 57, 119, 187	8 (0%)

All (102) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	69	GLY	14.7
1	G	74	SER	11.6
1	G	70	ALA	10.5
1	G	95	TYR	8.2
1	B	34	PRO	8.0
1	C	104	ALA	7.7
1	G	68	GLY	7.0
1	B	36	TYR	5.8
1	H	26	LEU	5.6
1	H	1	PRO	5.6
1	G	91	PRO	5.4
1	G	75	TYR	5.3
1	E	114	ALA	5.3
1	C	108	TRP	5.2
1	G	89	ILE	5.2

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Mol	Chain	Res	Type	RSRZ
1	C	106	VAL	4.9
1	E	103	ALA	4.8
1	G	94	VAL	4.8
1	G	84	ALA	4.7
1	G	78	LEU	4.6
1	G	76	SER	4.5
1	G	83	LEU	4.5
1	C	105	ASN	4.5
1	C	29	ALA	4.3
1	E	95	TYR	4.3
1	H	37	ILE	4.1
1	F	49	PHE	4.0
1	D	108	TRP	4.0
1	G	77	LYS	4.0
1	G	73	ARG	4.0
1	H	67	ILE	3.9
1	H	30	THR	3.8
1	G	98	TYR	3.8
1	G	72	ASN	3.7
1	I	106	VAL	3.6
1	G	71	GLN	3.5
1	F	64	ILE	3.5
1	B	31	GLY	3.4
1	D	114	ALA	3.3
1	F	113	PHE	3.3
1	C	114	ALA	3.2
1	I	48	ALA	3.2
1	G	28	GLN	3.2
1	H	3	PHE	3.1
1	H	61	LEU	3.1
1	H	38	ALA	3.1
1	H	2	MET	3.1
1	H	33	PRO	3.1
1	H	101	MET	3.0
1	G	58	LEU	3.0
1	B	70	ALA	2.9
1	G	9	VAL	2.9
1	H	95	TYR	2.9
1	G	50	GLY	2.8
1	H	97	ASN	2.8
1	B	35	GLN	2.8
1	D	101	MET	2.8

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Mol	Chain	Res	Type	RSRZ
1	D	64	ILE	2.8
1	F	95	TYR	2.8
1	B	69	GLY	2.7
1	H	80	CYS	2.7
1	E	65	GLY	2.7
1	I	36	TYR	2.7
1	I	102	ASN	2.7
1	B	68	GLY	2.7
1	I	108	TRP	2.6
1	G	100	ASP	2.6
1	H	75	TYR	2.6
1	B	28	GLN	2.6
1	I	104	ALA	2.6
1	C	64	ILE	2.5
1	E	104	ALA	2.5
1	H	73	ARG	2.4
1	E	70	ALA	2.4
1	F	99	TYR	2.4
1	G	85	GLU	2.4
1	G	29	ALA	2.3
1	F	77	LYS	2.3
1	G	88	ARG	2.3
1	G	97	ASN	2.3
1	H	111	SER	2.3
1	G	26	LEU	2.2
1	G	99	TYR	2.2
1	H	36	TYR	2.2
1	H	99	TYR	2.2
1	G	49	PHE	2.2
1	F	103	ALA	2.2
1	I	67	ILE	2.2
1	H	59	CYS	2.2
1	H	81	GLY	2.2
1	H	29	ALA	2.1
1	B	67	ILE	2.1
1	G	79	LEU	2.1
1	H	34	PRO	2.1
1	G	96	ILE	2.1
1	H	49	PHE	2.1
1	D	65	GLY	2.1
1	G	53	SER	2.1
1	G	87	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	G	57	ALA	2.1
1	H	88	ARG	2.0
1	I	107	GLY	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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	CL	E	201	1/1	0.84	0.18	100,100,100,100	0
2	CL	C	201	1/1	0.85	0.17	85,85,85,85	0
2	CL	D	203	1/1	0.90	0.33	76,76,76,76	0
2	CL	C	202	1/1	0.92	0.28	61,61,61,61	0
2	CL	D	201	1/1	0.95	0.43	55,55,55,55	0
2	CL	I	201	1/1	0.97	0.35	58,58,58,58	0
2	CL	A	201	1/1	0.98	0.37	66,66,66,66	0
2	CL	D	202	1/1	0.98	0.46	53,53,53,53	0

6.5 Other polymers [i](#)

There are no such residues in this entry.