Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 02:27 PM GMT

PDB ID	:	3ZJG
Title	:	A20 OTU domain with irreversibly oxidised Cys103 from 60 min H2O2 soak.
Authors	:	Kulathu, Y.; Garcia, F.J.; Mevissen, T.E.T.; Busch, M.; Arnaudo, N.; Carroll, K.S.; Barford, D.; Komander, D.
Deposited on	:	2013-01-17
Resolution	:	1.92 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:

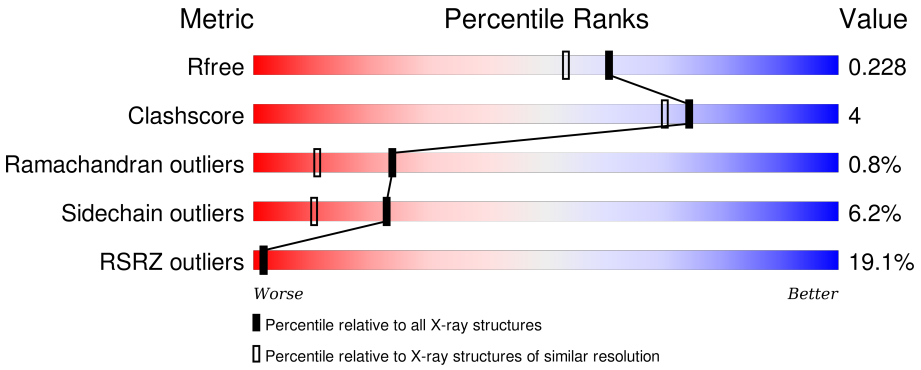
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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 1.92 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	5832 (1.94-1.90)
Clashscore	102246	6540 (1.94-1.90)
Ramachandran outliers	100387	6464 (1.94-1.90)
Sidechain outliers	100360	6465 (1.94-1.90)
RSRZ outliers	91569	5846 (1.94-1.90)

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	366	17% 78% 9% • 11%
2	B	366	17% 78% 10% • 10%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5495 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 TUMOR NECROSIS FACTOR ALPHA-INDUCED PROTEIN 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	327	Total	C	N	O	S	0	6	0
			2622	1687	450	469	16			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	114	SER	GLY	ENGINEERED MUTATION	UNP P21580

- Molecule 2 is a protein called TUMOR NECROSIS FACTOR ALPHA-INDUCED PROTEIN 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	328	Total	C	N	O	S	0	2	0
			2611	1680	454	462	15			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	114	SER	GLY	ENGINEERED MUTATION	UNP P21580

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	3	Total	Cl	0	0
			3	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	136	Total	O	0	0
			136	136		

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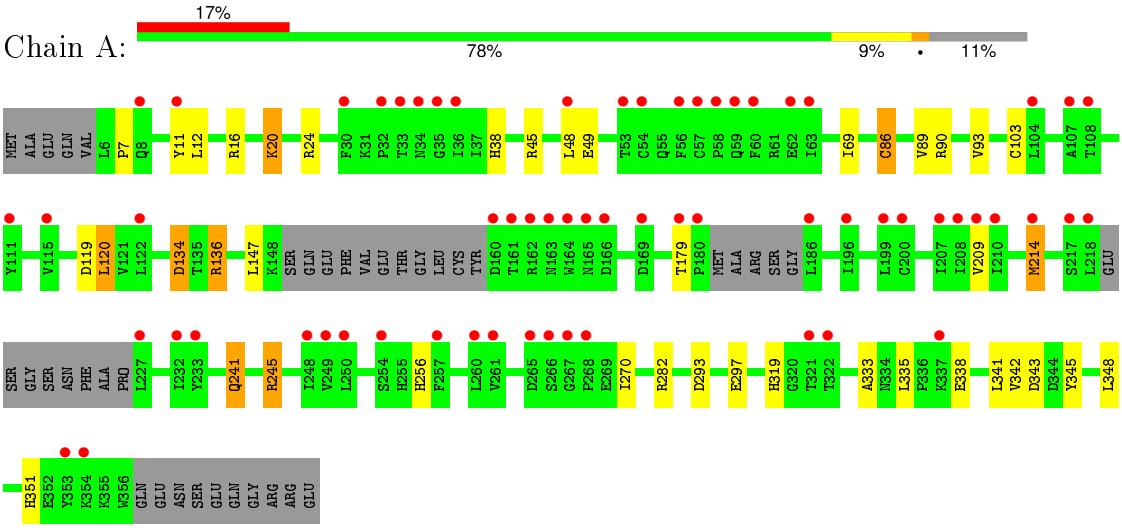
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	123	Total	O	0	0
			123	123		

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.

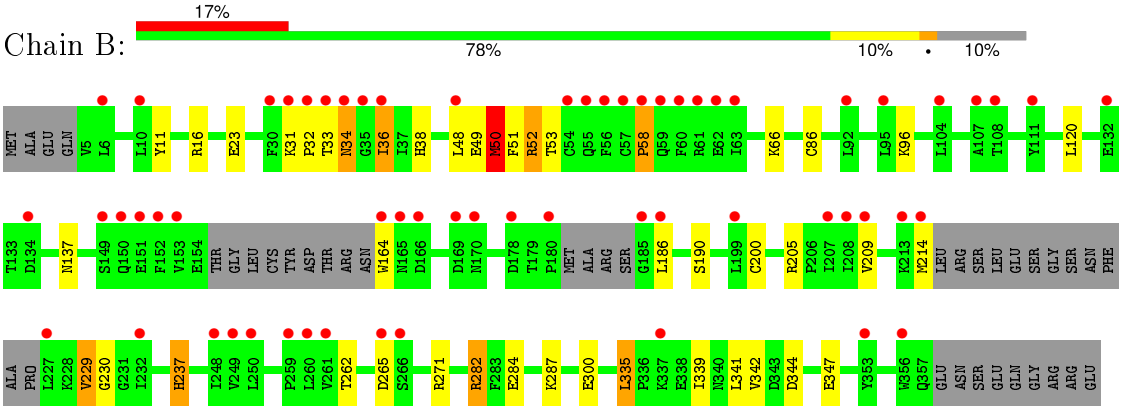
- Molecule 1: TUMOR NECROSIS FACTOR ALPHA-INDUCED PROTEIN 3

Chain A:



- Molecule 2: TUMOR NECROSIS FACTOR ALPHA-INDUCED PROTEIN 3

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	43.80Å 69.17Å 85.00Å 98.57° 100.51° 97.10°	Depositor
Resolution (Å)	34.00 – 1.92 34.00 – 1.92	Depositor EDS
% Data completeness (in resolution range)	95.3 (34.00-1.92) 89.9 (34.00-1.92)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.95 (at 1.92Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.184 , 0.220 0.194 , 0.228	Depositor DCC
R_{free} test set	3528 reflections (5.33%)	DCC
Wilson B-factor (Å^2)	31.6	Xtriage
Anisotropy	0.320	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 67.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Outliers	0 of 69728 reflections	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	5495	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 6.61% 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

Bond lengths and bond angles in the following residue types are not validated in this section: CSD, OCS, 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	0.87	3/2678 (0.1%)	0.87	3/3641 (0.1%)
2	B	0.75	1/2666 (0.0%)	0.79	1/3622 (0.0%)
All	All	0.81	4/5344 (0.1%)	0.83	4/7263 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	86[A]	CYS	CB-SG	-7.06	1.70	1.82
1	A	86[B]	CYS	CB-SG	-7.06	1.70	1.82
2	B	86	CYS	CB-SG	6.92	1.94	1.82
1	A	209	VAL	CB-CG1	5.54	1.64	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	245	ARG	NE-CZ-NH2	-6.74	116.93	120.30
2	B	50	MET	CG-SD-CE	6.37	110.39	100.20
1	A	245	ARG	NE-CZ-NH1	5.56	123.08	120.30
1	A	45	ARG	NE-CZ-NH2	-5.12	117.74	120.30

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	2622	0	2508	18	0
2	B	2611	0	2491	26	0
3	B	3	0	0	0	0
4	A	136	0	0	0	0
4	B	123	0	0	1	0
All	All	5495	0	4999	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 4.

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)
2:B:66:LYS:O	2:B:96:LYS:NZ	2.07	0.88
2:B:50:MET:HE2	2:B:51:PHE:H	1.51	0.76
2:B:237:HIS:HD2	4:B:2004:HOH:O	1.78	0.66
2:B:34:ASN:HD21	2:B:36:ILE:HG22	1.60	0.66
2:B:137:ASN:HD22	2:B:237:HIS:CE1	2.14	0.65
2:B:11:TYR:HA	2:B:341:LEU:HD23	1.79	0.65
1:A:134:ASP:OD1	1:A:136:ARG:HD3	1.97	0.63
2:B:282:ARG:NE	2:B:284:GLU:OE2	2.32	0.62
2:B:52:ARG:HE	2:B:53:THR:H	1.45	0.62
2:B:34:ASN:ND2	2:B:36:ILE:HG22	2.17	0.58
1:A:16:ARG:HG2	2:B:344:ASP:OD1	2.04	0.57
1:A:214[A]:MET:SD	1:A:214[A]:MET:N	2.75	0.57
1:A:49:GLU:HB2	1:A:333:ALA:HB2	1.86	0.56
2:B:52:ARG:HE	2:B:53:THR:N	2.03	0.56
1:A:7:PRO:HG2	1:A:345:TYR:CE2	2.42	0.55
2:B:11:TYR:HA	2:B:341:LEU:CD2	2.37	0.54
1:A:351:HIS:ND1	2:B:23:GLU:OE2	2.39	0.54
1:A:348:LEU:HD11	2:B:16:ARG:HA	1.91	0.51
2:B:50:MET:CE	2:B:50:MET:HA	2.41	0.51
2:B:214:MET:SD	2:B:287:LYS:HE3	2.52	0.50
1:A:241:GLN:H	1:A:241:GLN:CD	2.15	0.50
1:A:270:ILE:HG13	1:A:270:ILE:O	2.13	0.49
2:B:33:THR:O	2:B:34:ASN:HB3	2.12	0.48
2:B:214:MET:HB2	2:B:230:GLY:HA3	1.93	0.48
2:B:49:GLU:OE2	2:B:271:ARG:NH1	2.47	0.47
2:B:335:LEU:HD22	2:B:339:ILE:HG13	1.96	0.47
1:A:103:CSD:OD1	1:A:256:HIS:HA	2.15	0.47
2:B:48:LEU:HD11	2:B:342:VAL:HG21	1.97	0.46
2:B:49:GLU:OE2	2:B:262[A]:THR:OG1	2.32	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:20:LYS:HZ3	1:A:24:ARG:HD2	1.81	0.45
1:A:69:ILE:HD12	1:A:93[B]:VAL:CG2	2.47	0.45
2:B:209:VAL:HG11	2:B:229:VAL:HG22	1.99	0.44
1:A:293:ASP:O	1:A:297:GLU:HG2	2.17	0.44
1:A:20:LYS:NZ	1:A:24:ARG:HD2	2.32	0.44
2:B:200:CYS:HB2	2:B:205:ARG:O	2.16	0.44
2:B:32:PRO:HG2	2:B:36:ILE:HG12	2.01	0.43
1:A:11:TYR:HA	1:A:341:LEU:HD13	2.02	0.42
1:A:119:ASP:O	1:A:120:LEU:HB2	2.20	0.42
2:B:50:MET:HE2	2:B:51:PHE:N	2.27	0.41
1:A:48:LEU:HD11	1:A:342:VAL:CG2	2.51	0.40
1:A:48:LEU:HD11	1:A:342:VAL:HG21	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	324/366 (88%)	315 (97%)	7 (2%)	2 (1%)	30 16
2	B	321/366 (88%)	312 (97%)	6 (2%)	3 (1%)	21 9
All	All	645/732 (88%)	627 (97%)	13 (2%)	5 (1%)	24 11

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	319	HIS
2	B	34	ASN
1	A	338	GLU
2	B	265	ASP
2	B	58	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	272/335 (81%)	253 (93%)	19 (7%)	19 8
2	B	267/335 (80%)	251 (94%)	16 (6%)	24 11
All	All	539/670 (80%)	504 (94%)	35 (6%)	23 9

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	LEU
1	A	20	LYS
1	A	38	HIS
1	A	86[A]	CYS
1	A	86[B]	CYS
1	A	89	VAL
1	A	90	ARG
1	A	120	LEU
1	A	134	ASP
1	A	136	ARG
1	A	147	LEU
1	A	179	THR
1	A	214[A]	MET
1	A	214[B]	MET
1	A	241	GLN
1	A	245	ARG
1	A	282	ARG
1	A	335	LEU
1	A	343	ASP
2	B	31	LYS
2	B	36	ILE
2	B	38	HIS
2	B	50	MET
2	B	52	ARG
2	B	58	PRO
2	B	120	LEU
2	B	164	TRP

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Mol	Chain	Res	Type
2	B	186	LEU
2	B	190	SER
2	B	229	VAL
2	B	237	HIS
2	B	282	ARG
2	B	300	GLU
2	B	335	LEU
2	B	347	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	34	ASN
2	B	237	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	CSD	A	103	1	3,7,8	1.00	0	3,8,10	1.25	0
2	OCS	B	103	2	7,8,9	1.65	1 (14%)	7,11,13	1.60	3 (42%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	CSD	A	103	1	-	1/2/6/8	0/0/0/0
2	OCS	B	103	2	-	0/4/7/9	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	103	OCS	CB-SG	3.51	1.83	1.77

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	103	OCS	O-C-CA	-2.32	119.46	125.49
2	B	103	OCS	OD3-SG-CB	2.26	108.85	106.94
2	B	103	OCS	OD1-SG-CB	2.29	108.87	106.94

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	103	CSD	CA-CB-SG-OD1

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	103	CSD	1	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 3 ligands modelled in this entry, 3 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

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	326/366 (89%)	0.73	64 (19%) 1 2	16, 40, 77, 97	0
2	B	327/366 (89%)	0.78	61 (18%) 2 2	18, 45, 81, 100	0
All	All	653/732 (89%)	0.76	125 (19%) 2 2	16, 42, 80, 100	0

All (125) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	58	PRO	7.5
2	B	33	THR	6.7
1	A	266	SER	6.6
2	B	152	PHE	6.2
1	A	58	PRO	5.8
2	B	166	ASP	5.7
1	A	227	LEU	5.4
2	B	60	PHE	5.3
2	B	57	CYS	5.2
1	A	161	THR	5.1
1	A	54	CYS	4.9
1	A	33	THR	4.9
1	A	56	PHE	4.9
2	B	134	ASP	4.8
1	A	63	ILE	4.8
2	B	248	ILE	4.8
2	B	150	GLN	4.7
1	A	186	LEU	4.4
2	B	213	LYS	4.4
2	B	164	TRP	4.4
1	A	207	ILE	4.4
1	A	214[A]	MET	4.4
1	A	59	GLN	4.4
1	A	199	LEU	4.4

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Mol	Chain	Res	Type	RSRZ
1	A	321	THR	4.3
2	B	54	CYS	4.3
1	A	179	THR	4.3
1	A	57	CYS	4.2
2	B	56	PHE	4.1
2	B	59	GLN	4.1
2	B	207	ILE	4.0
2	B	180	PRO	3.9
2	B	153	VAL	3.9
2	B	249	VAL	3.9
1	A	8	GLN	3.9
2	B	266	SER	3.9
1	A	163	ASN	3.8
1	A	180	PRO	3.6
1	A	162	ARG	3.6
2	B	63	ILE	3.6
1	A	353	TYR	3.6
1	A	196	ILE	3.5
2	B	36	ILE	3.5
2	B	199	LEU	3.5
1	A	32	PRO	3.4
1	A	250	LEU	3.4
2	B	32	PRO	3.4
1	A	248	ILE	3.4
2	B	186	LEU	3.4
1	A	267	GLY	3.3
1	A	60	PHE	3.3
2	B	250	LEU	3.3
1	A	108	THR	3.2
1	A	249	VAL	3.2
2	B	34	ASN	3.2
2	B	165	ASN	3.1
1	A	217	SER	3.1
2	B	31	LYS	3.0
1	A	261[A]	VAL	3.0
2	B	108	THR	3.0
2	B	337	LYS	3.0
1	A	122	LEU	3.0
2	B	111	TYR	3.0
1	A	107	ALA	3.0
1	A	208	ILE	2.9
1	A	268	PRO	2.9

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Mol	Chain	Res	Type	RSRZ
2	B	208	ILE	2.9
2	B	30	PHE	2.9
1	A	104	LEU	2.8
1	A	11	TYR	2.8
1	A	164	TRP	2.8
1	A	35	GLY	2.8
2	B	356	TRP	2.8
1	A	166	ASP	2.7
1	A	30	PHE	2.7
2	B	48	LEU	2.7
2	B	209	VAL	2.7
1	A	233	TYR	2.7
1	A	265	ASP	2.6
1	A	169	ASP	2.6
2	B	261	VAL	2.6
2	B	151	GLU	2.6
2	B	169	ASP	2.6
1	A	115	VAL	2.6
1	A	209	VAL	2.6
1	A	165	ASN	2.5
1	A	111	TYR	2.4
2	B	55	GLN	2.4
2	B	35	GLY	2.4
2	B	353	TYR	2.4
2	B	170	ASN	2.3
2	B	227	LEU	2.3
2	B	178	ASP	2.3
2	B	132	GLU	2.3
1	A	200	CYS	2.3
1	A	218	LEU	2.3
1	A	34	ASN	2.3
1	A	160	ASP	2.3
2	B	61	ARG	2.3
1	A	257	PHE	2.3
1	A	232	ILE	2.3
2	B	62	GLU	2.2
2	B	265	ASP	2.2
2	B	185	GLY	2.2
2	B	6	LEU	2.2
2	B	10	LEU	2.2
1	A	53	THR	2.2
2	B	107	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
2	B	232	ILE	2.2
1	A	260	LEU	2.2
2	B	104	LEU	2.2
1	A	354	LYS	2.2
1	A	322	THR	2.2
2	B	260	LEU	2.2
1	A	36	ILE	2.1
1	A	337	LYS	2.1
1	A	254	SER	2.1
2	B	259	PRO	2.1
1	A	48	LEU	2.1
2	B	149	SER	2.1
2	B	214	MET	2.1
2	B	92	LEU	2.1
1	A	62	GLU	2.1
1	A	210[A]	ILE	2.0
2	B	95	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} 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	LLDF	B-factors(Å^2)	Q<0.9
1	CSD	A	103	8/9	0.97	0.10	-	18,23,45,48	0
2	OCS	B	103	9/10	0.94	0.12	-	34,35,52,54	0

6.3 Carbohydrates (i)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} 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	LLDF	B-factors(Å^2)	Q<0.9
3	CL	B	1359	1/1	1.00	0.07	-0.88	27,27,27,27	0
3	CL	B	1358	1/1	0.99	0.07	-0.96	23,23,23,23	0
3	CL	B	1360	1/1	0.99	0.04	-1.93	28,28,28,28	0

6.5 Other polymers (i)

There are no such residues in this entry.