wwPDB X-ray Structure Validation Summary Report (i)

May 26, 2020 – 06:20 am BST

PDB ID	:	5DPW
Title	:	Crystal structure of PLEKHM1 LIR in complex with human LC3C_8-125
Authors	:	Ravichandran, A.C.; Suzuki, H.; Dobson, R.C.J.
Deposited on	:	2015-09-14
Resolution	:	2.19 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
https://www.wwpdb.org/validation/2017/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:

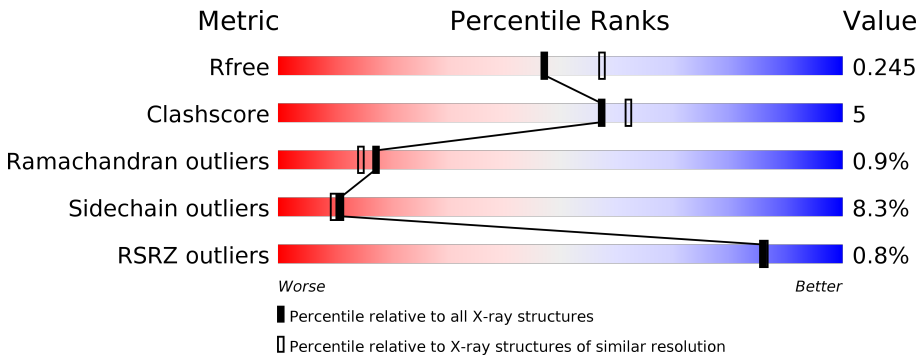
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 2.19 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	6864 (2.20-2.16)
Clashscore	141614	7689 (2.20-2.16)
Ramachandran outliers	138981	7564 (2.20-2.16)
Sidechain outliers	138945	7564 (2.20-2.16)
RSRZ outliers	127900	6738 (2.20-2.16)

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	118	79% 17% • •
1	C	118	2% 76% 17% • •
1	E	118	78% 19% •
1	G	118	78% 18% • •
1	I	118	% 73% 23% • •
1	K	118	% 83% 14% • •

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	M	118	75% 20%
1	O	118	86% 9%
2	B	14	43% 21% 36%
2	D	14	43% 7% 14% 36%
2	F	14	7% 50% 7% 7% 36%
2	H	14	7% 43% 21% 36%
2	J	14	7% 57% 7% 36%
2	L	14	7% 57% 7% 36%
2	N	14	29% 29% 7% 36%
2	P	14	43% 21% 36%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 16830 atoms, of which 8370 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 Microtubule-associated proteins 1A/1B light chain 3C.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	115	1924	614	974	161	170	5	0	0	0
1	C	115	1954	625	992	161	171	5	0	2	0
1	E	115	1926	614	976	161	170	5	0	0	0
1	G	115	1926	614	976	161	170	5	0	0	0
1	I	115	1970	631	996	163	175	5	0	5	0
1	K	115	1926	614	976	161	170	5	0	0	0
1	M	115	1926	614	976	161	170	5	0	0	0
1	O	115	1926	614	976	161	170	5	0	0	0

- Molecule 2 is a protein called Pleckstrin homology domain-containing family M member 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	H	N	O			
2	B	9	149	53	66	12	18	0	0	0
2	D	9	149	53	66	12	18	0	0	0
2	F	9	149	53	66	12	18	0	0	0
2	H	9	149	53	66	12	18	0	0	0
2	J	9	149	53	66	12	18	0	0	0
2	L	9	149	53	66	12	18	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	H	N	O			
2	N	9	149	53	66	12	18	0	0	0
			Total	C	H	N	O			
2	P	9	149	53	66	12	18	0	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	26	26	26	0	0
			Total	O		
3	B	2	2	2	0	0
			Total	O		
3	C	8	8	8	0	0
			Total	O		
3	D	2	2	2	0	0
			Total	O		
3	E	23	23	23	0	0
			Total	O		
3	F	2	2	2	0	0
			Total	O		
3	G	10	10	10	0	0
			Total	O		
3	H	1	1	1	0	0
			Total	O		
3	I	14	14	14	0	0
			Total	O		
3	J	1	1	1	0	0
			Total	O		
3	K	14	14	14	0	0
			Total	O		
3	L	2	2	2	0	0
			Total	O		
3	M	22	22	22	0	0
			Total	O		
3	O	28	28	28	0	0
			Total	O		
3	P	5	5	5	0	0

3 Residue-property plots (i)

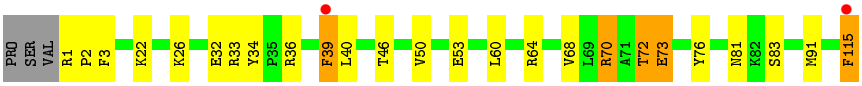
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: Microtubule-associated proteins 1A/1B light chain 3C

Chain A:

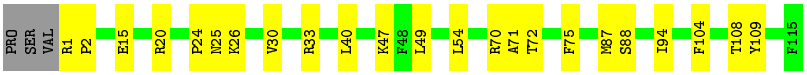
- Molecule 1: Microtubule-associated proteins 1A/1B light chain 3C

Chain C:



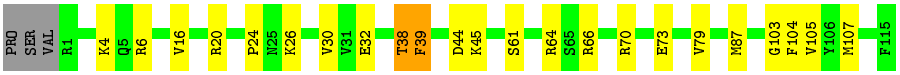
- Molecule 1: Microtubule-associated proteins 1A/1B light chain 3C

Chain E:



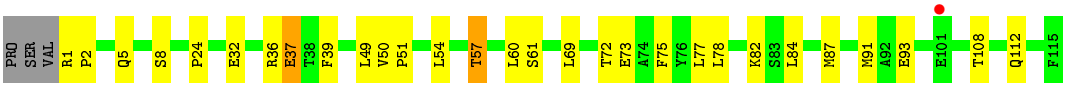
- Molecule 1: Microtubule-associated proteins 1A/1B light chain 3C

Chain G:



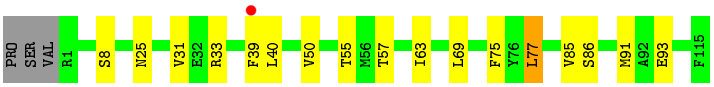
- Molecule 1: Microtubule-associated proteins 1A/1B light chain 3C

Chain I:



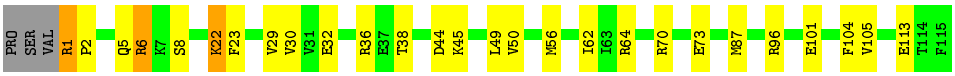
- Molecule 1: Microtubule-associated proteins 1A/1B light chain 3C

Chain K:



- Molecule 1: Microtubule-associated proteins 1A/1B light chain 3C

Chain M:

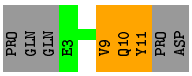


- Molecule 1: Microtubule-associated proteins 1A/1B light chain 3C

Chain O:

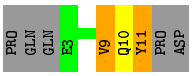
- Molecule 2: Pleckstrin homology domain-containing family M member 1

Chain B:



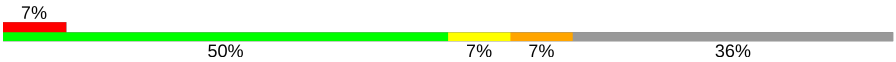
- Molecule 2: Pleckstrin homology domain-containing family M member 1

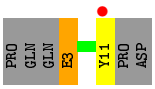
Chain D:



- Molecule 2: Pleckstrin homology domain-containing family M member 1

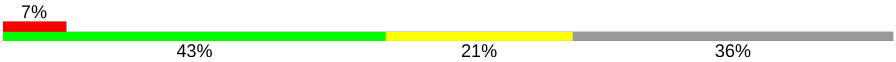
Chain F:

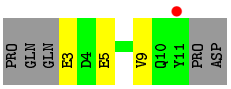




- Molecule 2: Pleckstrin homology domain-containing family M member 1

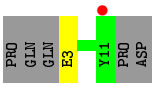
Chain H:





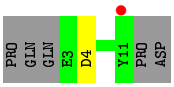
- Molecule 2: Pleckstrin homology domain-containing family M member 1

Chain J:

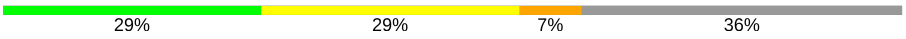


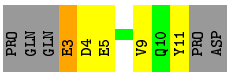
- Molecule 2: Pleckstrin homology domain-containing family M member 1

Chain L:

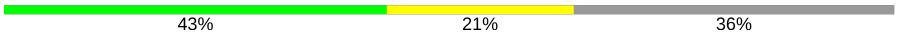


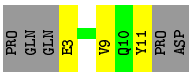
- Molecule 2: Pleckstrin homology domain-containing family M member 1

Chain N: 



- Molecule 2: Pleckstrin homology domain-containing family M member 1

Chain P: 



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	54.14Å 73.22Å 89.05Å 89.96° 89.99° 77.31°	Depositor
Resolution (Å)	38.61 – 2.19 38.61 – 2.18	Depositor EDS
% Data completeness (in resolution range)	98.6 (38.61-2.19) 91.5 (38.61-2.18)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.74 (at 2.18Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.200 , 0.246 0.201 , 0.245	Depositor DCC
R_{free} test set	1393 reflections (2.04%)	wwPDB-VP
Wilson B-factor (Å^2)	32.3	Xtriage
Anisotropy	0.805	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 35.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.468 for -h,-k,l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	16830	wwPDB-VP
Average B, all atoms (Å^2)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 75.82 % 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 1.1742e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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 (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	0.28	0/970	0.44	0/1308
1	C	0.27	0/989	0.49	0/1334
1	E	0.25	0/970	0.42	0/1308
1	G	0.26	0/970	0.47	0/1308
1	I	0.28	0/1017	0.48	0/1371
1	K	0.27	0/970	0.46	0/1308
1	M	0.26	0/970	0.45	0/1308
1	O	0.26	0/970	0.45	0/1308
2	B	0.29	0/85	0.43	0/116
2	D	0.22	0/85	0.40	0/116
2	F	0.25	0/85	0.39	0/116
2	H	0.25	0/85	0.47	0/116
2	J	0.27	0/85	0.43	0/116
2	L	0.29	0/85	0.40	0/116
2	N	0.34	0/85	0.42	0/116
2	P	0.28	0/85	0.44	0/116
All	All	0.27	0/8506	0.46	0/11481

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	950	974	978	10	1
1	C	962	992	994	13	1
1	E	950	976	978	11	0
1	G	950	976	978	13	0
1	I	974	996	980	11	0
1	K	950	976	978	6	1
1	M	950	976	978	13	0
1	O	950	976	978	7	1
2	B	83	66	66	2	0
2	D	83	66	66	2	0
2	F	83	66	66	1	0
2	H	83	66	66	2	0
2	J	83	66	66	0	0
2	L	83	66	66	0	0
2	N	83	66	66	4	0
2	P	83	66	66	2	0
3	A	26	0	0	1	0
3	B	2	0	0	0	0
3	C	8	0	0	0	0
3	D	2	0	0	0	0
3	E	23	0	0	1	0
3	F	2	0	0	1	0
3	G	10	0	0	1	0
3	H	1	0	0	0	0
3	I	14	0	0	0	0
3	J	1	0	0	0	0
3	K	14	0	0	0	0
3	L	2	0	0	0	0
3	M	22	0	0	1	0
3	O	28	0	0	0	0
3	P	5	0	0	0	0
All	All	8460	8370	8370	81	2

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.

The worst 5 of 81 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:70:ARG:NH1	1:C:53:GLU:OE2	1.76	1.18
1:O:6:ARG:NH1	1:O:32:GLU:OE2	1.96	0.98
1:A:26:LYS:NZ	2:B:9:VAL:O	2.00	0.95

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:33:ARG:NH1	1:C:40:LEU:O	2.03	0.91
1:K:93:GLU:OE2	1:M:96:ARG:NH2	2.04	0.88

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:85:VAL:O	1:O:76:TYR:HH[1_545]	1.58	0.02
1:A:53:GLU:OE2	1:C:70:ARG:NH1[1_565]	2.18	0.02

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	113/118 (96%)	109 (96%)	2 (2%)	2 (2%)	8	5
1	C	115/118 (98%)	107 (93%)	7 (6%)	1 (1%)	17	15
1	E	113/118 (96%)	108 (96%)	4 (4%)	1 (1%)	17	15
1	G	113/118 (96%)	108 (96%)	4 (4%)	1 (1%)	17	15
1	I	117/118 (99%)	112 (96%)	4 (3%)	1 (1%)	17	15
1	K	113/118 (96%)	109 (96%)	3 (3%)	1 (1%)	17	15
1	M	113/118 (96%)	109 (96%)	3 (3%)	1 (1%)	17	15
1	O	113/118 (96%)	110 (97%)	3 (3%)	0	100	100
2	B	7/14 (50%)	6 (86%)	1 (14%)	0	100	100
2	D	7/14 (50%)	6 (86%)	1 (14%)	0	100	100
2	F	7/14 (50%)	7 (100%)	0	0	100	100
2	H	7/14 (50%)	5 (71%)	1 (14%)	1 (14%)	0	0
2	J	7/14 (50%)	6 (86%)	1 (14%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	L	7/14 (50%)	6 (86%)	1 (14%)	0	100	100
2	N	7/14 (50%)	7 (100%)	0	0	100	100
2	P	7/14 (50%)	7 (100%)	0	0	100	100
All	All	966/1056 (92%)	922 (95%)	35 (4%)	9 (1%)	17	15

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	5	GLU
1	A	71	ALA
1	A	72	THR
1	G	39	PHE
1	K	39	PHE

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	105/108 (97%)	98 (93%)	7 (7%)	16	16
1	C	107/108 (99%)	95 (89%)	12 (11%)	6	4
1	E	105/108 (97%)	101 (96%)	4 (4%)	33	39
1	G	105/108 (97%)	100 (95%)	5 (5%)	25	29
1	I	110/108 (102%)	94 (86%)	16 (14%)	3	2
1	K	105/108 (97%)	98 (93%)	7 (7%)	16	16
1	M	105/108 (97%)	95 (90%)	10 (10%)	8	7
1	O	105/108 (97%)	100 (95%)	5 (5%)	25	29
2	B	9/14 (64%)	6 (67%)	3 (33%)	0	0
2	D	9/14 (64%)	7 (78%)	2 (22%)	1	0
2	F	9/14 (64%)	7 (78%)	2 (22%)	1	0
2	H	9/14 (64%)	9 (100%)	0	100	100
2	J	9/14 (64%)	8 (89%)	1 (11%)	6	4

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	L	9/14 (64%)	8 (89%)	1 (11%)	6 4
2	N	9/14 (64%)	7 (78%)	2 (22%)	1 0
2	P	9/14 (64%)	7 (78%)	2 (22%)	1 0
All	All	919/976 (94%)	840 (91%)	79 (9%)	11 9

5 of 79 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	5	GLN
1	I	72	THR
1	O	36	ARG
1	I	8	SER
1	I	57	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 (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	115/118 (97%)	0.00	0 100 100	26, 41, 74, 91	0
1	C	115/118 (97%)	0.01	2 (1%) 70 70	33, 49, 77, 113	0
1	E	115/118 (97%)	-0.04	0 100 100	25, 41, 77, 87	0
1	G	115/118 (97%)	-0.01	0 100 100	30, 49, 72, 98	0
1	I	115/118 (97%)	0.06	1 (0%) 84 84	27, 44, 67, 110	0
1	K	115/118 (97%)	0.04	1 (0%) 84 84	30, 48, 78, 117	0
1	M	115/118 (97%)	0.02	0 100 100	33, 48, 63, 99	0
1	O	115/118 (97%)	-0.09	0 100 100	29, 46, 67, 86	0
2	B	9/14 (64%)	0.55	0 100 100	57, 62, 96, 99	0
2	D	9/14 (64%)	0.61	0 100 100	57, 67, 98, 100	0
2	F	9/14 (64%)	0.62	1 (11%) 5 5	52, 59, 103, 106	0
2	H	9/14 (64%)	0.68	1 (11%) 5 5	52, 60, 102, 104	0
2	J	9/14 (64%)	0.49	1 (11%) 5 5	45, 59, 91, 96	0
2	L	9/14 (64%)	0.87	1 (11%) 5 5	46, 63, 98, 99	0
2	N	9/14 (64%)	0.26	0 100 100	49, 56, 94, 95	0
2	P	9/14 (64%)	0.26	0 100 100	48, 53, 87, 89	0
All	All	992/1056 (93%)	0.04	8 (0%) 86 86	25, 47, 81, 117	0

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	L	11	TYR	5.5
1	I	101	GLU	4.1
2	H	11	TYR	4.0
1	C	115	PHE	3.7
1	K	39	PHE	3.7

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.