



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 12:34 pm GMT

PDB ID : 5ABV
Title : Complex of D. melanogaster eIF4E with the 4E-binding protein Mextli
Authors : Peter, D.; Weichenrieder, O.
Deposited on : 2015-08-09
Resolution : 2.13 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
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

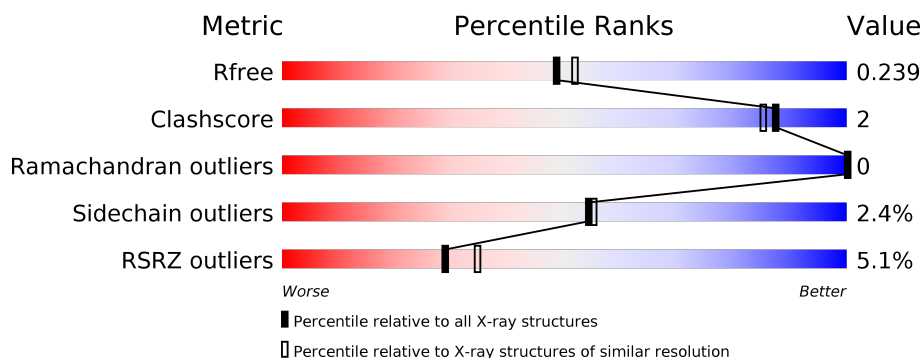
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.13 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}	100719	1915 (2.16-2.12)
Clashscore	112137	2047 (2.16-2.12)
Ramachandran outliers	110173	2020 (2.16-2.12)
Sidechain outliers	110143	2019 (2.16-2.12)
RSRZ outliers	101464	1921 (2.16-2.12)

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	184	<div> <div>5%</div> <div> <div></div> <div>90%</div> <div>8%</div> <div></div> </div> <div></div> </div>
1	C	184	<div> <div>3%</div> <div> <div></div> <div>83%</div> <div>11%</div> <div>5%</div> </div> <div></div> </div>
1	E	184	<div> <div>4%</div> <div> <div></div> <div>86%</div> <div>11%</div> <div></div> </div> <div></div> </div>
1	G	184	<div> <div>8%</div> <div> <div></div> <div>86%</div> <div>9%</div> <div></div> </div> <div></div> </div>
2	B	70	<div> <div>3%</div> <div> <div></div> <div>86%</div> <div>14%</div> </div> <div></div> </div>
2	D	70	<div> <div>6%</div> <div> <div></div> <div>83%</div> <div></div> <div>13%</div> </div> <div></div> </div>

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Mol	Chain	Length	Quality of chain
2	F	70	<div><div><div></div><div></div><div></div></div><div><div>6%</div><div>81%</div><div>16%</div></div></div>
2	H	70	<div><div><div></div><div></div><div></div></div><div><div>4%</div><div>83%</div><div>16%</div></div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7937 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 EUKARYOTIC TRANSLATION INITIATION FACTOR 4E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	179	Total	C	N	O	S	0	0	0
			1465	928	255	275	7			
1	C	174	Total	C	N	O	S	0	0	0
			1427	906	246	268	7			
1	E	179	Total	C	N	O	S	0	0	0
			1465	928	255	275	7			
1	G	176	Total	C	N	O	S	0	0	0
			1444	914	251	272	7			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	65	GLY	-	EXPRESSION TAG	UNP P48598
A	66	PRO	-	EXPRESSION TAG	UNP P48598
A	67	HIS	-	EXPRESSION TAG	UNP P48598
A	68	MET	-	EXPRESSION TAG	UNP P48598
C	65	GLY	-	EXPRESSION TAG	UNP P48598
C	66	PRO	-	EXPRESSION TAG	UNP P48598
C	67	HIS	-	EXPRESSION TAG	UNP P48598
C	68	MET	-	EXPRESSION TAG	UNP P48598
E	65	GLY	-	EXPRESSION TAG	UNP P48598
E	66	PRO	-	EXPRESSION TAG	UNP P48598
E	67	HIS	-	EXPRESSION TAG	UNP P48598
E	68	MET	-	EXPRESSION TAG	UNP P48598
G	65	GLY	-	EXPRESSION TAG	UNP P48598
G	66	PRO	-	EXPRESSION TAG	UNP P48598
G	67	HIS	-	EXPRESSION TAG	UNP P48598
G	68	MET	-	EXPRESSION TAG	UNP P48598

- Molecule 2 is a protein called GH11071P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	60	Total	C	N	O	S	0	0	0
			494	313	81	98	2			
2	D	61	Total	C	N	O	S	0	0	0
			506	319	85	100	2			
2	F	59	Total	C	N	O	S	0	0	0
			494	312	83	97	2			
2	H	59	Total	C	N	O	S	0	0	0
			495	313	83	97	2			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	571	GLY	-	EXPRESSION TAG	UNP Q9VR35
B	572	PRO	-	EXPRESSION TAG	UNP Q9VR35
B	573	HIS	-	EXPRESSION TAG	UNP Q9VR35
B	574	MET	-	EXPRESSION TAG	UNP Q9VR35
B	575	LEU	-	EXPRESSION TAG	UNP Q9VR35
B	576	GLU	-	EXPRESSION TAG	UNP Q9VR35
D	571	GLY	-	EXPRESSION TAG	UNP Q9VR35
D	572	PRO	-	EXPRESSION TAG	UNP Q9VR35
D	573	HIS	-	EXPRESSION TAG	UNP Q9VR35
D	574	MET	-	EXPRESSION TAG	UNP Q9VR35
D	575	LEU	-	EXPRESSION TAG	UNP Q9VR35
D	576	GLU	-	EXPRESSION TAG	UNP Q9VR35
F	571	GLY	-	EXPRESSION TAG	UNP Q9VR35
F	572	PRO	-	EXPRESSION TAG	UNP Q9VR35
F	573	HIS	-	EXPRESSION TAG	UNP Q9VR35
F	574	MET	-	EXPRESSION TAG	UNP Q9VR35
F	575	LEU	-	EXPRESSION TAG	UNP Q9VR35
F	576	GLU	-	EXPRESSION TAG	UNP Q9VR35
H	571	GLY	-	EXPRESSION TAG	UNP Q9VR35
H	572	PRO	-	EXPRESSION TAG	UNP Q9VR35
H	573	HIS	-	EXPRESSION TAG	UNP Q9VR35
H	574	MET	-	EXPRESSION TAG	UNP Q9VR35
H	575	LEU	-	EXPRESSION TAG	UNP Q9VR35
H	576	GLU	-	EXPRESSION TAG	UNP Q9VR35

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	35	Total	O	0	0
			35	35		
3	B	8	Total	O	0	0
			8	8		

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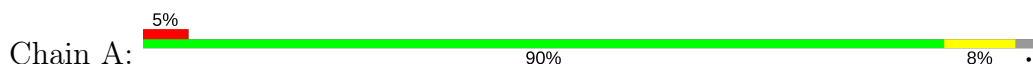
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	26	Total 26	O 26	0	0
3	D	3	Total 3	O 3	0	0
3	E	22	Total 22	O 22	0	0
3	F	4	Total 4	O 4	0	0
3	G	37	Total 37	O 37	0	0
3	H	12	Total 12	O 12	0	0

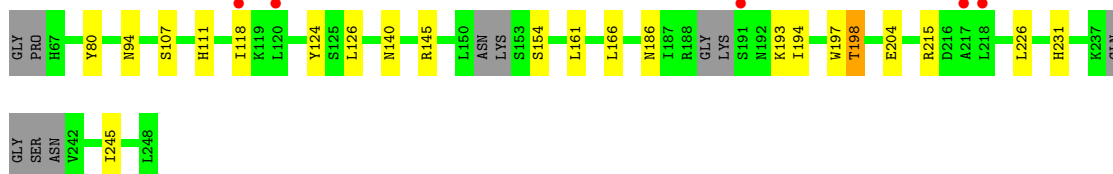
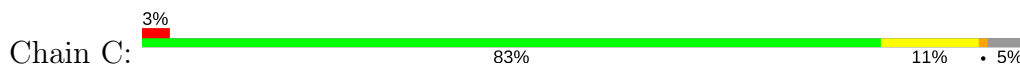
3 Residue-property plots [i](#)

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.

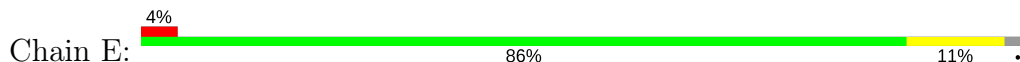
• Molecule 1: EUKARYOTIC TRANSLATION INITIATION FACTOR 4E



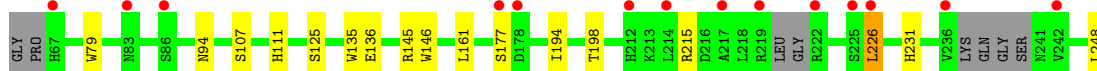
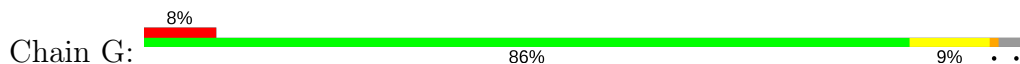
• Molecule 1: EUKARYOTIC TRANSLATION INITIATION FACTOR 4E



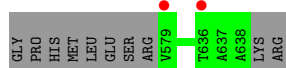
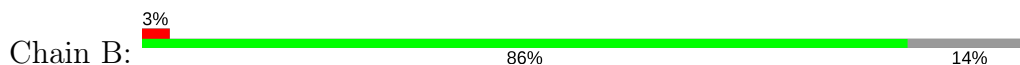
• Molecule 1: EUKARYOTIC TRANSLATION INITIATION FACTOR 4E



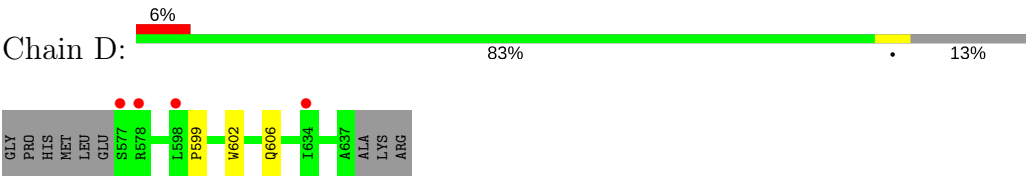
• Molecule 1: EUKARYOTIC TRANSLATION INITIATION FACTOR 4E



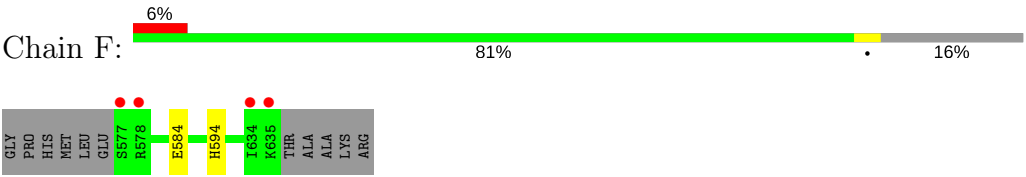
• Molecule 2: GH11071P



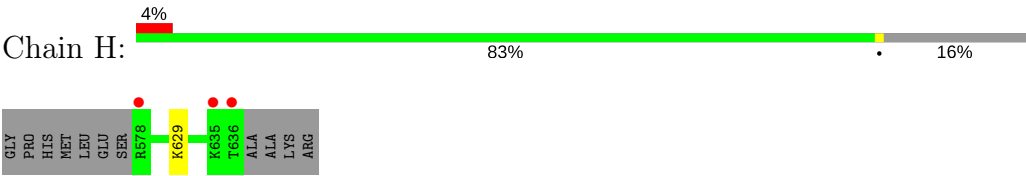
● Molecule 2: GH11071P



● Molecule 2: GH11071P



● Molecule 2: GH11071P



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	65.90Å 82.02Å 84.73Å 90.00° 90.13° 90.00°	Depositor
Resolution (Å)	43.96 – 2.13 43.96 – 2.13	Depositor EDS
% Data completeness (in resolution range)	98.2 (43.96-2.13) 97.6 (43.96-2.13)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.03 (at 2.14Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.192 , 0.232 0.200 , 0.239	Depositor DCC
R_{free} test set	2443 reflections (5.17%)	DCC
Wilson B-factor (Å ²)	41.5	Xtriage
Anisotropy	0.761	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 44.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.000 for -h,l,k 0.000 for -h,-l,-k 0.468 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7937	wwPDB-VP
Average B, all atoms (Å ²)	65.0	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 37.25 % 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 4.4133e-04. 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](#)

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	0.53	0/1498	0.68	0/2024
1	C	0.48	0/1458	0.67	0/1969
1	E	0.49	0/1498	0.67	0/2024
1	G	0.54	0/1476	0.69	0/1994
2	B	0.49	0/507	0.55	0/688
2	D	0.45	0/519	0.56	0/703
2	F	0.46	0/507	0.54	0/686
2	H	0.51	0/508	0.57	0/688
All	All	0.50	0/7971	0.65	0/10776

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	1465	0	1435	5	0
1	C	1427	0	1392	13	0
1	E	1465	0	1435	10	0
1	G	1444	0	1407	8	0
2	B	494	0	469	0	0
2	D	506	0	482	2	0
2	F	494	0	470	1	0
2	H	495	0	472	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	35	0	0	0	0
3	B	8	0	0	0	0
3	C	26	0	0	2	0
3	D	3	0	0	0	0
3	E	22	0	0	0	0
3	F	4	0	0	0	0
3	G	37	0	0	1	0
3	H	12	0	0	0	0
All	All	7937	0	7562	37	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 2.

The worst 5 of 37 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:E:150:LEU:HD11	1:E:161:LEU:HD22	1.63	0.79
1:C:145:ARG:HE	1:C:231:HIS:HE1	1.35	0.74
1:G:215:ARG:HG2	1:G:226:LEU:HD23	1.74	0.69
1:C:198:THR:HG23	3:C:2021:HOH:O	1.95	0.66
1:C:145:ARG:HE	1:C:231:HIS:CE1	2.15	0.65

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	175/184 (95%)	168 (96%)	7 (4%)	0	100	100
1	C	166/184 (90%)	162 (98%)	4 (2%)	0	100	100
1	E	175/184 (95%)	169 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	170/184 (92%)	164 (96%)	6 (4%)	0	100	100
2	B	58/70 (83%)	58 (100%)	0	0	100	100
2	D	59/70 (84%)	59 (100%)	0	0	100	100
2	F	57/70 (81%)	57 (100%)	0	0	100	100
2	H	57/70 (81%)	57 (100%)	0	0	100	100
All	All	917/1016 (90%)	894 (98%)	23 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	162/165 (98%)	157 (97%)	5 (3%)	45	43
1	C	158/165 (96%)	152 (96%)	6 (4%)	38	35
1	E	162/165 (98%)	158 (98%)	4 (2%)	53	53
1	G	160/165 (97%)	156 (98%)	4 (2%)	53	53
2	B	55/64 (86%)	55 (100%)	0	100	100
2	D	57/64 (89%)	57 (100%)	0	100	100
2	F	56/64 (88%)	55 (98%)	1 (2%)	64	66
2	H	56/64 (88%)	55 (98%)	1 (2%)	64	66
All	All	866/916 (94%)	845 (98%)	21 (2%)	54	55

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	215	ARG
1	E	84	ASP
1	G	136	GLU
1	C	198	THR
1	G	198	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	67	HIS
1	G	241	ASN
1	G	151	ASN
1	C	186	ASN
2	F	594	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](#)

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	179/184 (97%)	0.32	9 (5%) 30 36	31, 56, 104, 150	0
1	C	174/184 (94%)	0.36	5 (2%) 52 59	38, 60, 123, 159	0
1	E	179/184 (97%)	0.43	7 (3%) 40 46	38, 60, 121, 167	0
1	G	176/184 (95%)	0.39	14 (7%) 13 17	31, 54, 104, 135	0
2	B	60/70 (85%)	0.02	2 (3%) 47 54	39, 52, 97, 112	0
2	D	61/70 (87%)	0.67	4 (6%) 19 23	40, 78, 116, 133	0
2	F	59/70 (84%)	0.51	4 (6%) 18 22	40, 75, 118, 132	0
2	H	59/70 (84%)	0.22	3 (5%) 29 34	39, 51, 88, 120	0
All	All	947/1016 (93%)	0.37	48 (5%) 29 34	31, 60, 117, 167	0

The worst 5 of 48 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	242	VAL	5.2
1	G	217	ALA	5.0
1	A	222	ARG	4.9
1	E	190	LYS	4.8
2	F	634	ILE	4.3

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.