



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 12, 2024 – 08:35 PM EDT

PDB ID : 3D3K
Title : Crystal structure of human Edc3p
Authors : Ling, S.H.M.
Deposited on : 2008-05-12
Resolution : 2.20 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
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)	:	2.36.2

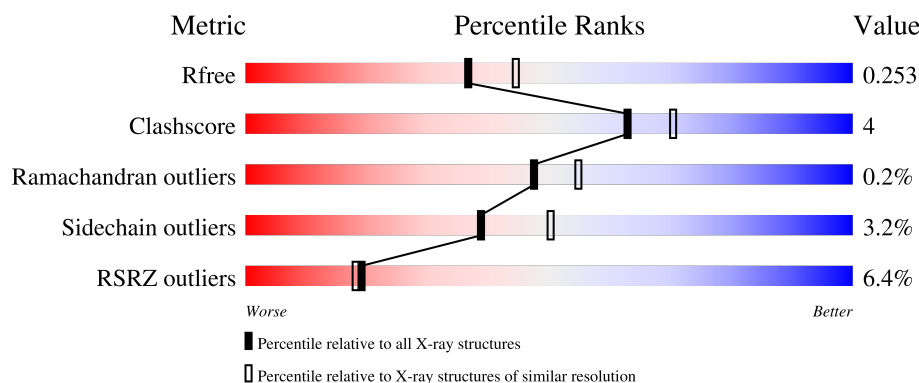
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


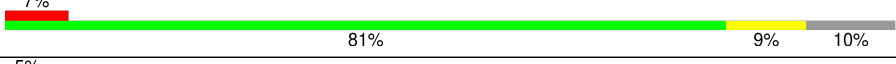


The reported resolution of this entry is 2.20 Å.

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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 of 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	259	
1	B	259	
1	C	259	
1	D	259	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7556 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 Enhancer of mRNA-decapping protein 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	233	Total	C	N	O	S	0	0	0
			1802	1158	312	321	11			
1	B	233	Total	C	N	O	S	0	0	0
			1802	1158	312	321	11			
1	C	233	Total	C	N	O	S	0	0	0
			1802	1158	312	321	11			
1	D	233	Total	C	N	O	S	0	0	0
			1802	1158	312	321	11			

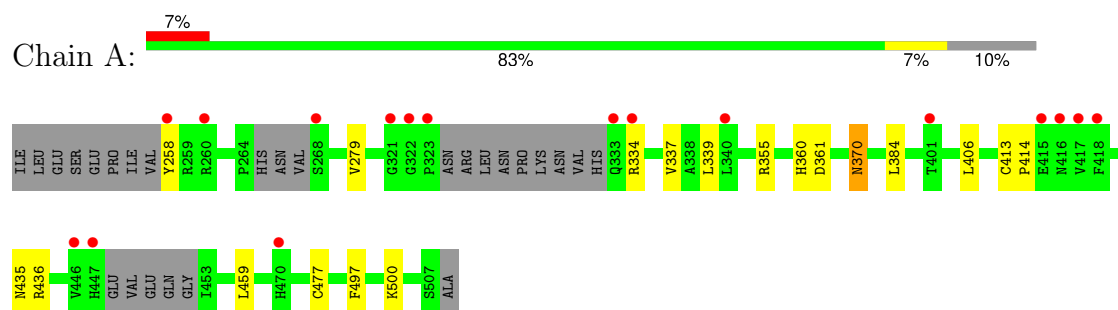
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	89	Total	O	0	0
			89	89		
2	B	94	Total	O	0	0
			94	94		
2	C	84	Total	O	0	0
			84	84		
2	D	81	Total	O	0	0
			81	81		

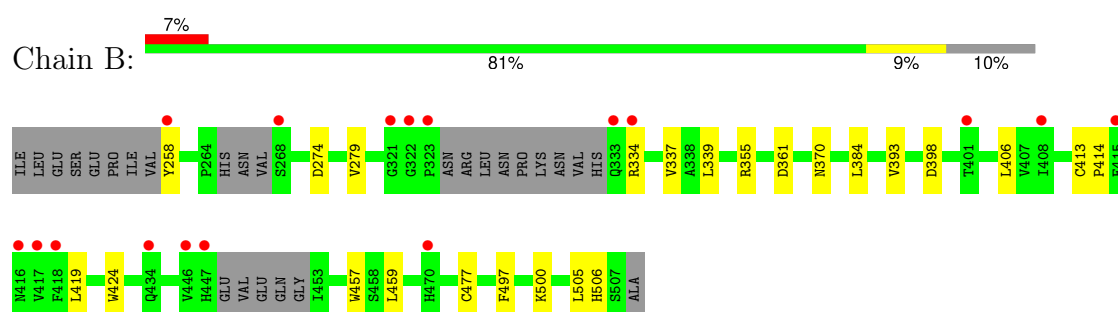
3 Residue-property plots [i](#)

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.

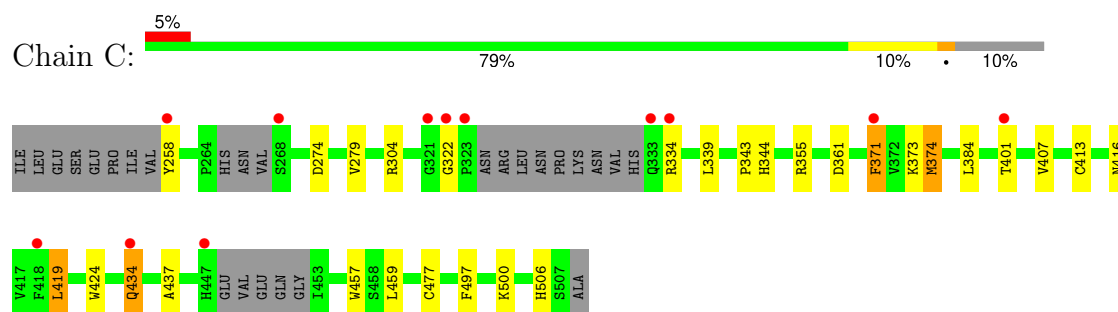
• Molecule 1: Enhancer of mRNA-decapping protein 3



• Molecule 1: Enhancer of mRNA-decapping protein 3

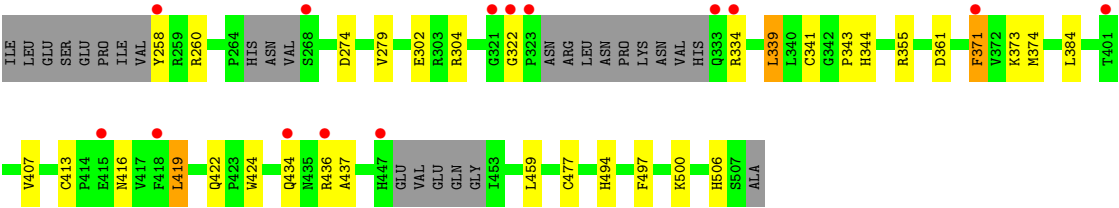


• Molecule 1: Enhancer of mRNA-decapping protein 3



• Molecule 1: Enhancer of mRNA-decapping protein 3





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	94.38Å 169.20Å 163.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.20 19.98 – 2.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (20.00-2.20) 100.0 (19.98-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.03 (at 2.19Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.228 , 0.256 0.223 , 0.253	Depositor DCC
R_{free} test set	3376 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	30.5	Xtriage
Anisotropy	0.101	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 45.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.000 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.000 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7556	wwPDB-VP
Average B, all atoms (Å ²)	28.0	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 49.95 % 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 6.9357e-05. 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	0.41	0/1844	0.53	0/2507
1	B	0.42	0/1844	0.53	0/2507
1	C	0.44	0/1844	0.56	0/2507
1	D	0.41	0/1844	0.56	0/2507
All	All	0.42	0/7376	0.55	0/10028

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	1802	0	1833	10	0
1	B	1802	0	1833	14	0
1	C	1802	0	1833	19	0
1	D	1802	0	1833	23	0
2	A	89	0	0	1	0
2	B	94	0	0	2	0
2	C	84	0	0	4	0
2	D	81	0	0	3	0
All	All	7556	0	7332	63	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 (63) 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:D:371:PHE:HD2	1:D:371:PHE:H	1.07	1.01
1:C:371:PHE:H	1:C:371:PHE:HD2	1.00	0.98
1:C:434:GLN:HG2	2:C:573:HOH:O	1.67	0.93
1:C:371:PHE:HD2	1:C:371:PHE:N	1.68	0.91
1:D:371:PHE:HD2	1:D:371:PHE:N	1.79	0.80
1:C:371:PHE:N	1:C:371:PHE:CD2	2.42	0.79
1:D:422:GLN:HE21	1:D:424:TRP:HE1	1.33	0.76
1:D:334:ARG:HG2	1:D:361:ASP:O	1.85	0.75
1:B:334:ARG:HG2	1:B:361:ASP:O	1.88	0.73
1:A:334:ARG:HG2	1:A:361:ASP:O	1.88	0.72
1:D:434:GLN:HG3	2:D:571:HOH:O	1.92	0.69
1:D:422:GLN:NE2	1:D:424:TRP:HE1	1.95	0.63
1:C:274:ASP:OD1	1:C:506:HIS:HE1	1.82	0.62
1:B:370:ASN:ND2	2:B:512:HOH:O	2.32	0.61
1:D:274:ASP:OD1	1:D:506:HIS:HE1	1.84	0.60
1:D:371:PHE:N	1:D:371:PHE:CD2	2.52	0.59
1:B:355:ARG:HD3	1:B:384:LEU:HB3	1.85	0.59
1:C:371:PHE:HE1	2:C:547:HOH:O	1.87	0.58
1:C:334:ARG:HG2	1:C:361:ASP:O	2.03	0.58
1:B:459:LEU:HD11	1:B:477:CYS:HB2	1.88	0.55
1:D:459:LEU:HD11	1:D:477:CYS:HB2	1.89	0.55
1:D:413:CYS:HB3	1:D:416:ASN:HD22	1.72	0.54
1:C:274:ASP:OD1	1:C:506:HIS:CE1	2.61	0.53
1:A:355:ARG:HD3	1:A:384:LEU:HB3	1.90	0.53
1:B:370:ASN:OD1	1:D:422:GLN:NE2	2.42	0.52
1:C:413:CYS:HB3	1:C:416:ASN:HD22	1.74	0.52
1:A:370:ASN:ND2	2:A:576:HOH:O	2.43	0.51
1:A:435:ASN:O	1:A:436:ARG:HB2	2.10	0.50
1:C:434:GLN:CG	2:C:573:HOH:O	2.40	0.49
1:D:343:PRO:HD2	1:D:419:LEU:HD21	1.95	0.49
1:B:274:ASP:OD1	1:B:506:HIS:HE1	1.96	0.49
1:C:459:LEU:HD11	1:C:477:CYS:HB2	1.96	0.48
1:D:274:ASP:OD1	1:D:506:HIS:CE1	2.66	0.48
1:A:497:PHE:HB3	1:A:500:LYS:O	2.14	0.48
1:D:416:ASN:O	1:D:419:LEU:HB2	2.13	0.48
1:D:260:ARG:HH21	1:D:494:HIS:CD2	2.32	0.47
1:D:497:PHE:HB3	1:D:500:LYS:O	2.14	0.47
1:B:419:LEU:HD11	1:B:424:TRP:HZ2	1.80	0.47
1:D:434:GLN:CG	2:D:571:HOH:O	2.57	0.47
1:B:370:ASN:HB2	2:B:512:HOH:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:497:PHE:HB3	1:C:500:LYS:O	2.16	0.46
1:C:304:ARG:NH2	2:C:582:HOH:O	2.49	0.45
1:D:304:ARG:NH2	2:D:550:HOH:O	2.50	0.45
1:A:459:LEU:HD11	1:A:477:CYS:HB2	1.99	0.44
1:B:279:VAL:HG11	1:B:505:LEU:HD22	2.00	0.44
1:B:497:PHE:HB3	1:B:500:LYS:O	2.17	0.44
1:A:337:VAL:HG22	1:A:406:LEU:HB3	1.99	0.43
1:A:370:ASN:OD1	1:C:424:TRP:CD1	2.71	0.43
1:D:416:ASN:HB3	1:D:419:LEU:HD13	1.99	0.43
1:B:413:CYS:SG	1:B:414:PRO:HD2	2.57	0.43
1:C:355:ARG:HD3	1:C:384:LEU:HB3	2.00	0.43
1:D:407:VAL:HG23	1:D:437:ALA:HB3	2.02	0.42
1:B:337:VAL:HG22	1:B:406:LEU:HB3	2.02	0.42
1:C:371:PHE:CZ	1:C:374:MET:HG2	2.55	0.42
1:C:407:VAL:HG23	1:C:437:ALA:HB3	2.02	0.42
1:B:393:VAL:HG11	1:B:398:ASP:HB3	2.02	0.42
1:A:413:CYS:SG	1:A:414:PRO:HD2	2.60	0.41
1:C:344:HIS:CG	1:C:413:CYS:HB2	2.55	0.41
1:D:344:HIS:CG	1:D:413:CYS:HB2	2.56	0.40
1:A:360:HIS:HE1	1:B:500:LYS:O	2.04	0.40
1:C:343:PRO:HD2	1:C:419:LEU:HD21	2.03	0.40
1:D:355:ARG:HD3	1:D:384:LEU:HB3	2.04	0.40
1:D:339:LEU:HD12	1:D:341:CYS:SG	2.61	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	225/259 (87%)	220 (98%)	5 (2%)	0	100	100
1	B	225/259 (87%)	222 (99%)	3 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	225/259 (87%)	220 (98%)	4 (2%)	1 (0%)	34	37
1	D	225/259 (87%)	220 (98%)	4 (2%)	1 (0%)	34	37
All	All	900/1036 (87%)	882 (98%)	16 (2%)	2 (0%)	47	55

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	322	GLY
1	D	322	GLY

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	203/227 (89%)	199 (98%)	4 (2%)	55	69
1	B	203/227 (89%)	200 (98%)	3 (2%)	65	78
1	C	203/227 (89%)	193 (95%)	10 (5%)	25	31
1	D	203/227 (89%)	194 (96%)	9 (4%)	28	35
All	All	812/908 (89%)	786 (97%)	26 (3%)	39	50

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	258	TYR
1	A	279	VAL
1	A	339	LEU
1	A	370	ASN
1	B	258	TYR
1	B	339	LEU
1	B	457	TRP
1	C	258	TYR
1	C	279	VAL
1	C	339	LEU

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Mol	Chain	Res	Type
1	C	371	PHE
1	C	373	LYS
1	C	374	MET
1	C	401	THR
1	C	419	LEU
1	C	434	GLN
1	C	457	TRP
1	D	258	TYR
1	D	279	VAL
1	D	302	GLU
1	D	339	LEU
1	D	371	PHE
1	D	373	LYS
1	D	374	MET
1	D	419	LEU
1	D	436	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	370	ASN
1	A	416	ASN
1	A	506	HIS
1	B	349	GLN
1	B	506	HIS
1	C	360	HIS
1	C	370	ASN
1	C	416	ASN
1	C	422	GLN
1	C	506	HIS
1	D	360	HIS
1	D	370	ASN
1	D	416	ASN
1	D	422	GLN
1	D	506	HIS

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 monosaccharides 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

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	233/259 (89%)	0.18	17 (7%)	15 14	19, 27, 41, 50	0
1	B	233/259 (89%)	0.17	17 (7%)	15 14	17, 27, 43, 53	0
1	C	233/259 (89%)	0.11	12 (5%)	27 26	18, 27, 38, 49	0
1	D	233/259 (89%)	0.20	14 (6%)	21 20	18, 26, 41, 50	0
All	All	932/1036 (89%)	0.17	60 (6%)	19 18	17, 27, 41, 53	0

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	258	TYR	7.5
1	C	322	GLY	7.3
1	D	323	PRO	7.1
1	C	321	GLY	6.2
1	B	323	PRO	6.1
1	B	322	GLY	6.0
1	C	418	PHE	5.7
1	A	258	TYR	5.6
1	B	333	GLN	5.6
1	B	447	HIS	5.6
1	D	418	PHE	5.5
1	C	323	PRO	5.3
1	A	333	GLN	5.2
1	A	323	PRO	5.2
1	A	447	HIS	4.8
1	A	322	GLY	4.8
1	B	418	PHE	4.8
1	A	417	VAL	4.8
1	D	371	PHE	4.7
1	D	333	GLN	4.6
1	C	447	HIS	4.5

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Mol	Chain	Res	Type	RSRZ
1	A	446	VAL	4.5
1	D	258	TYR	4.1
1	D	447	HIS	4.1
1	C	333	GLN	4.1
1	D	322	GLY	4.0
1	C	258	TYR	3.9
1	B	417	VAL	3.9
1	D	401	THR	3.9
1	A	418	PHE	3.9
1	D	321	GLY	3.8
1	C	371	PHE	3.8
1	A	321	GLY	3.7
1	A	268	SER	3.6
1	B	321	GLY	3.6
1	B	415	GLU	3.2
1	D	436	ARG	3.0
1	B	268	SER	3.0
1	A	415	GLU	3.0
1	B	434	GLN	2.8
1	D	268	SER	2.8
1	B	446	VAL	2.7
1	B	416	ASN	2.5
1	B	470	HIS	2.5
1	D	334	ARG	2.5
1	C	268	SER	2.4
1	C	334	ARG	2.3
1	A	334	ARG	2.3
1	A	470	HIS	2.3
1	C	434	GLN	2.3
1	D	434	GLN	2.3
1	A	416	ASN	2.2
1	B	401	THR	2.1
1	A	260	ARG	2.1
1	B	334	ARG	2.1
1	A	340	LEU	2.1
1	B	408	ILE	2.1
1	C	401	THR	2.0
1	A	401	THR	2.0
1	D	415	GLU	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.