



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2014 – 01:07 AM GMT

PDB ID : 2OCA
Title : The crystal structure of T4 UvsW
Authors : Kerr, I.D.; White, S.W.
Deposited on : 2006-12-20
Resolution : 2.70 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

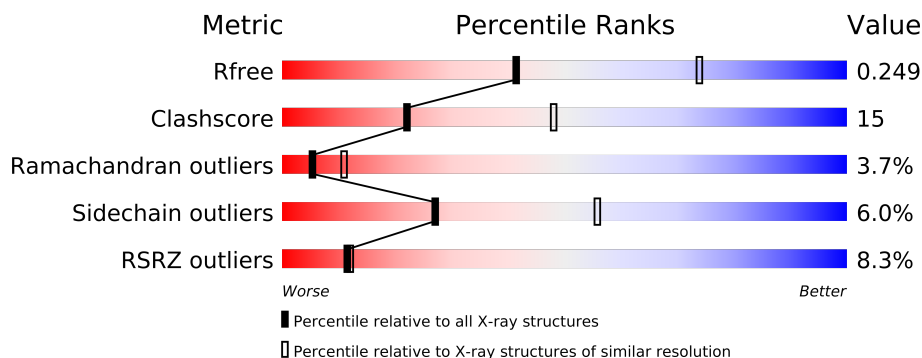
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.70 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}	66092	1557 (2.70-2.70)
Clashscore	79885	1939 (2.70-2.70)
Ramachandran outliers	78287	1905 (2.70-2.70)
Sidechain outliers	78261	1905 (2.70-2.70)
RSRZ outliers	66119	1559 (2.70-2.70)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	510	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4123 atoms, of which 0 are hydrogen and 0 are deuterium.

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 ATP-dependent DNA helicase uvsW.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	494	4017	2591	692	718	16	70	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	141	ARG	LYS	ENGINEERED	UNP P20703
A	457	ASP	SER	VARIANT	UNP P20703
A	503	LEU	-	EXPRESSION TAG	UNP P20703
A	504	GLU	-	EXPRESSION TAG	UNP P20703
A	505	HIS	-	EXPRESSION TAG	UNP P20703
A	506	HIS	-	EXPRESSION TAG	UNP P20703
A	507	HIS	-	EXPRESSION TAG	UNP P20703
A	508	HIS	-	EXPRESSION TAG	UNP P20703
A	509	HIS	-	EXPRESSION TAG	UNP P20703
A	510	HIS	-	EXPRESSION TAG	UNP P20703

- Molecule 2 is water.

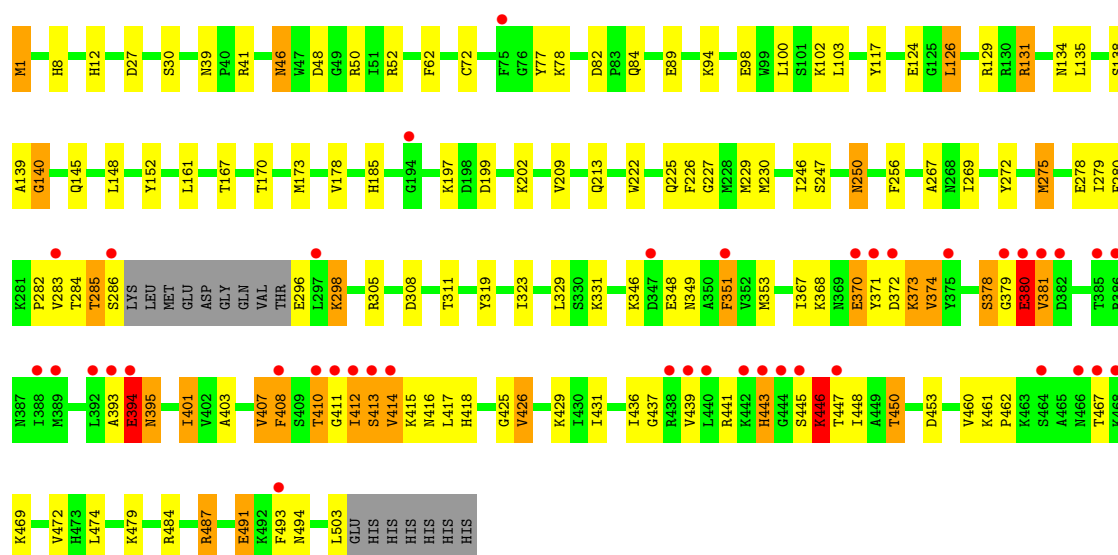
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	106	Total	O	0	0
			106	106		

3 Residue-property plots

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: ATP-dependent DNA helicase uvsW

Chain A: 



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	118.64Å 155.20Å 101.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.70 47.42 – 2.69	Depositor EDS
% Data completeness (in resolution range)	97.5 (30.00-2.70) 97.4 (47.42-2.69)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.30 (at 2.69Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.217 , 0.250 0.217 , 0.249	Depositor DCC
R_{free} test set	1292 reflections (5.08%)	DCC
Wilson B-factor (Å ²)	63.7	Xtriage
Anisotropy	0.620	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 52.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 25563 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4123	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.58% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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	0.38	0/4107	0.62	1/5526 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	446	LYS	N-CA-C	-5.22	96.91	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4017	0	4061	118	0
2	A	106	0	0	3	0
All	All	4123	0	4061	118	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 15.

All (118) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:349:ASN:H	1:A:418:HIS:CD2	1.86	0.92

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:349:ASN:H	1:A:418:HIS:HD2	0.98	0.92
1:A:414:VAL:HG11	1:A:417:LEU:HD22	1.54	0.88
1:A:410:THR:HG23	1:A:411:GLY:H	1.36	0.88
1:A:349:ASN:N	1:A:418:HIS:HD2	1.77	0.82
1:A:487:ARG:NH1	1:A:487:ARG:HB2	1.95	0.82
1:A:126:LEU:HD13	1:A:148:LEU:HD23	1.67	0.76
1:A:487:ARG:HH11	1:A:487:ARG:HB2	1.49	0.75
1:A:401:ILE:HD11	1:A:403:ALA:HB2	1.69	0.74
1:A:46:ASN:H	1:A:46:ASN:HD22	1.36	0.72
1:A:412:ILE:HB	1:A:439:VAL:HG13	1.71	0.72
1:A:351:PHE:CD2	1:A:353:MET:HE1	2.24	0.72
1:A:446:LYS:O	1:A:448:ILE:N	2.20	0.72
1:A:250:ASN:N	1:A:250:ASN:HD22	1.89	0.71
1:A:319:TYR:CZ	1:A:323:ILE:HD11	2.25	0.71
1:A:462:PRO:HB3	1:A:472:VAL:HG23	1.73	0.70
1:A:138:SER:O	1:A:139:ALA:HB3	1.90	0.70
1:A:412:ILE:CD1	1:A:443:HIS:HB2	2.22	0.69
1:A:414:VAL:HG12	1:A:417:LEU:HB2	1.73	0.69
1:A:282:PRO:O	1:A:284:THR:N	2.25	0.69
1:A:491:GLU:HB3	1:A:493:PHE:CE2	2.27	0.68
1:A:250:ASN:H	1:A:250:ASN:HD22	1.43	0.66
1:A:367:ILE:HG22	1:A:374:VAL:HG21	1.79	0.64
1:A:346:LYS:HE3	1:A:348:GLU:OE1	1.97	0.63
1:A:135:LEU:HD21	1:A:282:PRO:HG3	1.81	0.62
1:A:48:ASP:OD1	1:A:52:ARG:NH2	2.32	0.62
1:A:305:ARG:HH12	1:A:461:LYS:HE3	1.65	0.62
1:A:30:SER:OG	1:A:50:ARG:NH1	2.33	0.62
1:A:331:LYS:HD3	1:A:503:LEU:HD21	1.83	0.61
1:A:311:THR:CG2	1:A:460:VAL:HG22	2.30	0.61
1:A:425:GLY:HA2	2:A:594:HOH:O	2.02	0.60
1:A:351:PHE:HE2	1:A:408:PHE:HB2	1.68	0.59
1:A:126:LEU:HD13	1:A:148:LEU:CD2	2.33	0.58
1:A:319:TYR:OH	1:A:323:ILE:HD11	2.02	0.58
1:A:408:PHE:CZ	1:A:436:ILE:HG12	2.40	0.57
1:A:378:SER:HA	1:A:407:VAL:CG2	2.34	0.57
1:A:145:GLN:HE22	1:A:173:MET:HE1	1.69	0.57
1:A:410:THR:HG23	1:A:411:GLY:N	2.15	0.57
1:A:311:THR:HG23	1:A:460:VAL:HG22	1.86	0.56
1:A:161:LEU:HB2	1:A:226:PHE:CD2	2.40	0.56
1:A:446:LYS:C	1:A:448:ILE:H	2.08	0.56
1:A:412:ILE:HD11	1:A:443:HIS:HB2	1.88	0.54
1:A:100:LEU:HD12	1:A:103:LEU:HD12	1.89	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:408:PHE:HZ	1:A:436:ILE:HG12	1.71	0.54
1:A:410:THR:O	1:A:412:ILE:HG23	2.07	0.54
1:A:462:PRO:HB3	1:A:472:VAL:CG2	2.38	0.54
1:A:131:ARG:HG3	1:A:278:GLU:O	2.08	0.54
1:A:138:SER:O	1:A:139:ALA:CB	2.56	0.54
1:A:378:SER:HA	1:A:407:VAL:HG21	1.90	0.53
1:A:474:LEU:HD23	1:A:479:LYS:HG2	1.90	0.53
1:A:412:ILE:HD12	1:A:413:SER:N	2.24	0.53
1:A:135:LEU:CD2	1:A:282:PRO:HG3	2.38	0.53
1:A:429:LYS:HB3	1:A:431:ILE:HD13	1.91	0.53
1:A:491:GLU:HB3	1:A:493:PHE:CD2	2.44	0.53
1:A:431:ILE:HD12	1:A:431:ILE:N	2.24	0.52
1:A:296:GLU:OE1	1:A:441:ARG:HD2	2.10	0.52
1:A:445:SER:O	1:A:446:LYS:CB	2.56	0.52
1:A:269:ILE:HD11	1:A:279:ILE:HD11	1.91	0.52
1:A:308:ASP:O	1:A:311:THR:HB	2.10	0.51
1:A:311:THR:HG21	1:A:460:VAL:HA	1.92	0.51
1:A:487:ARG:HH11	1:A:487:ARG:CB	2.21	0.50
1:A:453:ASP:OD1	1:A:484:ARG:NH2	2.42	0.50
1:A:351:PHE:CE1	1:A:401:ILE:HG12	2.46	0.50
1:A:401:ILE:O	1:A:401:ILE:HG13	2.11	0.50
1:A:213:GLN:H	1:A:213:GLN:NE2	2.09	0.50
1:A:408:PHE:CD2	1:A:408:PHE:C	2.85	0.49
1:A:46:ASN:ND2	1:A:46:ASN:H	2.09	0.49
1:A:82:ASP:OD1	1:A:84:GLN:HG2	2.13	0.49
1:A:1:MET:HB2	1:A:78:LYS:O	2.12	0.49
1:A:152:TYR:OH	1:A:227:GLY:HA3	2.13	0.49
1:A:379:GLY:O	1:A:380:GLU:C	2.51	0.48
1:A:296:GLU:CD	1:A:441:ARG:HD2	2.34	0.48
1:A:199:ASP:HA	1:A:202:LYS:HE3	1.94	0.48
1:A:412:ILE:HD12	1:A:443:HIS:HB2	1.93	0.48
1:A:197:LYS:HG3	2:A:537:HOH:O	2.13	0.48
1:A:285:THR:HG21	1:A:494:ASN:HB2	1.96	0.48
1:A:39:ASN:OD1	1:A:41:ARG:HB2	2.14	0.48
1:A:250:ASN:H	1:A:250:ASN:ND2	2.10	0.47
1:A:445:SER:O	1:A:446:LYS:HB2	2.15	0.47
1:A:140:GLY:HA2	2:A:556:HOH:O	2.14	0.47
1:A:267:ALA:HB3	1:A:272:TYR:CZ	2.49	0.47
1:A:246:ILE:HG23	1:A:247:SER:N	2.31	0.46
1:A:431:ILE:H	1:A:431:ILE:CD1	2.29	0.46
1:A:394:GLU:O	1:A:395:ASN:HB2	2.14	0.45
1:A:8:HIS:HB3	1:A:12:HIS:O	2.17	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:98:GLU:HG3	1:A:102:LYS:HE3	1.99	0.45
1:A:170:THR:HG23	1:A:209:VAL:HG12	1.99	0.45
1:A:446:LYS:O	1:A:448:ILE:HG13	2.17	0.45
1:A:246:ILE:HD13	1:A:275:MET:SD	2.57	0.44
1:A:222:TRP:O	1:A:225:GLN:HG2	2.17	0.44
1:A:167:THR:O	1:A:170:THR:HB	2.18	0.43
1:A:413:SER:HA	1:A:443:HIS:HB3	2.01	0.43
1:A:124:GLU:HG3	1:A:280:PHE:CE2	2.53	0.43
1:A:124:GLU:HG3	1:A:280:PHE:CZ	2.53	0.43
1:A:298:LYS:O	1:A:450:THR:HA	2.17	0.43
1:A:412:ILE:O	1:A:413:SER:HB3	2.19	0.43
1:A:117:TYR:CE1	1:A:139:ALA:HB1	2.55	0.42
1:A:230:MET:HA	1:A:256:PHE:O	2.19	0.42
1:A:213:GLN:CD	1:A:213:GLN:H	2.22	0.42
1:A:379:GLY:O	1:A:381:VAL:N	2.52	0.42
1:A:437:GLY:O	1:A:441:ARG:HD3	2.20	0.42
1:A:89:GLU:HG2	1:A:129:ARG:HE	1.84	0.42
1:A:372:ASP:O	1:A:374:VAL:N	2.50	0.41
1:A:431:ILE:HD12	1:A:431:ILE:H	1.84	0.41
1:A:72:CYS:HB3	1:A:77:TYR:O	2.20	0.41
1:A:139:ALA:O	1:A:140:GLY:C	2.58	0.41
1:A:431:ILE:CD1	1:A:431:ILE:N	2.83	0.41
1:A:467:THR:HG22	1:A:469:LYS:H	1.85	0.41
1:A:296:GLU:O	1:A:448:ILE:HA	2.20	0.41
1:A:368:LYS:C	1:A:370:GLU:H	2.23	0.41
1:A:413:SER:OG	1:A:414:VAL:N	2.54	0.41
1:A:135:LEU:CG	1:A:282:PRO:HG3	2.52	0.40
1:A:178:VAL:HG11	1:A:185:HIS:CD2	2.56	0.40
1:A:311:THR:CG2	1:A:460:VAL:HA	2.51	0.40
1:A:393:ALA:HA	1:A:415:LYS:HB2	2.03	0.40
1:A:446:LYS:C	1:A:448:ILE:N	2.72	0.40
1:A:319:TYR:CZ	1:A:323:ILE:CD1	3.01	0.40
1:A:371:TYR:CE2	1:A:373:LYS:HB2	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	490/510 (96%)	453 (92%)	19 (4%)	18 (4%)	5	11

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	283	VAL
1	A	378	SER
1	A	381	VAL
1	A	394	GLU
1	A	395	ASN
1	A	413	SER
1	A	414	VAL
1	A	447	THR
1	A	140	GLY
1	A	416	ASN
1	A	426	VAL
1	A	446	LYS
1	A	410	THR
1	A	370	GLU
1	A	373	LYS
1	A	285	THR
1	A	380	GLU
1	A	407	VAL

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	434/449 (97%)	408 (94%)	26 (6%)	27	56

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

Mol	Chain	Res	Type
1	A	1	MET
1	A	27	ASP

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Mol	Chain	Res	Type
1	A	46	ASN
1	A	62	PHE
1	A	94	LYS
1	A	126	LEU
1	A	131	ARG
1	A	134	ASN
1	A	229	MET
1	A	250	ASN
1	A	275	MET
1	A	286	SER
1	A	298	LYS
1	A	329	LEU
1	A	351	PHE
1	A	374	VAL
1	A	380	GLU
1	A	394	GLU
1	A	401	ILE
1	A	408	PHE
1	A	412	ILE
1	A	426	VAL
1	A	443	HIS
1	A	450	THR
1	A	487	ARG
1	A	491	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	46	ASN
1	A	134	ASN
1	A	145	GLN
1	A	213	GLN
1	A	250	ASN
1	A	418	HIS
1	A	480	HIS

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

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, 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	494/510 (96%)	0.51	41 (8%) 11 12	44, 64, 100, 100	23 (4%)

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	443	HIS	7.5
1	A	408	PHE	7.5
1	A	393	ALA	5.6
1	A	392	LEU	5.5
1	A	412	ILE	5.5
1	A	389	MET	5.2
1	A	466	ASN	4.7
1	A	351	PHE	4.7
1	A	379	GLY	4.7
1	A	413	SER	4.5
1	A	442	LYS	4.3
1	A	447	THR	4.3
1	A	372	ASP	4.1
1	A	286	SER	3.7
1	A	394	GLU	3.6
1	A	386	ARG	3.5
1	A	439	VAL	3.4
1	A	385	THR	3.3
1	A	411	GLY	3.2
1	A	445	SER	3.1
1	A	347	ASP	3.1
1	A	283	VAL	3.1
1	A	381	VAL	3.0
1	A	438	ARG	3.0
1	A	382	ASP	2.8
1	A	380	GLU	2.8
1	A	444	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	414	VAL	2.6
1	A	440	LEU	2.5
1	A	370	GLU	2.5
1	A	75	PHE	2.4
1	A	371	TYR	2.4
1	A	493	PHE	2.3
1	A	194	GLY	2.3
1	A	297	LEU	2.3
1	A	410	THR	2.2
1	A	388	ILE	2.2
1	A	467	THR	2.1
1	A	464	SER	2.1
1	A	375	TYR	2.0
1	A	468	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.