Full wwPDB X-ray Structure Validation Report (i)

Jun 13, 2016 – 04:26 PM EDT

PDB ID	:	5IUT
Title	:	STRUCTURE OF P450 2B4 F202W MUTANT
Authors	:	Jang, H.-H.; Halpert, J.R.; Shah, M.B.
Deposited on	:	2016-03-18
Resolution	:	2.34 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:

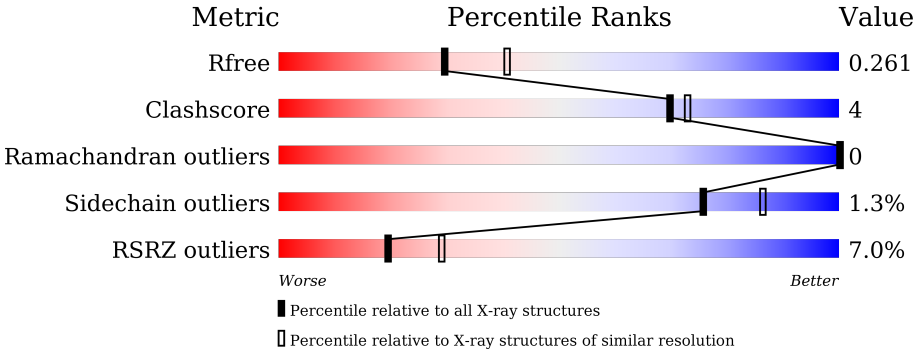
MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20027790
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027790

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

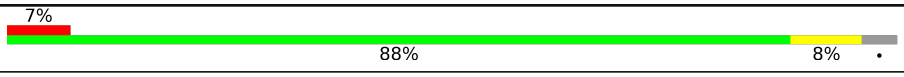
The reported resolution of this entry is 2.34 Å.

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	1406 (2.36-2.32)
Clashscore	102246	1509 (2.36-2.32)
Ramachandran outliers	100387	1490 (2.36-2.32)
Sidechain outliers	100360	1491 (2.36-2.32)
RSRZ outliers	91569	1412 (2.36-2.32)

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	478	

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 3900 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 Cytochrome P450 2B4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	460	3651	2352	630	659	10	0	0	0

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	21	ALA	GLU	engineered mutation	UNP P00178
A	?	-	PHE	DELETION	UNP P00178
A	?	-	SER	DELETION	UNP P00178
A	?	-	LEU	DELETION	UNP P00178
A	?	-	LEU	DELETION	UNP P00178
A	?	-	LEU	DELETION	UNP P00178
A	?	-	LEU	DELETION	UNP P00178
A	?	-	LEU	DELETION	UNP P00178
A	?	-	ALA	DELETION	UNP P00178
A	?	-	PHE	DELETION	UNP P00178
A	?	-	LEU	DELETION	UNP P00178
A	?	-	ALA	DELETION	UNP P00178
A	?	-	GLY	DELETION	UNP P00178
A	?	-	LEU	DELETION	UNP P00178
A	?	-	LEU	DELETION	UNP P00178
A	?	-	LEU	DELETION	UNP P00178
A	?	-	LEU	DELETION	UNP P00178
A	?	-	LEU	DELETION	UNP P00178
A	?	-	PHE	DELETION	UNP P00178
A	?	-	ARG	DELETION	UNP P00178
A	22	LYS	GLY	engineered mutation	UNP P00178
A	23	LYS	HIS	engineered mutation	UNP P00178
A	24	THR	PRO	engineered mutation	UNP P00178
A	25	SER	LYS	engineered mutation	UNP P00178
A	26	SER	ALA	engineered mutation	UNP P00178
A	27	LYS	HIS	engineered mutation	UNP P00178
A	29	LYS	ARG	engineered mutation	UNP P00178

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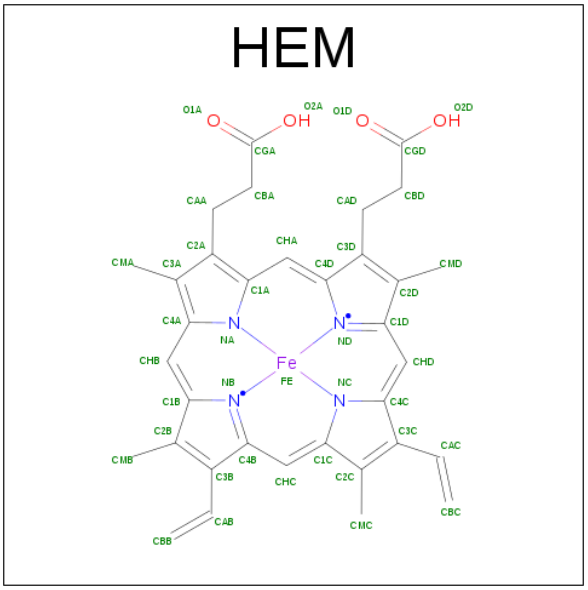
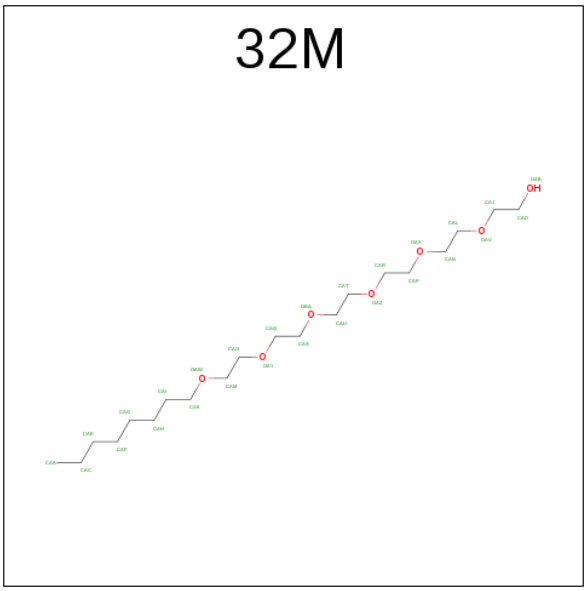
Chain	Residue	Modelled	Actual	Comment	Reference
A	202	TRP	PHE	engineered mutation	UNP P00178
A	221	SER	PRO	SEE REMARK 999	UNP P00178
A	226	TYR	HIS	engineered mutation	UNP P00178
A	492	HIS	-	expression tag	UNP P00178
A	493	HIS	-	expression tag	UNP P00178
A	494	HIS	-	expression tag	UNP P00178
A	495	HIS	-	expression tag	UNP P00178
A	496	HIS	-	expression tag	UNP P00178
A	497	HIS	-	expression tag	UNP P00178

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Fe	N	O		
2	A	1	43	34	1	4	4	0	0

- Molecule 3 is 3,6,9,12,15,18-hexaoxahexacosan-1-ol (three-letter code: 32M) (formula: $C_{20}H_{42}O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	27	20	7	0	0

- Molecule 4 is water.

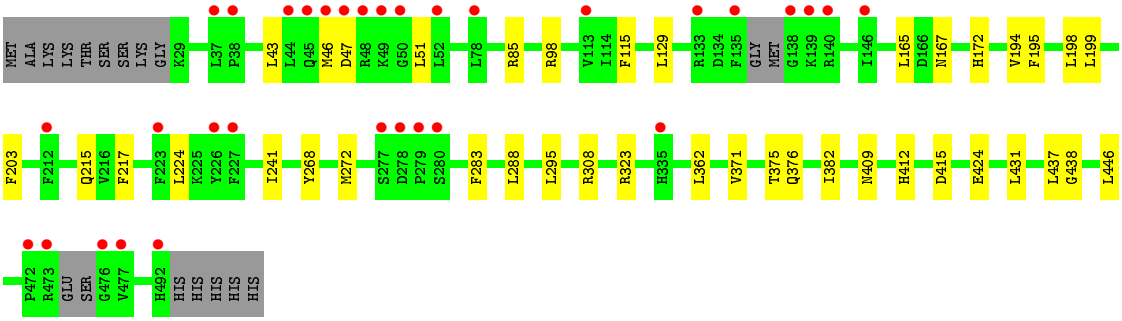
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	179	179	179	0	0

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 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: Cytochrome P450 2B4

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	91.17Å 91.17Å 151.14Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.34 19.85 – 2.34	Depositor EDS
% Data completeness (in resolution range)	97.4 (20.00-2.34) 97.4 (19.85-2.34)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.25 (at 2.33Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.216 , 0.265 0.213 , 0.261	Depositor DCC
R_{free} test set	1537 reflections (5.32%)	DCC
Wilson B-factor (Å^2)	50.9	Xtriage
Anisotropy	0.030	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 38.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	0.042 for -h,-k,l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	3900	wwPDB-VP
Average B, all atoms (Å^2)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.50% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, 32M

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	0.37	0/3743	0.53	0/5077

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	3651	0	3586	29	0
2	A	43	0	30	5	0
3	A	27	0	42	1	0
4	A	179	0	0	1	0
All	All	3900	0	3658	33	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 (33) 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:371:VAL:HG11	1:A:375:THR:HG21	1.74	0.70
1:A:129:LEU:HD13	1:A:437:LEU:CD1	2.22	0.69
1:A:129:LEU:HD13	1:A:437:LEU:HD12	1.76	0.68
1:A:46:MET:HB2	1:A:47:ASP:HA	1.74	0.68
2:A:501:HEM:HMC2	2:A:501:HEM:HBC2	1.77	0.66
1:A:198:LEU:HD13	1:A:241:ILE:HD13	1.83	0.60
2:A:501:HEM:HMB2	2:A:501:HEM:HBB2	1.85	0.58
2:A:501:HEM:CMC	2:A:501:HEM:HBC2	2.37	0.55
1:A:215:GLN:HA	1:A:215:GLN:NE2	2.22	0.55
1:A:371:VAL:CG1	1:A:375:THR:HG21	2.34	0.55
1:A:194:VAL:O	1:A:198:LEU:HD23	2.08	0.54
1:A:195:PHE:CE1	1:A:199:LEU:HD11	2.44	0.52
1:A:98:ARG:HG2	1:A:115:PHE:HA	1.92	0.51
2:A:501:HEM:CMB	2:A:501:HEM:HBB2	2.42	0.50
1:A:268:TYR:CG	1:A:288:LEU:HD13	2.46	0.50
1:A:165:LEU:HD12	1:A:165:LEU:C	2.34	0.48
1:A:198:LEU:CD1	1:A:241:ILE:HD13	2.44	0.48
1:A:85:ARG:NH2	1:A:424:GLU:O	2.47	0.47
1:A:375:THR:HG23	1:A:382:ILE:HB	1.98	0.45
1:A:217:PHE:HA	1:A:224:LEU:HD12	1.99	0.45
1:A:167:ASN:OD1	1:A:308:ARG:HG3	2.17	0.45
1:A:438:GLY:HA3	2:A:501:HEM:C3C	2.52	0.45
1:A:46:MET:HE1	1:A:51:LEU:HD13	2.00	0.44
1:A:46:MET:HB2	1:A:47:ASP:CA	2.46	0.43
1:A:129:LEU:HD13	1:A:437:LEU:HD11	1.99	0.43
1:A:409:ASN:HB3	1:A:412:HIS:CE1	2.52	0.43
1:A:268:TYR:CE1	1:A:288:LEU:HB2	2.53	0.43
1:A:215:GLN:HA	1:A:215:GLN:HE21	1.82	0.42
1:A:172:HIS:HB3	1:A:203:PHE:CE2	2.55	0.41
1:A:43:LEU:HD11	3:A:502:32M:H5	2.02	0.41
1:A:415:ASP:C	1:A:415:ASP:OD1	2.59	0.41
1:A:323:ARG:NH2	4:A:612:HOH:O	2.53	0.41
1:A:272:MET:HG2	1:A:283:PHE:O	2.21	0.41

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	454/478 (95%)	436 (96%)	18 (4%)	0	100 100

There are no Ramachandran outliers to report.

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	394/423 (93%)	389 (99%)	5 (1%)	76 86

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	295	LEU
1	A	362	LEU
1	A	376	GLN
1	A	431	LEU
1	A	446	LEU

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

Mol	Chain	Res	Type
1	A	172	HIS
1	A	215	GLN

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)

2 ligands 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	$\#\|Z\| > 2$
2	HEM	A	501	1,3	24,50,50	2.21	5 (20%)	16,82,82	1.71	4 (25%)
3	32M	A	502	2	26,26,26	0.59	0	25,25,25	1.00	2 (8%)

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
2	HEM	A	501	1,3	-	0/6/54/54	0/0/8/8
3	32M	A	502	2	-	0/24/24/24	0/0/0/0

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	HEM	C3B-C2B	-4.68	1.34	1.40
2	A	501	HEM	C3C-C2C	-4.53	1.34	1.40
2	A	501	HEM	C3B-CAB	3.31	1.54	1.47
2	A	501	HEM	C3C-CAC	3.52	1.55	1.47
2	A	501	HEM	C3D-C2D	5.15	1.52	1.37

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	501	HEM	CBD-CAD-C3D	-3.81	105.78	112.47
2	A	501	HEM	CAA-CBA-CGA	-2.83	107.28	112.78
2	A	501	HEM	C3C-CAC-CBC	-2.58	121.21	126.40
3	A	502	32M	CAE-CAF-CAG	-2.46	101.76	114.54
3	A	502	32M	CAG-CAH-CAI	-2.36	102.26	114.54
2	A	501	HEM	C3B-CAB-CBB	-2.11	122.16	126.40

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	HEM	5	0
3	A	502	32M	1	0

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	460/478 (96%)	0.23	32 (6%) 19 29	30, 45, 78, 97	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	48	ARG	5.9
1	A	49	LYS	4.8
1	A	492	HIS	4.8
1	A	135	PHE	4.6
1	A	277	SER	4.6
1	A	473	ARG	4.2
1	A	279	PRO	4.0
1	A	223	PHE	3.9
1	A	50	GLY	3.9
1	A	226	TYR	3.7
1	A	47	ASP	3.5
1	A	46	MET	3.4
1	A	139	LYS	3.3
1	A	476	GLY	3.3
1	A	212	PHE	3.2
1	A	44	LEU	3.1
1	A	472	PRO	3.0
1	A	140	ARG	2.8
1	A	227	PHE	2.7
1	A	280	SER	2.7
1	A	37	LEU	2.7
1	A	335	HIS	2.7
1	A	45	GLN	2.5
1	A	113	VAL	2.4
1	A	133	ARG	2.3
1	A	477	VAL	2.2
1	A	78	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	38	PRO	2.2
1	A	52	LEU	2.1
1	A	278	ASP	2.1
1	A	146	ILE	2.0
1	A	138	GLY	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 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, 95th 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	32M	A	502	27/27	0.75	0.28	1.38	77,91,97,97	0
2	HEM	A	501	43/43	0.98	0.10	-1.06	29,31,35,37	0

6.5 Other polymers (i)

There are no such residues in this entry.