



# Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 03:00 AM GMT

PDB ID : 2YDF  
Title : HUMAN SERUM ALBUMIN COMPLEXED WITH IOPHENOXIC ACID  
Authors : Ryan, A.J.; Curry, S.  
Deposited on : 2011-03-18  
Resolution : 2.75 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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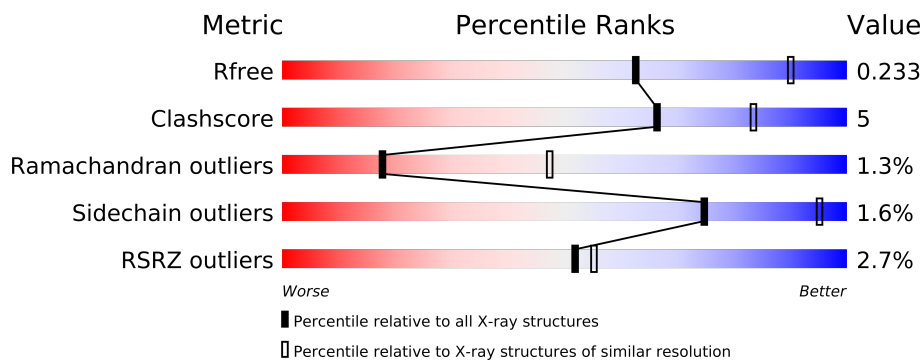
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.75 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	2406 (2.80-2.72)
Clashscore	79885	2995 (2.80-2.72)
Ramachandran outliers	78287	2941 (2.80-2.72)
Sidechain outliers	78261	2944 (2.80-2.72)
RSRZ outliers	66119	2409 (2.80-2.72)

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  $\geq 3$ , 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	585	
1	B	585	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	IO3	B	2004	-	X

## 2 Entry composition i

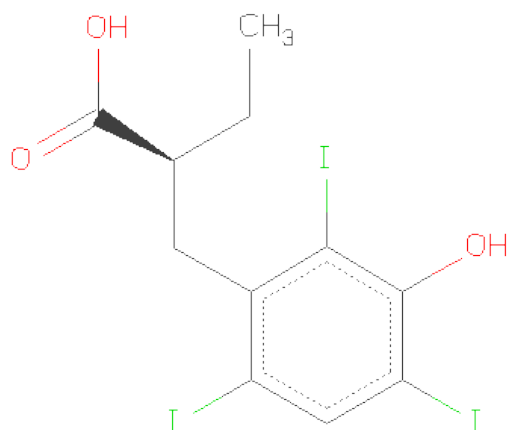
There are 3 unique types of molecules in this entry. The entry contains 8442 atoms, of which 0 are hydrogen and 0 are deuterium.

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 SERUM ALBUMIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	569	Total	C	N	O	S	0	0	0
			4177	2640	704	794	39			
1	B	566	Total	C	N	O	S	0	0	0
			4106	2590	685	792	39			

- Molecule 2 is IOPHENOXIC ACID (three-letter code: IO3) (formula: C<sub>11</sub>H<sub>11</sub>I<sub>3</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	I	O	0	0
			17	11	3	3		
2	A	1	Total	C	I	O	0	0
			17	11	3	3		
2	A	1	Total	C	I	O	0	0
			17	11	3	3		
2	A	1	Total	C	I	O	0	0
			17	11	3	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	I	O	0	0
			17	11	3	3		
2	B	1	Total	C	I	O	0	0
			17	11	3	3		
2	B	1	Total	C	I	O	0	0
			17	11	3	3		
2	B	1	Total	C	I	O	0	0
			17	11	3	3		

- Molecule 3 is water.

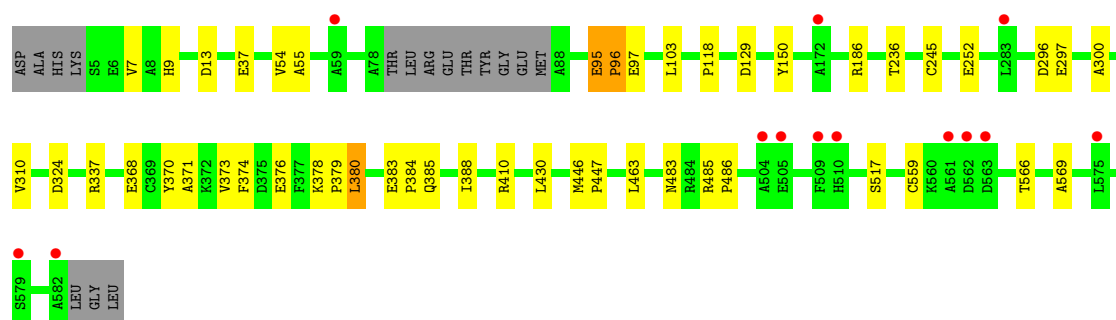
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	12	Total	O	0	0
			12	12		
3	B	11	Total	O	0	0
			11	11		

### 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.

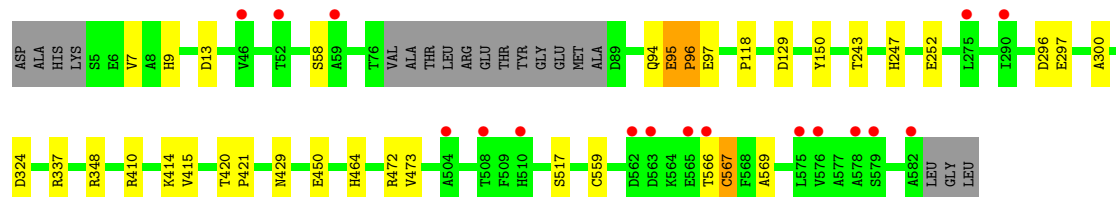
#### • Molecule 1: SERUM ALBUMIN

Chain A: 



#### • Molecule 1: SERUM ALBUMIN

Chain B: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	55.07Å 55.44Å 119.84Å 81.00° 90.83° 64.52°	Depositor
Resolution (Å)	35.12 – 2.75 49.23 – 2.35	Depositor EDS
% Data completeness (in resolution range)	94.7 (35.12-2.75) 95.5 (49.23-2.35)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.00 (at 2.34Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.207 , 0.239 0.202 , 0.233	Depositor DCC
$R_{free}$ test set	1476 reflections (4.73%)	DCC
Wilson B-factor (Å <sup>2</sup> )	65.6	Xtriage
Anisotropy	0.276	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 39.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 52313 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	8442	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.01% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: IO3

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	0.22	0/4257	0.37	0/5798
1	B	0.22	0/4184	0.37	0/5709
All	All	0.22	0/8441	0.37	0/11507

There are no bond length outliers.

There are no bond angle outliers.

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	4177	0	472	22	0
1	B	4106	0	311	17	0
2	A	68	0	40	8	0
2	B	68	0	40	4	0
3	A	12	0	0	0	0
3	B	11	0	0	0	0
All	All	8442	0	863	47	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 5.

All (47) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:2001:IO3:I3	2:A:2001:IO3:H6	2.44	0.87
2:A:2003:IO3:H7	2:A:2003:IO3:I3	2.51	0.80
2:B:2001:IO3:H6	2:B:2001:IO3:I3	2.53	0.79
1:A:378:LYS:HB3	1:A:379:PRO:HD3	1.72	0.70
1:A:388:ILE:CD1	2:A:2002:IO3:H3	2.28	0.64
1:A:383:GLU:HB3	1:A:384:PRO:HD3	1.84	0.60
2:B:2004:IO3:I3	2:B:2004:IO3:H8	2.73	0.59
1:B:95:GLU:O	1:B:97:GLU:N	2.35	0.59
1:A:485:ARG:HB3	1:A:486:PRO:HD3	1.87	0.57
1:A:95:GLU:O	1:A:97:GLU:N	2.38	0.56
1:A:95:GLU:CB	1:A:96:PRO:CD	2.83	0.56
2:A:2004:IO3:H6	2:A:2004:IO3:I3	2.76	0.55
2:A:2004:IO3:C8	2:A:2004:IO3:I3	3.27	0.53
1:B:95:GLU:CB	1:B:96:PRO:CD	2.87	0.51
2:B:2003:IO3:H7	2:B:2003:IO3:I1	2.81	0.51
1:A:376:GLU:O	1:A:380:LEU:HD12	2.11	0.51
2:A:2004:IO3:I3	2:A:2004:IO3:H7	2.82	0.50
1:B:296:ASP:OD1	1:B:297:GLU:N	2.47	0.48
1:B:410:ARG:CD	2:B:2004:IO3:H11	2.44	0.48
1:B:464:HIS:CG	1:B:473:VAL:HG11	2.49	0.48
1:A:296:ASP:OD1	1:A:297:GLU:N	2.47	0.48
1:B:420:THR:HB	1:B:421:PRO:HD3	1.97	0.47
1:B:252:GLU:OE1	1:B:252:GLU:N	2.47	0.47
1:A:385:GLN:HG3	1:A:446:MET:CE	2.45	0.47
1:B:9:HIS:CE1	1:B:13:ASP:OD2	2.68	0.47
1:A:252:GLU:N	1:A:252:GLU:OE1	2.48	0.46
1:B:429:ASN:HD22	1:B:429:ASN:N	2.15	0.45
1:B:243:THR:O	1:B:247:HIS:ND1	2.50	0.45
1:A:324:ASP:N	1:A:324:ASP:OD1	2.48	0.44
1:A:446:MET:HB3	1:A:447:PRO:HD3	2.00	0.44
1:A:566:THR:O	1:A:569:ALA:N	2.50	0.44
1:A:37:GLU:N	1:A:37:GLU:OE1	2.51	0.44
1:B:415:VAL:O	1:B:415:VAL:HG23	2.19	0.43
1:B:566:THR:O	1:B:569:ALA:N	2.52	0.43
1:A:186:ARG:CG	2:A:2003:IO3:H11	2.49	0.42
1:B:94:GLN:O	1:B:95:GLU:O	2.37	0.42
1:B:566:THR:O	1:B:567:CYS:C	2.58	0.42
1:A:9:HIS:CE1	1:A:13:ASP:OD2	2.73	0.42
1:A:483:ASN:C	1:A:486:PRO:HD2	2.40	0.42
1:B:324:ASP:OD1	1:B:324:ASP:N	2.53	0.42
1:A:54:VAL:CG2	1:A:55:ALA:N	2.83	0.41
1:A:410:ARG:NH2	2:A:2002:IO3:O3	2.53	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:348:ARG:NH2	1:B:450:GLU:OE2	2.54	0.41
1:A:310:VAL:O	1:A:370:TYR:HE1	2.04	0.41
1:A:373:VAL:HG13	1:A:374:PHE:CD1	2.56	0.41
1:A:368:GLU:HA	1:A:371:ALA:HB2	2.03	0.40
1:B:414:LYS:O	1:B:472:ARG:NH1	2.55	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	565/585 (97%)	525 (93%)	33 (6%)	7 (1%)	19	50
1	B	562/585 (96%)	524 (93%)	30 (5%)	8 (1%)	16	45
All	All	1127/1170 (96%)	1049 (93%)	63 (6%)	15 (1%)	18	47

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	96	PRO
1	A	300	ALA
1	A	517	SER
1	B	96	PRO
1	B	300	ALA
1	B	517	SER
1	A	95	GLU
1	B	95	GLU
1	B	129	ASP
1	A	129	ASP
1	A	150	TYR
1	B	567	CYS
1	B	150	TYR
1	B	118	PRO
1	A	118	PRO

### 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	401/511 (78%)	392 (98%)	9 (2%)	64	92
1	B	390/511 (76%)	386 (99%)	4 (1%)	85	97
All	All	791/1022 (77%)	778 (98%)	13 (2%)	75	95

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	VAL
1	A	103	LEU
1	A	236	THR
1	A	245	CYS
1	A	337	ARG
1	A	380	LEU
1	A	430	LEU
1	A	463	LEU
1	A	559	CYS
1	B	7	VAL
1	B	58	SER
1	B	337	ARG
1	B	559	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	429	ASN

### 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 ⓘ

8 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	IO3	A	2001	-	17,17,17	0.89	1 (5%)	24,24,24	1.48	5 (20%)
2	IO3	A	2002	-	17,17,17	0.92	1 (5%)	24,24,24	1.64	1 (4%)
2	IO3	A	2003	-	17,17,17	0.90	1 (5%)	24,24,24	1.35	2 (8%)
2	IO3	A	2004	-	17,17,17	0.81	1 (5%)	24,24,24	1.46	3 (12%)
2	IO3	B	2001	-	17,17,17	0.87	1 (5%)	24,24,24	1.38	5 (20%)
2	IO3	B	2002	-	17,17,17	0.93	1 (5%)	24,24,24	1.32	3 (12%)
2	IO3	B	2003	-	17,17,17	0.89	1 (5%)	24,24,24	1.66	5 (20%)
2	IO3	B	2004	-	17,17,17	0.87	1 (5%)	24,24,24	1.43	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	IO3	A	2001	-	-	0/10/10/10	0/1/1/1
2	IO3	A	2002	-	-	0/10/10/10	0/1/1/1
2	IO3	A	2003	-	-	0/10/10/10	0/1/1/1
2	IO3	A	2004	-	-	0/10/10/10	0/1/1/1
2	IO3	B	2001	-	-	0/10/10/10	0/1/1/1
2	IO3	B	2002	-	-	0/10/10/10	0/1/1/1
2	IO3	B	2003	-	-	0/10/10/10	0/1/1/1
2	IO3	B	2004	-	-	0/10/10/10	0/1/1/1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2003	IO3	C7-C8	-2.41	1.49	1.53
2	A	2002	IO3	C7-C8	-2.37	1.49	1.53
2	B	2004	IO3	C7-C8	-2.31	1.49	1.53
2	A	2001	IO3	C7-C8	-2.24	1.49	1.53
2	B	2001	IO3	C7-C8	-2.13	1.49	1.53
2	A	2003	IO3	C7-C8	-2.11	1.49	1.53
2	A	2004	IO3	C7-C8	-2.03	1.49	1.53
2	B	2002	IO3	C7-C8	-2.02	1.49	1.53

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2002	IO3	C1-C7-C8	6.59	123.82	113.83
2	A	2004	IO3	C1-C7-C8	5.14	121.61	113.83
2	B	2003	IO3	C1-C7-C8	5.03	121.45	113.83
2	B	2004	IO3	C1-C7-C8	4.67	120.91	113.83
2	B	2002	IO3	C1-C7-C8	4.59	120.78	113.83
2	A	2003	IO3	C1-C7-C8	4.26	120.29	113.83
2	A	2001	IO3	C1-C7-C8	3.98	119.86	113.83
2	B	2001	IO3	C1-C7-C8	3.90	119.74	113.83
2	A	2001	IO3	C1-C6-I3	3.12	123.13	119.00
2	B	2003	IO3	C7-C1-C2	-3.10	118.08	123.56
2	B	2003	IO3	C6-C1-C2	2.83	120.09	116.84
2	B	2004	IO3	C6-C1-C2	2.77	120.03	116.84
2	B	2003	IO3	C1-C6-I3	2.72	122.61	119.00
2	A	2001	IO3	C5-C6-I3	-2.39	116.39	119.27
2	B	2001	IO3	C1-C6-I3	2.37	122.15	119.00
2	A	2003	IO3	C6-C1-C2	2.34	119.53	116.84
2	A	2001	IO3	O3-C9-C8	2.22	120.82	114.44
2	B	2001	IO3	O3-C9-O2	-2.22	119.05	124.07
2	B	2001	IO3	C7-C1-C2	-2.20	119.67	123.56
2	B	2002	IO3	O3-C9-O2	-2.17	119.16	124.07
2	A	2004	IO3	C7-C1-C2	-2.15	119.76	123.56
2	B	2003	IO3	O3-C9-C8	2.14	120.59	114.44
2	A	2004	IO3	C6-C1-C2	2.12	119.28	116.84
2	B	2001	IO3	C5-C6-I3	-2.10	116.74	119.27
2	B	2002	IO3	O3-C9-C8	2.05	120.32	114.44
2	A	2001	IO3	C7-C1-C2	-2.03	119.97	123.56

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	569/585 (97%)	-0.18	13 (2%) 57 61	1, 30, 164, 266	0
1	B	566/585 (96%)	-0.15	17 (3%) 48 52	2, 35, 163, 261	0
All	All	1135/1170 (97%)	-0.16	30 (2%) 52 57	1, 32, 165, 266	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	510	HIS	9.5
1	B	562	ASP	8.4
1	A	504	ALA	8.1
1	B	566	THR	7.1
1	B	563	ASP	6.2
1	A	562	ASP	5.9
1	A	561	ALA	5.2
1	B	510	HIS	4.9
1	B	504	ALA	4.8
1	B	578	ALA	4.4
1	B	575	LEU	3.9
1	A	505	GLU	3.8
1	B	508	THR	3.2
1	B	59	ALA	3.1
1	A	509	PHE	3.0
1	A	563	ASP	3.0
1	B	579	SER	3.0
1	A	59	ALA	2.8
1	B	290	ILE	2.8
1	B	576	VAL	2.8
1	B	582	ALA	2.7
1	B	52	THR	2.6
1	B	565	GLU	2.5
1	B	46	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	283	LEU	2.5
1	A	575	LEU	2.5
1	A	579	SER	2.4
1	A	582	ALA	2.4
1	A	172	ALA	2.3
1	B	275	LEU	2.1

## 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 ⓘ

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, 95<sup>th</sup> 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	IO3	B	2004	17/17	0.34	3.55	109,111,171,173	0
2	IO3	A	2004	17/17	0.28	0.99	90,94,120,205	0
2	IO3	A	2003	17/17	0.18	0.33	71,86,184,201	0
2	IO3	B	2003	17/17	0.17	-0.04	57,72,102,132	0
2	IO3	B	2002	17/17	0.16	-0.22	26,36,52,52	0
2	IO3	A	2002	17/17	0.14	-0.38	25,30,41,48	0
2	IO3	B	2001	17/17	0.14	-0.82	9,17,27,28	0
2	IO3	A	2001	17/17	0.15	-0.83	0,16,27,27	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.