



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:20 AM GMT

PDB ID : 2QAB  
Title : Crystal Structure of Estrogen Receptor Alpha Ligand Binding Domain Mutant 537S Complexed with an Ethyl Indazole Compound  
Authors : Nettles, K.W.; Bruning, J.B.; Nowak, J.; Sharma, S.K.; Hahm, J.B.; Shi, Y.; Kulp, K.; Hochberg, R.B.; Zhou, H.; Katzenellenbogen, J.A.; Katzenellenbogen, B.S.; Kim, Y.; Joachmiak, A.; Greene, G.L.  
Deposited on : 2007-06-14  
Resolution : 1.89 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](mailto: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.

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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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
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) : trunk26865



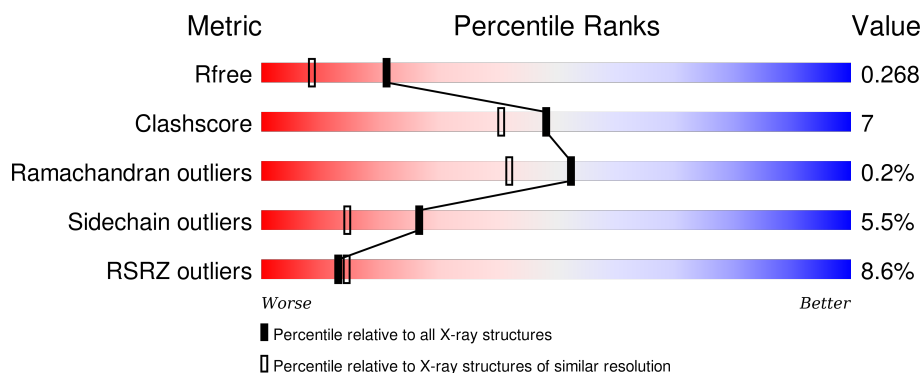
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.89 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	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (1.90-1.90)

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. 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	258	<div> <div>7%</div> <div>76%</div> <div>13%</div> <div>•</div> <div>9%</div> </div>
1	B	258	<div> <div>8%</div> <div>79%</div> <div>14%</div> <div>•</div> <div>5%</div> </div>
2	C	13	<div> <div>23%</div> <div>38%</div> <div>46%</div> <div>15%</div> </div>
2	D	13	<div> <div>8%</div> <div>54%</div> <div>8%</div> <div>8%</div> <div>31%</div> </div>



## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4099 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 Estrogen receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	236	Total	C	N	O	S	0	6	0
			1908	1220	329	339	20			
1	B	245	Total	C	N	O	S	0	5	0
			1964	1257	337	351	19			

There are 4 discrepancies between the modelled and reference sequences:

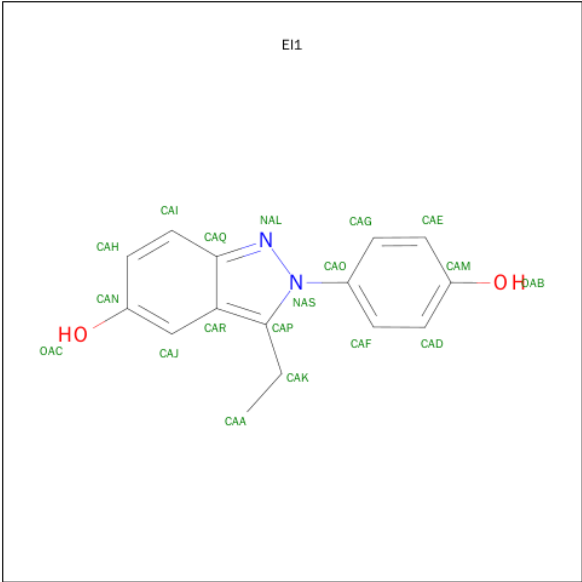
Chain	Residue	Modelled	Actual	Comment	Reference
A	297	SER	-	EXPRESSION TAG	UNP P03372
A	537	SER	TYR	ENGINEERED	UNP P03372
B	297	SER	-	EXPRESSION TAG	UNP P03372
B	537	SER	TYR	ENGINEERED	UNP P03372

- Molecule 2 is a protein called nuclear receptor coactivator 2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	11	Total	C	N	O	0	0	0
			94	60	20	14			
2	D	9	Total	C	N	O	0	0	0
			79	51	16	12			

- Molecule 3 is 3-ETHYL-2-(4-HYDROXYPHENYL)-2H-INDAZOL-5-OL (three-letter code: EI1) (formula: C<sub>15</sub>H<sub>14</sub>N<sub>2</sub>O<sub>2</sub>).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			19	15	2	2		
3	B	1	Total	C	N	O	0	0
			19	15	2	2		

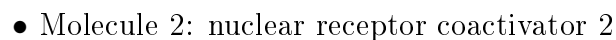
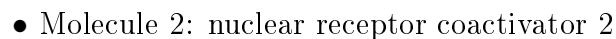
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	13	Total	O	0	0
			13	13		
4	B	3	Total	O	0	0
			3	3		





- Molecule 1: Estrogen receptor





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	55.82Å 83.08Å 58.30Å 90.00° 109.13° 90.00°	Depositor
Resolution (Å)	19.54 – 1.89 19.54 – 1.89	Depositor EDS
% Data completeness (in resolution range)	98.6 (19.54-1.89) 98.6 (19.54-1.89)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.27 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.224 , 0.270 0.224 , 0.268	Depositor DCC
$R_{free}$ test set	2012 reflections (5.34%)	DCC
Wilson B-factor (Å <sup>2</sup> )	31.7	Xtriage
Anisotropy	0.089	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 59.2	EDS
Estimated twinning fraction	0.027 for l,-k,h	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 39668 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	4099	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.23% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: EI1

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	0/1970	0.54	0/2661
1	B	0.45	1/2014 (0.0%)	0.52	0/2722
2	C	0.73	0/95	0.59	0/126
2	D	0.36	0/79	0.55	0/104
All	All	0.43	1/4158 (0.0%)	0.53	0/5613

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	467	LYS	CE-NZ	9.80	1.73	1.49

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	1908	0	1940	25	0
1	B	1964	0	2013	34	0
2	C	94	0	97	4	0
2	D	79	0	88	2	0
3	A	19	0	13	1	0
3	B	19	0	12	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	13	0	0	0	0
4	B	3	0	0	0	0
All	All	4099	0	4163	60	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 7.

All (60) 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:B:467:LYS:NZ	1:B:467:LYS:CE	1.73	1.51
1:A:528:MET:HE3	1:A:533:VAL:HG21	1.37	1.04
1:A:519:ASN:HD22	1:B:519:ASN:HD22	1.06	0.99
1:B:377:HIS:NE2	1:B:460:THR:HB	1.90	0.87
1:A:519:ASN:ND2	1:B:519:ASN:HD22	1.82	0.78
1:B:308:LEU:HD21	1:B:477:ARG:HB3	1.67	0.77
1:B:377:HIS:CE1	1:B:460:THR:HB	2.24	0.73
1:A:519:ASN:HD22	1:B:519:ASN:ND2	1.86	0.71
1:B:331:TYR:CE1	1:B:333:PRO:HA	2.27	0.70
1:B:331:TYR:CZ	1:B:333:PRO:HA	2.27	0.69
1:B:348:ASN:HD21	1:B:352:ARG:HH21	1.45	0.62
1:B:348:ASN:ND2	1:B:352:ARG:HH21	1.98	0.62
3:B:1:EI1:HAK2	3:B:1:EI1:HAF	1.81	0.61
1:B:467:LYS:NZ	1:B:467:LYS:CD	2.61	0.61
1:B:330:GLU:HG2	1:B:348:ASN:ND2	2.18	0.59
1:A:528:MET:CE	1:A:533:VAL:HG21	2.23	0.58
1:A:418:VAL:HG13	1:A:528:MET:CE	2.35	0.57
1:B:310:LEU:HD22	1:B:314:GLN:HB3	1.86	0.57
1:A:455:ASN:O	1:A:458:VAL:HG12	2.07	0.55
3:B:1:EI1:HAK2	3:B:1:EI1:CAF	2.35	0.55
1:A:322:ALA:HA	1:A:363:ARG:HE	1.72	0.54
1:B:458:VAL:HG22	1:B:472:LYS:HD3	1.89	0.54
1:A:418:VAL:HG13	1:A:528:MET:HE1	1.90	0.54
1:B:308:LEU:HA	1:B:481:LYS:HD2	1.90	0.54
1:A:392:VAL:HG11	1:A:431:THR:HG22	1.91	0.52
1:B:465:THR:O	1:B:469:LEU:HD13	2.10	0.52
1:B:455:ASN:O	1:B:458:VAL:HG12	2.10	0.52
2:C:691:HIS:O	2:C:695:GLN:HG2	2.10	0.51
1:A:418:VAL:CG1	1:A:528:MET:HE2	2.41	0.51
1:B:396:MET:CE	1:B:436:ARG:HA	2.42	0.49
1:B:464:SER:O	1:B:467:LYS:HE3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:366:GLY:O	1:B:474:HIS:HE1	1.95	0.48
2:C:689:ILE:HG23	2:C:692:ARG:HH12	1.79	0.46
1:B:396:MET:HE1	1:B:436:ARG:HA	1.97	0.45
1:A:401:LYS:HD3	1:A:409:LEU:HG	1.98	0.45
1:A:516:HIS:HA	1:B:519:ASN:HD21	1.82	0.45
1:B:497:LEU:HG	1:B:501[B]:HIS:HE1	1.81	0.44
1:A:332:ASP:OD2	1:A:334:THR:OG1	2.26	0.44
2:D:688:LYS:HB2	2:D:688:LYS:HE2	1.77	0.44
1:B:472:LYS:HE3	1:B:472:LYS:HB2	1.68	0.44
1:B:331:TYR:CE1	1:B:333:PRO:CA	2.99	0.44
2:C:689:ILE:HG23	2:C:692:ARG:NH1	2.33	0.44
1:A:330:GLU:O	1:A:331:TYR:C	2.57	0.43
1:A:359:ASN:HB3	1:A:363:ARG:HH12	1.84	0.43
1:A:331:TYR:CZ	1:A:333:PRO:HA	2.54	0.43
1:B:470:GLU:OE2	1:B:470:GLU:HA	2.19	0.43
1:B:313:ASP:OD1	1:B:488:HIS:NE2	2.49	0.43
1:A:424:ILE:HA	1:A:427:MET:HE2	2.00	0.43
1:B:358:ILE:CD1	2:D:693:LEU:HD23	2.49	0.43
1:A:358:ILE:CD1	2:C:693:LEU:HD13	2.49	0.42
1:A:308:LEU:HA	1:A:308:LEU:HD12	1.75	0.42
1:B:369:ASP:HB2	1:B:474:HIS:CE1	2.54	0.42
1:B:539:LEU:O	1:B:543:MET:HG2	2.19	0.42
1:A:470:GLU:HG2	1:A:471:GLU:N	2.34	0.42
1:A:306:LEU:N	1:A:306:LEU:HD22	2.34	0.41
1:A:459:TYR:CD2	1:B:513[A]:HIS:CE1	3.08	0.41
3:A:1:EI1:CAF	3:A:1:EI1:HAK2	2.50	0.41
1:A:498:GLN:HA	1:A:501[A]:HIS:CE1	2.56	0.41
1:B:371:THR:O	1:B:375:GLN:HG3	2.21	0.41
1:A:459:TYR:CE1	1:B:434:ARG:HD3	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	238/258 (92%)	234 (98%)	3 (1%)	1 (0%)	39	27
1	B	246/258 (95%)	239 (97%)	7 (3%)	0	100	100
2	C	9/13 (69%)	8 (89%)	1 (11%)	0	100	100
2	D	7/13 (54%)	7 (100%)	0	0	100	100
All	All	500/542 (92%)	488 (98%)	11 (2%)	1 (0%)	52	42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	331	TYR

### 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	218/233 (94%)	203 (93%)	15 (7%)	19	8
1	B	224/233 (96%)	215 (96%)	9 (4%)	38	26
2	C	10/13 (77%)	9 (90%)	1 (10%)	9	3
2	D	9/13 (69%)	8 (89%)	1 (11%)	8	2
All	All	461/492 (94%)	435 (94%)	26 (6%)	27	14

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

Mol	Chain	Res	Type
1	A	308	LEU
1	A	310	LEU
1	A	321	ASP
1	A	345	LEU
1	A	432	SER
1	A	470	GLU
1	A	471	GLU
1	A	481	LYS
1	A	497	LEU
1	A	501[A]	HIS

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Mol	Chain	Res	Type
1	A	501[B]	HIS
1	A	520	LYS
1	A	532	ASN
1	A	534	VAL
1	A	545	ASP
1	B	306	LEU
1	B	321[A]	ASP
1	B	348	ASN
1	B	460	THR
1	B	462	LEU
1	B	472	LYS
1	B	473	ASP
1	B	477	ARG
1	B	541	LEU
2	C	688	LYS
2	D	693	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	398	HIS
1	A	532	ASN
1	B	348	ASN
1	B	398	HIS
1	B	474	HIS
1	B	498	GLN
1	B	519	ASN
2	C	695	GLN
2	D	691	HIS
2	D	695	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules 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 [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	$\# Z  > 2$
3	EI1	A	1	-	19,21,21	2.63	3 (15%)	22,30,30	1.50	2 (9%)
3	EI1	B	1	-	19,21,21	2.56	3 (15%)	22,30,30	1.60	6 (27%)

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
3	EI1	A	1	-	-	0/6/6/6	0/3/3/3
3	EI1	B	1	-	-	0/6/6/6	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1	EI1	NAL-NAS	-8.04	1.24	1.39
3	B	1	EI1	NAL-NAS	-8.00	1.25	1.39
3	A	1	EI1	OAB-CAM	-5.71	1.23	1.37
3	B	1	EI1	OAB-CAM	-5.61	1.23	1.37
3	A	1	EI1	CAO-NAS	-4.19	1.35	1.44
3	B	1	EI1	CAO-NAS	-3.88	1.36	1.44

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1	EI1	CAN-CAJ-CAR	-2.13	119.25	120.53

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Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
3	B	1	EI1	CAG-CAO-CAF	-2.04	118.04	121.21
3	B	1	EI1	CAJ-CAR-CAQ	2.40	121.29	120.34
3	A	1	EI1	CAI-CAQ-NAL	2.62	133.49	129.94
3	B	1	EI1	CAI-CAQ-NAL	2.66	133.54	129.94
3	B	1	EI1	CAD-CAF-CAO	2.70	121.98	119.23
3	B	1	EI1	CAK-CAP-NAS	4.26	127.85	119.75
3	A	1	EI1	CAK-CAP-NAS	5.15	129.55	119.75

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1	EI1	1	0
3	B	1	EI1	2	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

### 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	236/258 (91%)	0.38	18 (7%) 17 18	20, 29, 52, 72	0
1	B	245/258 (94%)	0.45	21 (8%) 13 14	21, 29, 52, 80	2 (0%)
2	C	11/13 (84%)	1.57	3 (27%) 1 1	23, 30, 56, 67	0
2	D	9/13 (69%)	0.98	1 (11%) 7 8	27, 35, 44, 55	0
All	All	501/542 (92%)	0.45	43 (8%) 13 14	20, 29, 55, 80	2 (0%)

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	549	LEU	12.2
1	B	466	LEU	8.5
1	B	465	THR	7.7
1	A	334	THR	7.3
1	B	462	LEU	6.4
1	B	334	THR	5.9
2	C	686	LYS	5.6
2	D	696	ASP	5.3
1	B	333	PRO	5.0
1	B	306	LEU	4.7
1	A	336	PRO	4.6
1	A	533	VAL	4.3
2	C	687	HIS	3.8
1	B	463	SER	3.8
1	A	306	LEU	3.5
2	C	696	ASP	3.5
1	B	461	PHE	3.4
1	B	460	THR	3.4
1	A	346	LEU	3.3
1	B	468	SER	3.2
1	A	531	LYS	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	305	SER	3.2
1	B	335	ARG	3.0
1	A	333	PRO	2.9
1	B	467	LYS	2.9
1	A	305	SER	2.9
1	A	459	TYR	2.9
1	B	469	LEU	2.8
1	A	332	ASP	2.8
1	A	335	ARG	2.8
1	B	437	MET	2.7
1	B	501[A]	HIS	2.6
1	A	340	ALA	2.6
1	A	397	GLU	2.5
1	A	331	TYR	2.5
1	B	548	ARG	2.3
1	A	482	ILE	2.3
1	A	501[A]	HIS	2.2
1	A	337	PHE	2.2
1	B	482	ILE	2.1
1	A	470	GLU	2.1
1	B	470	GLU	2.1
1	B	332	ASP	2.1

## 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, 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	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	EI1	B	1	19/19	0.94	0.14	1.44	8,14,20,20	0
3	EI1	A	1	19/19	0.93	0.12	0.07	10,25,31,31	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.