



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:29 AM GMT

PDB ID : 2QXS  
Title : Crystal Structure of Antagonizing Mutant 536S of the Estrogen Receptor Alpha Ligand Binding Domain Complexed to Raloxifene  
Authors : Bruning, J.B.; Gil, G.; Nowak, J.; Katzenellenbogen, J.; Nettles, K.W.  
Deposited on : 2007-08-12  
Resolution : 1.70 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

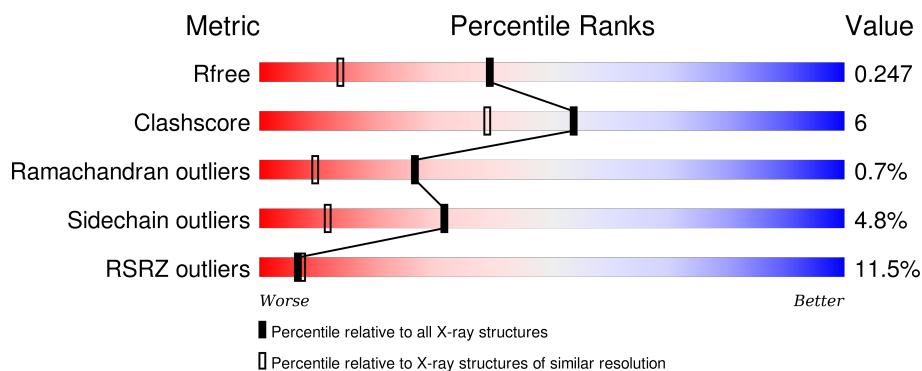
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.70 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))
$R_{free}$	91344	3190 (1.70-1.70)
Clashscore	102246	3585 (1.70-1.70)
Ramachandran outliers	100387	3527 (1.70-1.70)
Sidechain outliers	100360	3527 (1.70-1.70)
RSRZ outliers	91569	3200 (1.70-1.70)

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  $\geq 3$ , 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>11%</div> <div>79%</div> <div>11%</div> <div>•</div> <div>8%</div> </div>
1	B	258	<div> <div>9%</div> <div>74%</div> <div>13%</div> <div>•</div> <div>12%</div> </div>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4077 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.

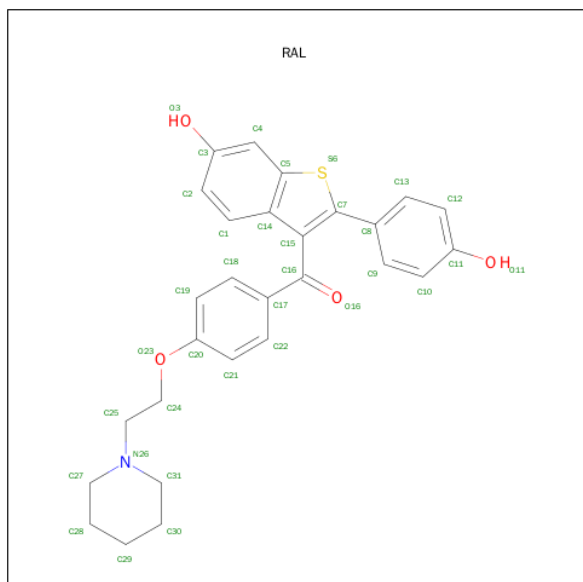
- Molecule 1 is a protein called Estrogen receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	237	Total	C	N	O	S	8	10	0
			1902	1222	319	340	21			
1	B	226	Total	C	N	O	S	7	7	0
			1807	1160	306	319	22			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	297	SER	-	EXPRESSION TAG	UNP P03372
A	536	SER	LEU	ENGINEERED	UNP P03372
B	297	SER	-	EXPRESSION TAG	UNP P03372
B	536	SER	LEU	ENGINEERED	UNP P03372

- Molecule 2 is RALOXIFENE (three-letter code: RAL) (formula:  $C_{28}H_{27}NO_4S$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			34	28	1	4	1		
2	B	1	Total	C	N	O	S	0	0
			34	28	1	4	1		

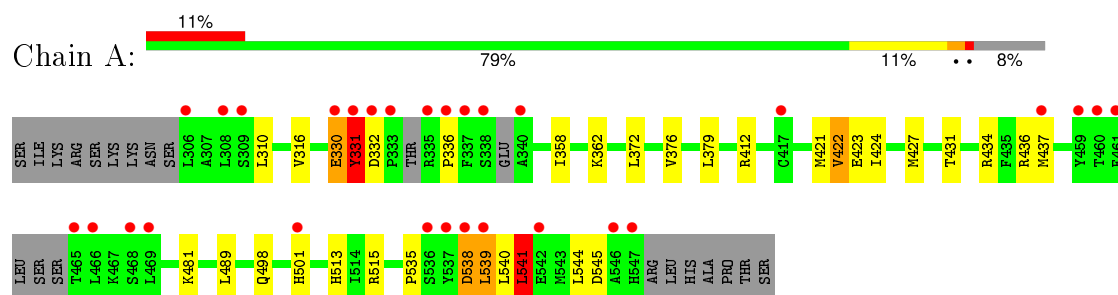
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	153	Total	O	0	0
			153	153		
3	B	147	Total	O	0	0
			147	147		

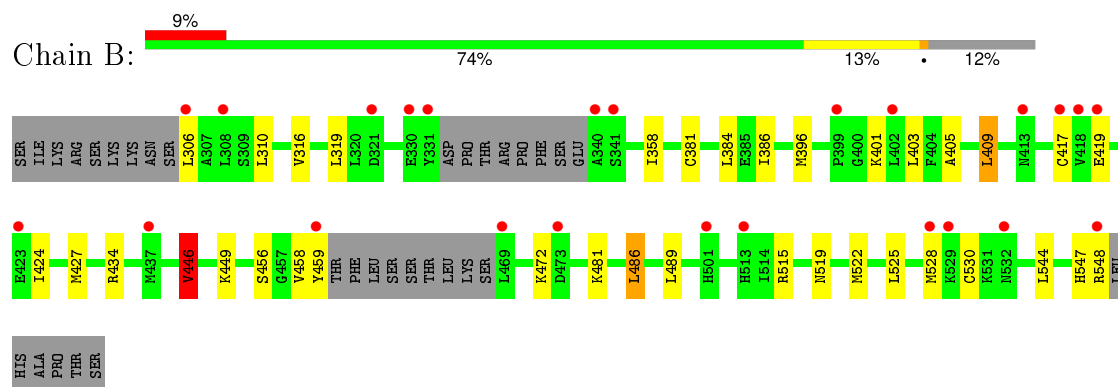
### 3 Residue-property plots [i](#)

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: Estrogen receptor



#### • Molecule 1: Estrogen receptor



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	101.59Å 58.10Å 87.95Å 90.00° 102.66° 90.00°	Depositor
Resolution (Å)	15.00 – 1.70 14.95 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.8 (15.00-1.70) 99.8 (14.95-1.70)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.81 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.183 , 0.216 0.220 , 0.247	Depositor DCC
$R_{free}$ test set	2795 reflections (5.35%)	DCC
Wilson B-factor (Å <sup>2</sup> )	16.9	Xtriage
Anisotropy	0.048	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.44 , 53.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 55018 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	4077	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	10.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.90% 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 ⓘ

### 5.1 Standard geometry ⓘ

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

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	0.57	0/1953	0.72	4/2638 (0.2%)
1	B	0.53	1/1852 (0.1%)	0.70	2/2499 (0.1%)
All	All	0.56	1/3805 (0.0%)	0.71	6/5137 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	1	1
1	B	0	1
All	All	1	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	548	ARG	C-O	6.80	1.36	1.23

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	436	ARG	NE-CZ-NH2	-6.60	117.00	120.30
1	A	436	ARG	NE-CZ-NH1	6.00	123.30	120.30
1	B	486	LEU	CA-CB-CG	5.70	128.40	115.30
1	A	331	TYR	N-CA-CB	5.68	120.83	110.60
1	A	541	LEU	CA-CB-CG	5.68	128.36	115.30
1	B	446	VAL	CG1-CB-CG2	5.31	119.40	110.90

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	332	ASP	CA

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	330	GLU	Peptide
1	B	547	HIS	Peptide

## 5.2 Too-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 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	1902	0	1935	27	0
1	B	1807	0	1850	25	0
2	A	34	0	25	0	0
2	B	34	0	27	0	0
3	A	153	0	0	12	0
3	B	147	0	0	7	0
All	All	4077	0	3837	49	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 6.

All (49) 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:545:ASP:HB2	3:A:722:HOH:O	1.34	1.22
1:B:386:ILE:HG12	3:B:719:HOH:O	1.54	1.07
1:A:421:MET:HE1	3:A:738:HOH:O	1.62	0.98
1:A:541:LEU:HD13	3:A:722:HOH:O	1.68	0.92
1:A:372[A]:LEU:HD21	3:A:722:HOH:O	1.72	0.87
1:A:539:LEU:HB3	3:A:733:HOH:O	1.73	0.87
1:A:310:LEU:O	1:A:481:LYS:HE3	1.79	0.82
1:B:519:ASN:ND2	3:B:707:HOH:O	2.17	0.76
1:A:541:LEU:O	1:A:545:ASP:N	2.19	0.74
1:B:515:ARG:NH2	3:B:738:HOH:O	2.20	0.74
1:A:362:LYS:HE2	3:A:624:HOH:O	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:459:TYR:HB2	3:B:685:HOH:O	1.90	0.70
1:A:540:LEU:HG	3:A:733:HOH:O	1.93	0.68
1:B:515:ARG:HD2	3:B:707:HOH:O	1.95	0.67
1:A:423:GLU:HB2	3:A:657:HOH:O	2.00	0.61
1:A:422:VAL:HG22	3:A:628:HOH:O	2.02	0.60
1:B:401:LYS:HB3	1:B:409:LEU:HD22	1.84	0.60
1:B:403:LEU:CD2	1:B:409:LEU:HG	2.31	0.59
1:B:319:LEU:HB3	1:B:446:VAL:HG13	1.87	0.56
1:B:310:LEU:O	1:B:481:LYS:CE	2.55	0.55
1:A:424:ILE:HA	1:A:427:MET:CE	2.38	0.54
1:B:316:VAL:HG21	1:B:489:LEU:HD21	1.90	0.54
1:B:403:LEU:HD23	1:B:409:LEU:HG	1.90	0.54
1:A:513[B]:HIS:CE1	1:B:459:TYR:CD1	2.96	0.53
1:A:541:LEU:O	1:A:545:ASP:CB	2.56	0.53
1:A:535:PRO:HB2	3:A:733:HOH:O	2.08	0.53
1:A:372[A]:LEU:HD11	3:A:722:HOH:O	2.09	0.52
1:B:528:MET:HE2	1:B:530:CME:SG	2.51	0.51
1:A:424:ILE:HA	1:A:427:MET:HE3	1.93	0.51
1:A:310:LEU:O	1:A:481:LYS:CE	2.57	0.50
1:A:538:ASP:HA	1:A:541:LEU:HB2	1.94	0.49
1:B:449:LYS:HG3	3:B:719:HOH:O	2.12	0.49
1:B:310:LEU:O	1:B:481:LYS:HE3	2.14	0.48
1:A:498:GLN:HA	1:A:501[B]:HIS:CE1	2.49	0.47
1:A:379:LEU:HD12	1:A:544:LEU:HD11	1.96	0.46
1:B:358:ILE:HG23	1:B:544:LEU:HD23	1.97	0.46
1:A:513[B]:HIS:CG	1:B:459:TYR:CE1	3.03	0.45
1:A:513[B]:HIS:CE1	1:B:459:TYR:CE1	3.05	0.45
1:B:403:LEU:HD22	1:B:409:LEU:HG	1.99	0.44
1:A:316:VAL:HG21	1:A:489:LEU:HD21	1.99	0.44
1:B:319:LEU:CB	1:B:446:VAL:HG13	2.49	0.42
1:B:424:ILE:HA	1:B:427:MET:CE	2.49	0.42
1:A:412:ARG:HB2	3:A:636:HOH:O	2.19	0.42
1:B:381[B]:CYS:SG	1:B:456:SER:O	2.78	0.41
1:A:431:THR:OG1	1:A:513[A]:HIS:CD2	2.74	0.41
1:B:384:LEU:HD23	1:B:522:MET:HG2	2.03	0.41
1:B:405:ALA:HA	3:B:732:HOH:O	2.22	0.40
1:B:458:VAL:O	1:B:472:LYS:HE2	2.21	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	237/258 (92%)	233 (98%)	1 (0%)	3 (1%)	15	2
1	B	226/258 (88%)	223 (99%)	3 (1%)	0	100	100
All	All	463/516 (90%)	456 (98%)	4 (1%)	3 (1%)	26	12

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	331	TYR
1	A	332	ASP
1	A	336	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	213/232 (92%)	203 (95%)	10 (5%)	32	12
1	B	201/232 (87%)	191 (95%)	10 (5%)	30	11
All	All	414/464 (89%)	394 (95%)	20 (5%)	31	12

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	330	GLU
1	A	331	TYR
1	A	358	ILE

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Mol	Chain	Res	Type
1	A	422	VAL
1	A	434	ARG
1	A	437	MET
1	A	515	ARG
1	A	538	ASP
1	A	539	LEU
1	A	541	LEU
1	B	306	LEU
1	B	396	MET
1	B	409	LEU
1	B	417[A]	CYS
1	B	417[B]	CYS
1	B	419	GLU
1	B	434	ARG
1	B	446	VAL
1	B	486	LEU
1	B	525	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	488	HIS
1	A	502	GLN
1	A	547	HIS
1	B	502	GLN
1	B	513	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	$\# Z  > 2$
1	CME	A	530	1	8,9,10	0.75	0	6,9,11	1.44	1 (16%)
1	CME	B	530	1	4,5,10	0.74	0	3,5,11	1.30	1 (33%)

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
1	CME	A	530	1	-	0/5/8/10	0/0/0/0
1	CME	B	530	1	-	0/1/4/10	0/0/0/0

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	530	CME	O-C-CA	-2.26	119.59	125.49
1	B	530	CME	O-C-CA	-2.12	119.97	125.49

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	530	CME	1	0

## 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	RAL	A	600	-	33,38,38	0.84	1 (3%)	40,53,53	1.36	3 (7%)
2	RAL	B	600	-	33,38,38	0.97	1 (3%)	40,53,53	1.11	1 (2%)

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	RAL	A	600	-	-	0/15/26/26	0/5/5/5
2	RAL	B	600	-	-	0/15/26/26	0/5/5/5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	600	RAL	C4-C3	2.15	1.41	1.37
2	B	600	RAL	C4-C3	2.17	1.41	1.37

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	600	RAL	C2-C1-C14	-3.96	115.93	121.13
2	B	600	RAL	C2-C1-C14	-3.39	116.68	121.13
2	A	600	RAL	C3-C4-C5	-2.63	117.59	120.36
2	A	600	RAL	C25-N26-C27	-2.20	105.61	111.27

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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	236/258 (91%)	0.69	29 (12%)	5 6	2, 5, 20, 49	3 (1%)
1	B	225/258 (87%)	0.73	24 (10%)	8 8	2, 8, 24, 31	2 (0%)
All	All	461/516 (89%)	0.71	53 (11%)	6 7	2, 7, 21, 49	5 (1%)

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	340	ALA	12.0
1	A	340	ALA	9.4
1	B	306	LEU	8.8
1	B	331	TYR	7.9
1	B	459	TYR	7.4
1	A	338	SER	6.0
1	A	337	PHE	5.5
1	A	335	ARG	5.5
1	A	537	TYR	5.3
1	B	532	ASN	5.1
1	A	417	CYS	5.1
1	A	460	THR	5.1
1	A	461	PHE	4.8
1	B	417[A]	CYS	4.8
1	B	437	MET	4.7
1	A	336	PRO	4.6
1	A	465	THR	4.5
1	B	469	LEU	4.2
1	A	547	HIS	4.1
1	B	501[A]	HIS	4.0
1	A	542	GLU	3.7
1	A	459	TYR	3.6
1	B	308	LEU	3.6
1	A	538	ASP	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	332	ASP	3.2
1	A	437	MET	3.2
1	A	331	TYR	3.2
1	A	306	LEU	3.1
1	A	466	LEU	3.1
1	A	539	LEU	3.0
1	A	501[A]	HIS	2.7
1	A	333	PRO	2.7
1	B	528	MET	2.7
1	B	413	ASN	2.7
1	A	536	SER	2.6
1	A	330	GLU	2.5
1	A	469	LEU	2.5
1	B	419	GLU	2.5
1	A	309[A]	SER	2.5
1	B	513	HIS	2.5
1	B	341	SER	2.4
1	B	548	ARG	2.4
1	B	330	GLU	2.4
1	B	473	ASP	2.3
1	B	529	LYS	2.3
1	A	546	ALA	2.2
1	B	418	VAL	2.2
1	A	468	SER	2.2
1	A	308	LEU	2.2
1	B	399	PRO	2.1
1	B	321	ASP	2.1
1	B	402	LEU	2.1
1	B	423	GLU	2.0

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

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(Å <sup>2</sup> )	Q<0.9
1	CME	B	530	6/11	0.68	0.22	-	14,15,15,22	0
1	CME	A	530	10/11	0.83	0.13	-	14,15,29,29	0



### 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
2	RAL	B	600	34/34	0.95	0.11	-0.02	6,10,14,16	0
2	RAL	A	600	34/34	0.96	0.10	-0.33	4,6,13,14	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.