



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 02:13 pm GMT

PDB ID : 4ZNV  
Title : Crystal Structure of the ER-alpha Ligand-binding Domain (Y537S) in complex with a 2-Methoxy-substituted OBHS derivative  
Authors : Nwachukwu, J.C.; Srinivasan, S.; Zheng, Y.; Wang, S.; Min, J.; Dong, C.; Liao, Z.; Cavett, V.; Nowak, J.; Houtman, R.; Carlson, K.E.; Josan, J.S.; Elemento, O.; Katzenellenbogen, J.A.; Zhou, H.B.; Nettles, K.W.  
Deposited on : 2015-05-05  
Resolution : 1.77 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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : recalc28949

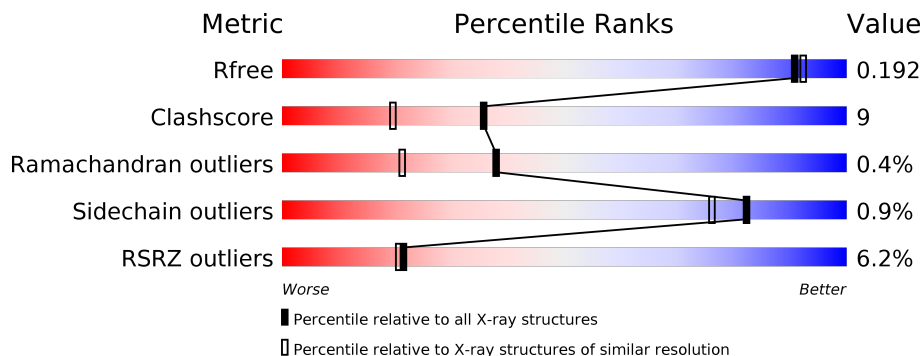
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.77 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))
$R_{free}$	100719	7172 (1.80-1.76)
Clashscore	112137	8247 (1.80-1.76)
Ramachandran outliers	110173	8154 (1.80-1.76)
Sidechain outliers	110143	8153 (1.80-1.76)
RSRZ outliers	101464	7262 (1.80-1.76)

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	259	<div> <div>5%</div> <div> <div></div> <div>77%</div> <div>14%</div> <div>8%</div> </div> </div>
1	B	259	<div> <div>7%</div> <div> <div></div> <div>79%</div> <div>15%</div> <div>6%</div> </div> </div>
2	C	13	<div> <div></div> <div> <div></div> <div>54%</div> <div>15%</div> <div>31%</div> </div> </div>
2	D	13	<div> <div>8%</div> <div> <div></div> <div>54%</div> <div>23%</div> <div>23%</div> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4421 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	0	2	0
			1891	1210	328	334	19			
1	B	243	Total	C	N	O	S	0	7	0
			1969	1261	342	347	19			

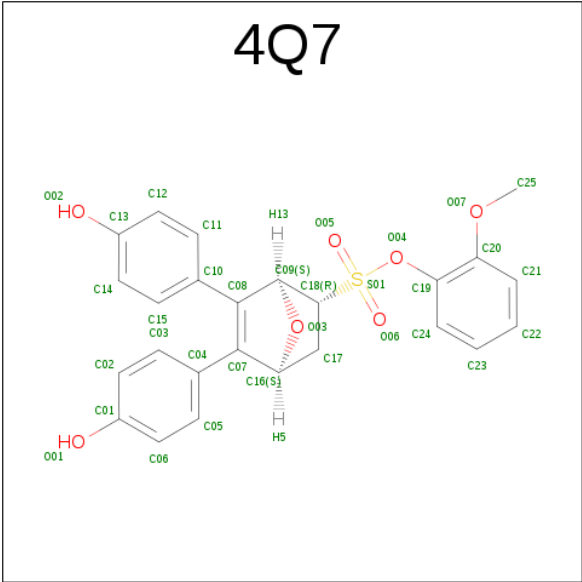
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	537	SER	TYR	engineered mutation	UNP P03372
B	537	SER	TYR	engineered mutation	UNP P03372

- Molecule 2 is a protein called Nuclear receptor-interacting peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	9	Total	C	N	O	0	0	0
			79	51	16	12			
2	D	10	Total	C	N	O	0	0	0
			89	57	19	13			

- Molecule 3 is 2-methoxyphenyl (1S,2R,4S)-5,6-bis(4-hydroxyphenyl)-7-oxabicyclo[2.2.1]hept-5-ene-2-sulfonate (three-letter code: 4Q7) (formula: C<sub>25</sub>H<sub>22</sub>O<sub>7</sub>S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	S	0	0
			33	25	7	1		
3	B	1	Total	C	O	S	0	0
			33	25	7	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	181	Total	O	0	0
			181	181		
4	B	135	Total	O	0	0
			135	135		
4	C	6	Total	O	0	0
			6	6		
4	D	5	Total	O	0	0
			5	5		



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	54.82Å 81.22Å 58.59Å 90.00° 111.21° 90.00°	Depositor
Resolution (Å)	32.59 – 1.77 32.59 – 1.77	Depositor EDS
% Data completeness (in resolution range)	96.3 (32.59-1.77) 96.1 (32.59-1.77)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.15 (at 1.77Å)	Xtriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.178 , 0.197 0.177 , 0.192	Depositor DCC
$R_{free}$ test set	1934 reflections (4.51%)	DCC
Wilson B-factor (Å <sup>2</sup> )	28.5	Xtriage
Anisotropy	0.104	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 48.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	4421	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.50% 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, 0.333 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: 4Q7

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	0.34	0/1933	0.48	0/2612
1	B	0.32	0/2024	0.46	0/2735
2	C	0.21	0/79	0.45	0/104
2	D	0.30	0/90	0.53	0/119
All	All	0.33	0/4126	0.47	0/5570

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	1891	0	1934	43	0
1	B	1969	0	2032	41	0
2	C	79	0	88	2	0
2	D	89	0	95	4	0
3	A	33	0	0	0	0
3	B	33	0	0	1	0
4	A	181	0	0	12	1
4	B	135	0	0	9	1
4	C	6	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	5	0	0	0	0
All	All	4421	0	4149	76	1

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 9.

All (76) 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:459:TYR:HE1	1:B:513:HIS:CD2	1.81	0.97
1:B:390:GLY:O	1:B:394[B]:ARG:HD2	1.69	0.93
1:A:334:THR:HG22	1:A:335:ARG:H	1.37	0.88
1:A:373[A]:HIS:ND1	4:A:703:HOH:O	2.07	0.88
1:B:363[A]:ARG:NH1	4:B:701:HOH:O	2.08	0.87
1:B:473:ASP:OD2	1:B:477:ARG:NH1	2.12	0.82
1:A:459:TYR:CE1	1:B:513:HIS:CD2	2.69	0.81
2:D:688:LYS:HD2	2:D:691:HIS:HE1	1.49	0.77
2:D:688:LYS:HB2	2:D:691:HIS:ND1	1.99	0.77
1:A:397:GLU:OE1	4:A:701:HOH:O	2.04	0.75
2:C:695:GLN:OE1	4:C:701:HOH:O	2.06	0.73
2:D:688:LYS:HD2	2:D:691:HIS:CE1	2.26	0.71
1:A:415:GLY:HA2	1:A:421:MET:HE3	1.76	0.67
1:A:490:MET:HB3	1:A:495:LEU:HD12	1.79	0.65
1:A:392:VAL:HG13	1:A:432:SER:HA	1.79	0.64
1:B:530:CYS:SG	4:B:813:HOH:O	2.09	0.64
1:A:531:LYS:NZ	4:A:702:HOH:O	2.19	0.64
1:A:373[A]:HIS:CE1	4:A:703:HOH:O	2.50	0.60
1:A:520:LYS:NZ	4:A:707:HOH:O	2.30	0.60
1:B:363[A]:ARG:NH2	4:B:702:HOH:O	2.16	0.60
1:A:456:SER:HA	1:A:515:ARG:NH2	2.16	0.60
1:A:459:TYR:CD1	1:B:513:HIS:CE1	2.91	0.59
1:A:459:TYR:CE1	1:B:513:HIS:CG	2.92	0.57
1:A:473:ASP:OD2	1:A:477:ARG:HD2	2.05	0.57
1:A:459:TYR:HD1	1:B:513:HIS:CE1	2.25	0.55
1:B:343:MET:SD	3:B:601:4Q7:C25	2.95	0.55
1:A:459:TYR:HD1	1:B:513:HIS:ND1	2.04	0.55
1:A:392:VAL:HG13	1:A:432:SER:CA	2.37	0.55
1:A:548:ARG:NE	4:A:702:HOH:O	2.06	0.54
1:B:539:LEU:O	1:B:543:MET:HG2	2.08	0.53
1:B:335[A]:ARG:CZ	4:B:705:HOH:O	2.55	0.53
1:B:347[A]:THR:HG23	1:B:540:LEU:CD1	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:513:HIS:CE1	1:B:459:TYR:HD2	2.28	0.51
1:B:477:ARG:NH2	4:B:703:HOH:O	2.25	0.51
1:B:363[A]:ARG:NE	4:B:702:HOH:O	2.36	0.51
1:A:545:ASP:OD1	1:A:549:LEU:HD13	2.11	0.50
1:B:308:LEU:HA	1:B:481:LYS:CD	2.42	0.50
1:B:396:MET:O	1:B:436:ARG:HD3	2.12	0.50
1:B:415:GLY:HA2	1:B:421:MET:HE2	1.94	0.49
1:B:473:ASP:OD2	1:B:477:ARG:CZ	2.60	0.49
1:B:308:LEU:HA	1:B:481:LYS:HD2	1.94	0.49
1:A:334:THR:HG22	1:A:335:ARG:N	2.16	0.48
1:B:351:ASP:OD1	1:B:537:SER:OG	2.20	0.48
1:A:455:ASN:O	1:B:513:HIS:CE1	2.67	0.48
1:B:356:HIS:HD2	4:B:815:HOH:O	1.97	0.47
1:A:513:HIS:CE1	1:B:459:TYR:CD2	3.03	0.47
1:A:498:GLN:HA	1:A:501:HIS:CE1	2.49	0.47
1:A:459:TYR:CD1	1:B:513:HIS:ND1	2.82	0.47
1:A:392:VAL:HG11	1:A:431:THR:HG22	1.96	0.47
1:A:550:HIS:CD2	4:A:778:HOH:O	2.68	0.47
1:A:548:ARG:HD2	4:A:763:HOH:O	2.15	0.46
1:B:347[A]:THR:HG23	1:B:540:LEU:HD13	1.98	0.46
1:A:456:SER:HA	1:A:515:ARG:HH22	1.80	0.45
1:B:347[B]:THR:HG22	4:B:735:HOH:O	2.17	0.45
1:A:459:TYR:CE1	1:B:513:HIS:NE2	2.84	0.45
1:A:542:GLU:OE2	4:A:704:HOH:O	2.21	0.45
1:A:339:GLU:HG2	1:A:533:VAL:HG11	1.98	0.45
1:B:403:LEU:HA	1:B:409:LEU:HD12	2.00	0.44
1:B:347[A]:THR:HG21	1:B:536:LEU:CD2	2.47	0.44
1:A:451:ILE:HG13	1:A:482:ILE:HG21	2.00	0.43
1:A:550:HIS:HD2	4:A:778:HOH:O	2.00	0.43
1:B:516:HIS:O	1:B:520:LYS:HG2	2.19	0.43
1:B:347[A]:THR:HG21	1:B:536:LEU:HD22	2.00	0.43
1:B:389:ILE:HA	1:B:392:VAL:HG22	2.00	0.43
1:A:373[A]:HIS:CE1	4:A:732:HOH:O	2.72	0.42
1:A:459:TYR:CD1	1:B:513:HIS:CG	3.07	0.42
1:A:376:VAL:HG13	2:D:690:LEU:HD23	2.01	0.42
1:B:456:SER:HA	1:B:515:ARG:NH2	2.35	0.42
1:B:372[B]:LEU:CD2	2:C:691:HIS:CE1	3.03	0.42
1:A:549:LEU:HA	1:A:549:LEU:HD12	1.75	0.41
1:A:381:CYS:SG	4:A:870:HOH:O	2.09	0.41
1:B:401:LYS:HD3	1:B:411:ASP:HB3	2.03	0.41
1:A:424:ILE:HD13	1:A:427:MET:CE	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:415:GLY:HA2	1:A:421:MET:CE	2.45	0.40
1:B:368:VAL:HG22	4:B:740:HOH:O	2.20	0.40
1:A:448:LEU:HD11	1:A:507:LEU:HD22	2.04	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:816:HOH:O	4:B:775:HOH:O[2_555]	1.98	0.22

## 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	233/259 (90%)	228 (98%)	4 (2%)	1 (0%)	38	21
1	B	246/259 (95%)	240 (98%)	5 (2%)	1 (0%)	38	21
2	C	7/13 (54%)	7 (100%)	0	0	100	100
2	D	8/13 (62%)	7 (88%)	1 (12%)	0	100	100
All	All	494/544 (91%)	482 (98%)	10 (2%)	2 (0%)	38	21

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	334	THR
1	B	336	PRO

### 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	212/231 (92%)	208 (98%)	4 (2%)	62	48
1	B	222/231 (96%)	221 (100%)	1 (0%)	91	89
2	C	9/13 (69%)	9 (100%)	0	100	100
2	D	10/13 (77%)	10 (100%)	0	100	100
All	All	453/488 (93%)	448 (99%)	5 (1%)	82	70

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

Mol	Chain	Res	Type
1	A	373[A]	HIS
1	A	373[B]	HIS
1	A	526	TYR
1	A	549	LEU
1	B	497	LEU

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

Mol	Chain	Res	Type
2	C	691	HIS
2	D	691	HIS

### 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 ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

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	4Q7	A	601	-	33,37,37	2.14	9 (27%)	44,55,55	2.46	12 (27%)
3	4Q7	B	601	-	33,37,37	2.39	16 (48%)	44,55,55	2.74	15 (34%)

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	4Q7	A	601	-	-	0/19/45/45	0/3/5/5
3	4Q7	B	601	-	-	0/19/45/45	0/3/5/5

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	601	4Q7	C10-C08	-6.34	1.35	1.48
3	B	601	4Q7	C04-C07	-5.72	1.37	1.48
3	A	601	4Q7	C04-C07	-5.48	1.37	1.48
3	A	601	4Q7	C10-C08	-5.38	1.37	1.48
3	B	601	4Q7	C20-C19	-2.67	1.35	1.40
3	A	601	4Q7	C20-C19	-2.54	1.35	1.40
3	A	601	4Q7	O04-C19	-2.49	1.36	1.42
3	B	601	4Q7	C03-C04	-2.32	1.35	1.39
3	B	601	4Q7	C02-C03	-2.30	1.34	1.38
3	B	601	4Q7	C14-C13	-2.22	1.34	1.38
3	B	601	4Q7	C14-C15	-2.20	1.34	1.38
3	B	601	4Q7	C22-C21	-2.19	1.34	1.38
3	B	601	4Q7	C11-C10	-2.19	1.35	1.39
3	A	601	4Q7	C23-C24	-2.18	1.34	1.38
3	B	601	4Q7	C23-C24	-2.17	1.34	1.38
3	B	601	4Q7	C15-C10	-2.17	1.35	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	601	4Q7	C24-C19	-2.16	1.35	1.39
3	A	601	4Q7	C22-C21	-2.13	1.34	1.38
3	B	601	4Q7	C06-C01	-2.07	1.34	1.38
3	A	601	4Q7	C14-C15	-2.04	1.35	1.38
3	B	601	4Q7	C21-C20	-2.01	1.35	1.39
3	A	601	4Q7	O05-S01	2.66	1.46	1.43
3	B	601	4Q7	O06-S01	2.68	1.46	1.43
3	A	601	4Q7	O04-S01	3.02	1.64	1.60
3	B	601	4Q7	O04-S01	3.32	1.65	1.60

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	601	4Q7	O06-S01-C18	-12.56	97.32	109.24
3	A	601	4Q7	O06-S01-C18	-9.64	100.09	109.24
3	B	601	4Q7	O05-S01-C18	-7.91	101.73	109.24
3	A	601	4Q7	O05-S01-C18	-7.73	101.91	109.24
3	A	601	4Q7	C09-C08-C07	-3.41	102.39	108.28
3	A	601	4Q7	C11-C10-C15	-2.85	114.64	118.58
3	B	601	4Q7	C05-C04-C03	-2.73	114.79	118.58
3	B	601	4Q7	C09-C08-C07	-2.42	104.11	108.28
3	A	601	4Q7	O03-C16-C17	-2.38	100.65	104.88
3	B	601	4Q7	C16-C07-C08	-2.37	102.86	107.11
3	B	601	4Q7	C11-C10-C15	-2.14	115.62	118.58
3	B	601	4Q7	O03-C16-C17	-2.11	101.14	104.88
3	A	601	4Q7	C05-C04-C03	-2.02	115.78	118.58
3	B	601	4Q7	O04-S01-O06	2.03	113.04	106.69
3	B	601	4Q7	C11-C10-C08	2.08	123.61	120.91
3	A	601	4Q7	C14-C15-C10	2.10	123.14	120.79
3	B	601	4Q7	C11-C12-C13	2.21	122.38	119.88
3	A	601	4Q7	C04-C07-C08	2.35	133.59	128.28
3	B	601	4Q7	C14-C15-C10	2.43	123.51	120.79
3	A	601	4Q7	O04-S01-O05	2.48	114.44	106.69
3	B	601	4Q7	C06-C05-C04	2.55	123.65	120.79
3	B	601	4Q7	C04-C07-C08	2.60	134.15	128.28
3	A	601	4Q7	C25-O07-C20	2.63	121.32	117.54
3	A	601	4Q7	O04-S01-O06	2.78	115.37	106.69
3	B	601	4Q7	C10-C08-C07	3.36	135.86	128.28
3	B	601	4Q7	O04-S01-O05	3.58	117.88	106.69
3	A	601	4Q7	C10-C08-C07	4.31	138.01	128.28

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
3	B	601	4Q7	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, 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	237/259 (91%)	0.08	12 (5%) 29 28	20, 34, 61, 108	0
1	B	243/259 (93%)	0.22	18 (7%) 15 15	21, 36, 71, 84	0
2	C	9/13 (69%)	0.49	0 100 100	35, 52, 62, 71	0
2	D	10/13 (76%)	0.30	1 (10%) 8 7	33, 37, 72, 82	0
All	All	499/544 (91%)	0.16	31 (6%) 21 21	20, 35, 70, 108	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	534	VAL	6.2
1	B	306	LEU	6.1
1	B	533	VAL	4.8
1	A	333	PRO	4.7
1	A	458	VAL	3.9
1	B	528	MET	3.9
1	B	468	SER	3.7
1	B	536	LEU	3.6
1	B	372[A]	LEU	3.3
1	A	514	ILE	3.3
1	A	472	LYS	3.3
2	D	696	ASP	3.2
1	B	337	PHE	2.9
1	B	511	LEU	2.8
1	A	457	GLY	2.8
1	B	335[A]	ARG	2.6
1	A	509	LEU	2.6
1	A	460	THR	2.5
1	B	368	VAL	2.5
1	A	310	LEU	2.5
1	B	373	HIS	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	509	LEU	2.5
1	A	373[A]	HIS	2.4
1	B	529	LYS	2.3
1	B	532	ASN	2.1
1	B	535	PRO	2.1
1	A	510	ILE	2.1
1	A	516	HIS	2.1
1	B	334	THR	2.0
1	B	467	LYS	2.0
1	A	550	HIS	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, 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
3	4Q7	A	601	33/33	0.96	0.11	0.32	19,22,29,38	0
3	4Q7	B	601	33/33	0.95	0.09	-0.17	23,28,41,42	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.