



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 06:25 AM GMT

PDB ID : 2HWQ
Title : Structural basis for the structure-activity relationships of Peroxisome Proliferator-Activated Receptor agonists
Authors : Peng, Y.H.; Lu, I.L.; Mahindroo, N.; Lin, C.H.; Hsieh, H.P.; Wu, S.Y.
Deposited on : 2006-08-01
Resolution : 1.97 Å (reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

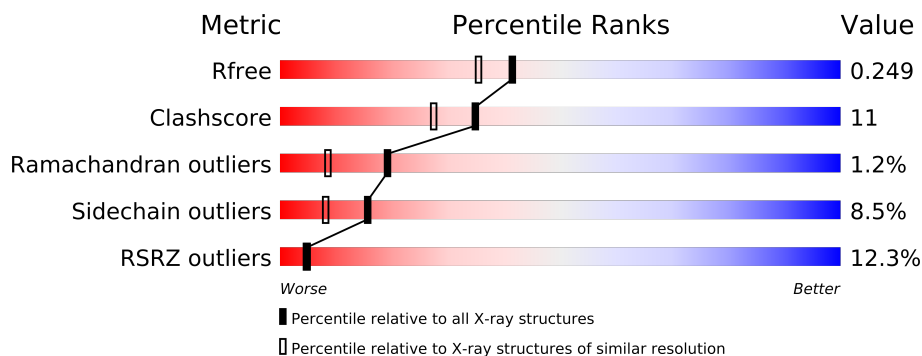
The following versions of software and data (see [references](#)) were used in the production of this report:

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 1.97 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	6577 (2.00-1.96)
Clashscore	79885	8091 (2.00-1.96)
Ramachandran outliers	78287	7989 (2.00-1.96)
Sidechain outliers	78261	7987 (2.00-1.96)
RSRZ outliers	66119	6578 (2.00-1.96)

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. 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	271	
1	B	271	

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	DRY	A	1101	-	X

2 Entry composition i

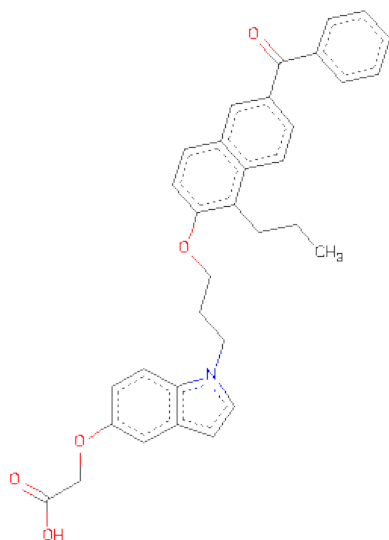
There are 3 unique types of molecules in this entry. The entry contains 4347 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Peroxisome proliferator-activated receptor gamma.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	261	Total	C	N	O	S	0	0	0
			2096	1355	340	391	10			
1	B	253	Total	C	N	O	S	0	0	0
			2017	1296	331	380	10			

- Molecule 2 is [(1-{3-[(6-BENZOYL-1-PROPYL-2-NAPHTHYL)OXY]PROPYL}-1H-INDO L-5-YL)OXY]ACETICACID (three-letter code: DRY) (formula: C₃₃H₃₁NO₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			39	33	1	5		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	82	Total	O	0	0
			82	82		

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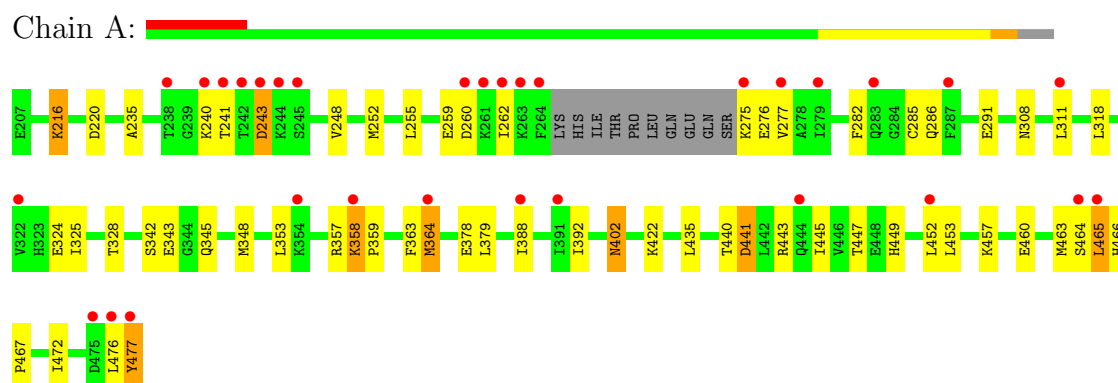
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	113	Total 113	O 113	0	0

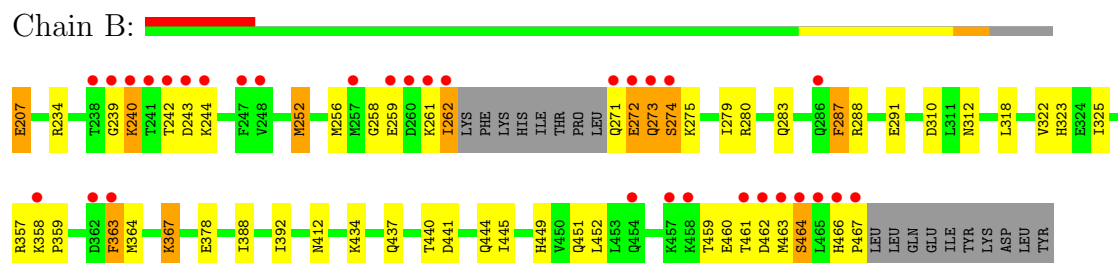
3 Residue-property plots

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: Peroxisome proliferator-activatedreceptor gamma



- Molecule 1: Peroxisome proliferator-activatedreceptor gamma



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	56.02Å 88.67Å 58.02Å 90.00° 90.24° 90.00°	Depositor
Resolution (Å)	30.00 – 1.97 26.14 – 1.97	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-1.97) 99.2 (26.14-1.97)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.90 (at 1.96Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.239 , 0.265 0.227 , 0.249	Depositor DCC
R_{free} test set	1999 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	28.4	Xtriage
Anisotropy	0.091	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 47.0	EDS
Estimated twinning fraction	0.000 for l,k,-h 0.032 for h,-k,-l 0.019 for l,-k,h	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 39914 reflections (0.003%)	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4347	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.38% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities 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: DRY

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	0.52	1/2131 (0.0%)	0.64	0/2868
1	B	0.44	0/2049	0.67	0/2759
All	All	0.48	1/4180 (0.0%)	0.66	0/5627

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	477	TYR	C-OXT	14.37	1.50	1.23

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	2096	0	2157	48	0
1	B	2017	0	2069	42	0
2	A	39	0	30	9	0
3	A	82	0	0	4	0
3	B	113	0	0	14	0
All	All	4347	0	4256	90	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 11.

All (90) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:207:GLU:HB3	3:B:196:HOH:O	1.47	1.11
1:B:444:GLN:HB3	3:B:197:HOH:O	1.66	0.95
1:A:353:LEU:HD22	1:A:364:MET:SD	2.08	0.92
1:A:364:MET:SD	2:A:1101:DRY:HAC1	2.18	0.84
1:A:282:PHE:CE1	2:A:1101:DRY:HAJ	2.17	0.80
1:A:364:MET:HA	2:A:1101:DRY:HAA2	1.64	0.80
1:B:378:GLU:HG2	3:B:148:HOH:O	1.86	0.74
1:B:252:MET:HE1	3:B:173:HOH:O	1.88	0.73
1:A:466:HIS:CG	1:A:467:PRO:HD2	2.23	0.73
1:B:275:LYS:HE3	1:B:462:ASP:OD1	1.90	0.72
1:A:276:GLU:OE2	1:A:357:ARG:HD3	1.92	0.69
1:A:216:LYS:HE2	1:A:216:LYS:O	1.94	0.68
1:A:282:PHE:CD1	2:A:1101:DRY:HAJ	2.32	0.64
1:A:443:ARG:O	1:A:447:THR:HG23	1.98	0.63
1:A:325:ILE:HD11	1:A:392:ILE:HG13	1.81	0.63
1:A:364:MET:HB3	2:A:1101:DRY:HAB1	1.84	0.60
1:A:358:LYS:HB3	1:A:359:PRO:HD3	1.84	0.58
1:B:357:ARG:HG2	1:B:359:PRO:HD2	1.86	0.58
1:B:288:ARG:HH11	1:B:291:GLU:HB3	1.68	0.58
1:B:258:GLY:HA2	1:B:261:LYS:HB2	1.84	0.57
1:A:325:ILE:HG12	1:A:388:ILE:HG23	1.86	0.57
1:A:364:MET:CA	2:A:1101:DRY:HAA2	2.34	0.57
1:B:252:MET:O	1:B:256:MET:HG2	2.05	0.56
1:B:207:GLU:HG3	3:B:170:HOH:O	2.05	0.56
1:B:283:GLN:NE2	1:B:462:ASP:OD2	2.38	0.56
1:A:364:MET:HB3	2:A:1101:DRY:CAB	2.36	0.56
1:B:325:ILE:HD11	1:B:392:ILE:HG13	1.87	0.56
1:B:271:GLN:HG3	1:B:272:GLU:N	2.21	0.55
1:A:422:LYS:HG3	3:A:125:HOH:O	2.06	0.54
1:A:457:LYS:HG3	3:A:172:HOH:O	2.07	0.54
1:B:261:LYS:HG2	3:B:137:HOH:O	2.09	0.53
1:B:310:ASP:OD1	1:B:312:ASN:HB2	2.09	0.53
1:B:412:ASN:HB3	3:B:122:HOH:O	2.09	0.53
1:A:348:MET:SD	1:A:353:LEU:HD21	2.49	0.52
1:B:363:PHE:CE2	1:B:452:LEU:HG	2.44	0.52
1:B:262:ILE:HG22	3:B:137:HOH:O	2.10	0.52
1:B:288:ARG:NH1	1:B:291:GLU:HB3	2.24	0.51
1:B:325:ILE:HD11	1:B:392:ILE:CG1	2.41	0.51
1:A:308:ASN:ND2	1:B:291:GLU:OE2	2.40	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:255:LEU:HD21	1:A:277:VAL:HG13	1.93	0.51
1:B:259:GLU:OE1	1:B:280:ARG:NH2	2.34	0.50
1:A:363:PHE:CD1	1:A:452:LEU:HD23	2.48	0.49
1:A:357:ARG:NH2	1:A:460:GLU:OE1	2.47	0.48
1:B:367:LYS:N	1:B:367:LYS:HD2	2.27	0.48
1:A:363:PHE:CE1	1:A:452:LEU:HB3	2.49	0.47
1:B:412:ASN:CB	3:B:122:HOH:O	2.62	0.47
1:A:449:HIS:HE1	2:A:1101:DRY:CAL	2.28	0.47
1:B:467:PRO:HG3	3:B:131:HOH:O	2.13	0.47
1:A:466:HIS:CE1	1:A:467:PRO:HG2	2.50	0.46
1:B:364:MET:O	1:B:367:LYS:HB2	2.15	0.46
1:A:243:ASP:OD1	1:A:243:ASP:N	2.49	0.46
1:B:467:PRO:HB3	3:B:131:HOH:O	2.15	0.46
1:A:282:PHE:O	1:A:285:CYS:HB2	2.15	0.46
1:A:325:ILE:HG12	1:A:388:ILE:HD12	1.98	0.45
1:B:279:ILE:HD13	1:B:462:ASP:CB	2.46	0.45
1:A:325:ILE:HD11	1:A:392:ILE:CG1	2.46	0.45
1:B:259:GLU:CD	1:B:280:ARG:HH22	2.19	0.45
1:B:287:PHE:HB3	3:B:138:HOH:O	2.15	0.45
1:A:342:SER:O	1:A:345:GLN:HG2	2.17	0.45
1:B:273:GLN:O	1:B:274:SER:HB3	2.17	0.45
1:B:325:ILE:HG12	1:B:388:ILE:HG23	1.99	0.44
1:A:465:LEU:HD13	1:A:465:LEU:N	2.32	0.44
1:B:434:LYS:HA	1:B:437:GLN:HE21	1.82	0.44
1:A:472:ILE:O	1:A:476:LEU:HD13	2.17	0.44
1:A:286:GLN:NE2	1:A:465:LEU:HD12	2.32	0.44
1:B:363:PHE:HE1	1:B:449:HIS:CE1	2.35	0.44
1:B:258:GLY:HA2	1:B:261:LYS:CB	2.48	0.44
1:B:467:PRO:N	3:B:118:HOH:O	2.50	0.44
2:A:1101:DRY:HAB2	2:A:1101:DRY:HAN	1.92	0.43
1:A:357:ARG:O	1:A:359:PRO:HD2	2.18	0.43
1:A:452:LEU:HD12	1:A:452:LEU:HA	1.86	0.43
1:A:328:THR:HG21	1:A:388:ILE:HD11	2.00	0.42
1:A:311:LEU:HD12	1:A:311:LEU:O	2.19	0.42
1:B:463:MET:O	1:B:464:SER:CB	2.67	0.42
1:A:363:PHE:CZ	1:A:452:LEU:HB3	2.54	0.42
1:A:255:LEU:HD21	1:A:277:VAL:CG1	2.49	0.42
1:B:240:LYS:HB2	1:B:240:LYS:HE3	1.75	0.42
1:A:353:LEU:HD22	1:A:364:MET:CE	2.49	0.42
1:B:243:ASP:OD1	1:B:244:LYS:HG2	2.20	0.41
1:A:402:ASN:ND2	3:A:168:HOH:O	2.52	0.41
1:A:358:LYS:HB3	1:A:359:PRO:CD	2.48	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:459:THR:O	1:B:460:GLU:HG2	2.20	0.41
1:B:363:PHE:HE1	1:B:449:HIS:ND1	2.18	0.41
1:A:262:ILE:HG12	3:A:177:HOH:O	2.19	0.41
1:A:441:ASP:O	1:A:445:ILE:HG12	2.21	0.41
1:A:259:GLU:O	1:A:262:ILE:HG13	2.20	0.41
1:A:379:LEU:HD11	1:A:435:LEU:HD13	2.02	0.41
1:A:235:ALA:HB1	1:A:240:LYS:HD3	2.04	0.40
1:B:445:ILE:HD13	3:B:182:HOH:O	2.21	0.40
1:A:324:GLU:OE2	1:A:443:ARG:HD3	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	257/271 (95%)	248 (96%)	7 (3%)	2 (1%)	27	16
1	B	249/271 (92%)	236 (95%)	9 (4%)	4 (2%)	14	5
All	All	506/542 (93%)	484 (96%)	16 (3%)	6 (1%)	19	8

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	358	LYS
1	A	464	SER
1	B	274	SER
1	B	464	SER
1	B	242	THR
1	B	239	GLY

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	234/244 (96%)	214 (92%)	20 (8%)	15	8
1	B	226/244 (93%)	207 (92%)	19 (8%)	16	8
All	All	460/488 (94%)	421 (92%)	39 (8%)	15	8

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	216	LYS
1	A	220	ASP
1	A	241	THR
1	A	243	ASP
1	A	248	VAL
1	A	252	MET
1	A	260	ASP
1	A	275	LYS
1	A	291	GLU
1	A	318	LEU
1	A	343	GLU
1	A	364	MET
1	A	378	GLU
1	A	402	ASN
1	A	440	THR
1	A	441	ASP
1	A	453	LEU
1	A	463	MET
1	A	465	LEU
1	A	477	TYR
1	B	207	GLU
1	B	234	ARG
1	B	240	LYS
1	B	252	MET
1	B	262	ILE
1	B	272	GLU
1	B	273	GLN
1	B	287	PHE
1	B	318	LEU
1	B	322	VAL
1	B	323	HIS
1	B	358	LYS
1	B	363	PHE

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Mol	Chain	Res	Type
1	B	367	LYS
1	B	440	THR
1	B	441	ASP
1	B	451	GLN
1	B	461	THR
1	B	466	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	283	GLN
1	A	294	GLN
1	A	402	ASN
1	A	449	HIS
1	A	451	GLN
1	B	273	GLN
1	B	402	ASN
1	B	437	GLN
1	B	454	GLN

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 ⓘ

1 ligand is 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	DRY	A	1101	-	43,43,43	1.63	4 (9%)	59,59,59	1.21	6 (10%)

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	DRY	A	1101	-	-	0/23/23/23	0/1/5/5

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1101	DRY	CAH-NAM	-6.85	1.33	1.39
2	A	1101	DRY	CAN-NAM	-3.31	1.33	1.38
2	A	1101	DRY	CAV-CAU	2.82	1.54	1.49
2	A	1101	DRY	CAT-CAU	2.36	1.53	1.49

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1101	DRY	CBJ-OBI-CAI	-3.56	110.99	117.73
2	A	1101	DRY	CAG-CAH-NAM	-3.15	105.80	108.61
2	A	1101	DRY	CAZ-CAY-CBD	-3.04	118.77	122.77
2	A	1101	DRY	CAV-CAU-CAT	2.31	124.18	120.26
2	A	1101	DRY	CBD-CAY-CAX	2.17	121.97	119.55
2	A	1101	DRY	CAK-CAH-NAM	2.01	133.96	130.29

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, 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	261/271 (96%)	0.74	31 (11%) 5 5	15, 30, 63, 89	0
1	B	253/271 (93%)	0.89	32 (12%) 4 4	14, 27, 75, 92	0
All	All	514/542 (94%)	0.81	63 (12%) 5 5	14, 29, 70, 92	0

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	264	PHE	17.9
1	B	465	LEU	13.6
1	B	241	THR	11.3
1	A	262	ILE	9.2
1	B	467	PRO	7.8
1	B	240	LYS	7.4
1	B	260	ASP	7.3
1	B	242	THR	7.1
1	B	243	ASP	6.6
1	B	273	GLN	6.6
1	A	477	TYR	6.0
1	B	363	PHE	5.8
1	B	259	GLU	5.4
1	B	463	MET	5.2
1	B	239	GLY	5.1
1	B	461	THR	5.0
1	B	274	SER	5.0
1	A	242	THR	4.8
1	A	358	LYS	4.6
1	A	465	LEU	4.1
1	B	272	GLU	4.1
1	A	243	ASP	4.1
1	B	464	SER	3.9
1	B	244	LYS	3.8

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Mol	Chain	Res	Type	RSRZ
1	B	358	LYS	3.8
1	A	263	LYS	3.8
1	A	244	LYS	3.7
1	A	452	LEU	3.6
1	A	279	ILE	3.3
1	B	262	ILE	3.3
1	A	240	LYS	3.2
1	B	466	HIS	3.2
1	B	458	LYS	3.2
1	B	462	ASP	3.2
1	A	241	THR	3.2
1	B	261	LYS	3.1
1	A	476	LEU	2.9
1	A	364	MET	2.9
1	B	457	LYS	2.8
1	B	247	PHE	2.7
1	A	261	LYS	2.7
1	A	260	ASP	2.6
1	B	362	ASP	2.6
1	A	283	GLN	2.6
1	A	277	VAL	2.5
1	B	271	GLN	2.5
1	A	287	PHE	2.4
1	A	238	THR	2.4
1	A	311	LEU	2.4
1	A	475	ASP	2.3
1	A	464	SER	2.3
1	B	454	GLN	2.3
1	A	444	GLN	2.3
1	A	391	ILE	2.3
1	B	257	MET	2.2
1	A	388	ILE	2.2
1	A	245	SER	2.2
1	B	238	THR	2.2
1	A	275	LYS	2.1
1	B	248	VAL	2.1
1	A	354	LYS	2.1
1	A	322	VAL	2.0
1	B	286	GLN	2.0

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, 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	DRY	A	1101	39/39	0.48	6.57	65,76,79,80	0

6.5 Other polymers ⓘ

There are no such residues in this entry.