



Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 02:17 pm BST

PDB ID : 4E4Q
Title : Crystal structure of PPARgamma with the ligand FS214
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Deposited on : 2012-03-13
Resolution : 2.50 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

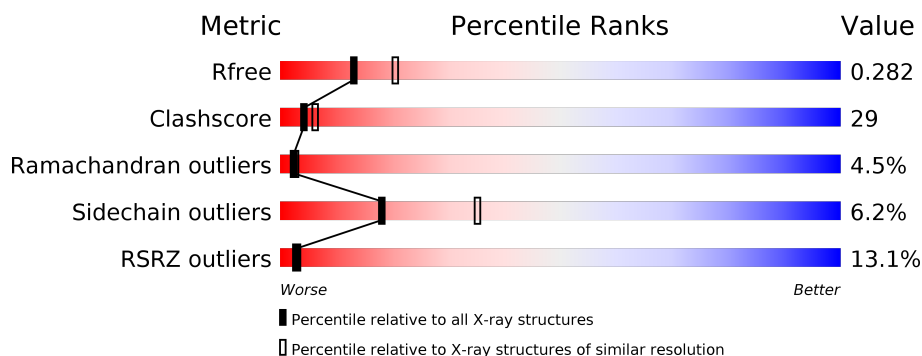
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 respectively. 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	287	
1	B	287	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	RRH	A	501	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4465 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.

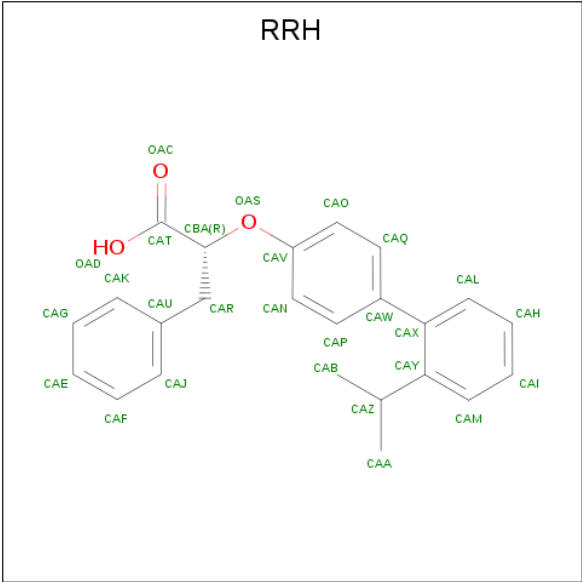
- Molecule 1 is a protein called Peroxisome proliferator-activated receptor gamma.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	268	Total	C	N	O	S	0	0	0
			2149	1387	352	400	10			
1	B	268	Total	C	N	O	S	28	0	0
			2149	1387	352	400	10			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	191	GLY	-	EXPRESSION TAG	UNP P37231
A	192	SER	-	EXPRESSION TAG	UNP P37231
A	193	HIS	-	EXPRESSION TAG	UNP P37231
A	194	MET	-	EXPRESSION TAG	UNP P37231
B	191	GLY	-	EXPRESSION TAG	UNP P37231
B	192	SER	-	EXPRESSION TAG	UNP P37231
B	193	HIS	-	EXPRESSION TAG	UNP P37231
B	194	MET	-	EXPRESSION TAG	UNP P37231

- Molecule 2 is (2R)-3-phenyl-2-([2'-(propan-2-yl)biphenyl-4-yl]oxy)propanoic acid (three-letter code: RRH) (formula: C₂₄H₂₄O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			27	24	3		

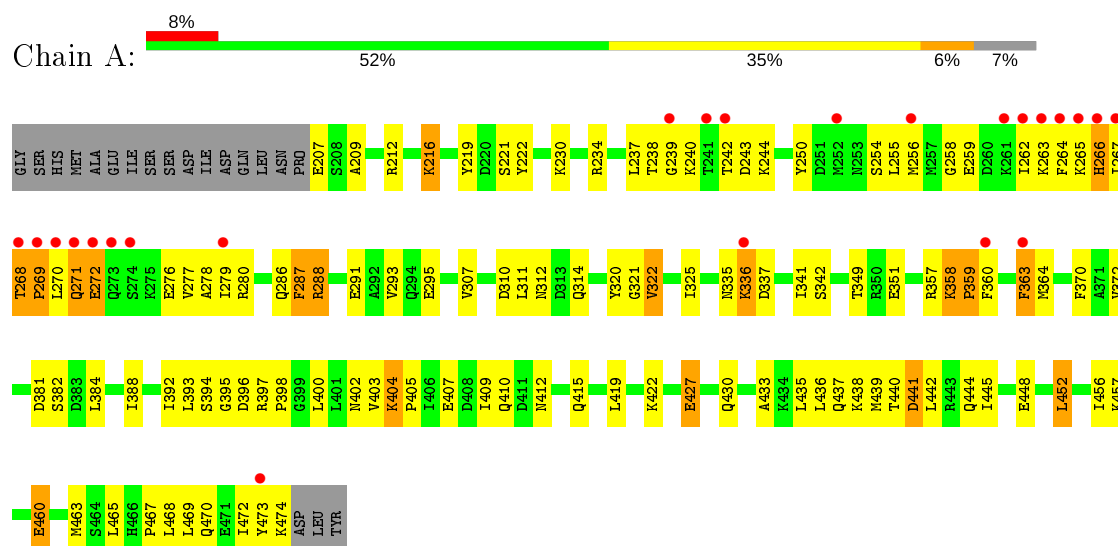
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	67	Total	O	0	0
			67	67		
3	B	73	Total	O	0	0
			73	73		

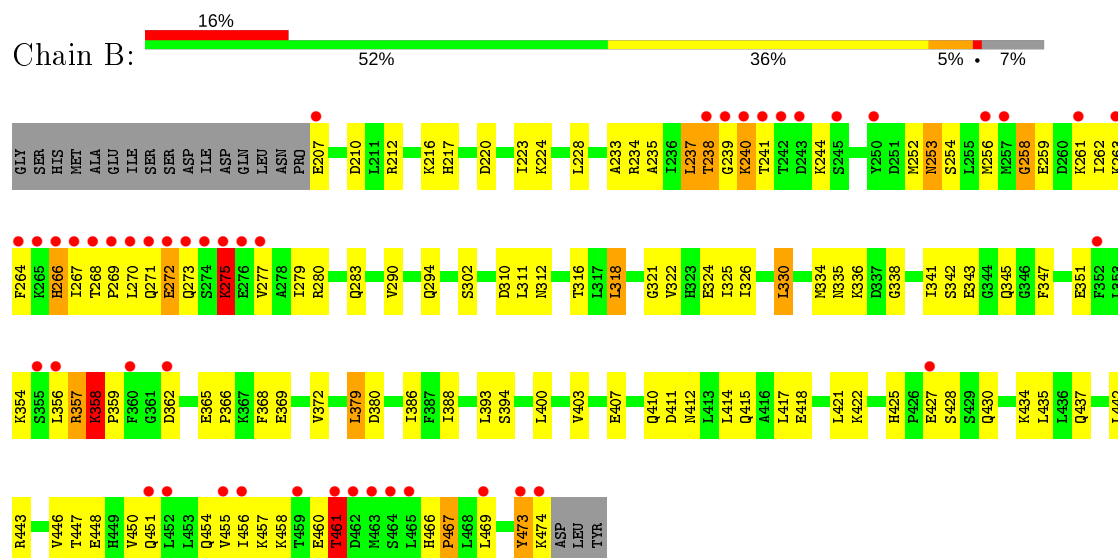
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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-activated receptor gamma



- Molecule 1: Peroxisome proliferator-activated receptor gamma



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	92.77Å 61.27Å 118.28Å 90.00° 102.15° 90.00°	Depositor
Resolution (Å)	10.00 – 2.50 48.64 – 2.50	Depositor EDS
% Data completeness (in resolution range)	(Not available) (10.00-2.50) 98.8 (48.64-2.50)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.25 (at 2.51Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.242 , 0.298 0.234 , 0.282	Depositor DCC
R_{free} test set	1091 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å ²)	47.3	Xtriage
Anisotropy	0.609	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 65.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4465	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.81% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: RRH

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	0.43	0/2186	0.62	0/2945
1	B	0.49	1/2186 (0.0%)	0.72	3/2945 (0.1%)
All	All	0.46	1/4372 (0.0%)	0.67	3/5890 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	473	TYR	CA-C	5.31	1.66	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	357	ARG	N-CA-CB	6.86	122.95	110.60
1	B	357	ARG	N-CA-C	-6.33	93.92	111.00
1	B	356	LEU	N-CA-C	5.54	125.96	111.00

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	2149	0	2217	146	0
1	B	2149	0	2217	102	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	27	0	23	23	0
3	A	67	0	0	16	0
3	B	73	0	0	13	0
All	All	4465	0	4457	257	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 29.

All (257) 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)
2:A:501:RRH:H4	2:A:501:RRH:H14	1.13	1.07
2:A:501:RRH:CAZ	2:A:501:RRH:H14	1.90	1.01
1:B:275:LYS:HE3	1:B:275:LYS:HA	1.46	0.97
1:A:266:HIS:CE1	2:A:501:RRH:H24	2.03	0.93
1:B:466:HIS:N	1:B:467:PRO:HD2	1.79	0.93
1:A:325:ILE:HG23	1:A:388:ILE:HD12	1.50	0.93
1:A:336:LYS:HG2	1:A:372:VAL:HG21	1.52	0.89
2:A:501:RRH:H4	2:A:501:RRH:CAP	2.00	0.88
1:A:268:THR:H	1:A:269:PRO:HD2	1.38	0.88
1:A:271:GLN:HB2	1:A:276:GLU:HA	1.57	0.85
1:A:320:TYR:HB3	1:A:397:ARG:HH11	1.41	0.83
1:A:381:ASP:HA	3:A:657:HOH:O	1.78	0.82
1:A:363:PHE:CE2	1:A:456:ILE:HD11	2.15	0.82
1:A:212:ARG:O	1:A:216:LYS:HD3	1.78	0.81
1:A:271:GLN:HE21	1:A:277:VAL:H	1.28	0.81
1:A:473:TYR:O	1:A:474:LYS:HG3	1.82	0.79
1:A:384:LEU:HB2	3:A:657:HOH:O	1.82	0.78
1:A:470:GLN:HB3	3:A:620:HOH:O	1.83	0.78
1:A:363:PHE:HE2	1:A:456:ILE:HD11	1.49	0.77
1:A:256:MET:HG2	1:A:268:THR:O	1.86	0.76
1:A:440:THR:O	1:A:444:GLN:HG2	1.86	0.76
1:B:268:THR:HB	1:B:269:PRO:HD2	1.67	0.75
1:A:392:ILE:HG22	1:A:393:LEU:HD22	1.70	0.74
1:B:358:LYS:NZ	1:B:358:LYS:HA	2.04	0.73
1:A:270:LEU:HD13	1:A:271:GLN:N	2.03	0.72
1:A:336:LYS:HG2	1:A:372:VAL:CG2	2.19	0.72
1:A:363:PHE:CE2	1:A:452:LEU:HD22	2.26	0.71
1:A:266:HIS:NE2	2:A:501:RRH:H24	2.05	0.71
1:A:271:GLN:NE2	1:A:277:VAL:HG12	2.05	0.71
1:B:447:THR:O	1:B:450:VAL:HG22	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:501:RRH:H2O	2:A:501:RRH:OAD	1.92	0.70
1:A:437:GLN:O	1:A:440:THR:HG22	1.92	0.70
1:A:272:GLU:HA	1:A:276:GLU:HB3	1.72	0.69
1:B:264:PHE:CZ	1:B:266:HIS:HB3	2.27	0.69
1:B:451:GLN:O	1:B:454:GLN:HG2	1.92	0.69
1:A:243:ASP:HB3	3:A:639:HOH:O	1.93	0.68
1:A:259:GLU:HA	1:A:264:PHE:HB2	1.76	0.68
1:A:265:LYS:NZ	1:A:265:LYS:HB3	2.09	0.67
1:B:269:PRO:HA	1:B:280:ARG:HH22	1.59	0.65
1:B:269:PRO:O	1:B:270:LEU:HD23	1.96	0.65
1:A:276:GLU:CD	1:A:357:ARG:HH21	1.99	0.65
1:A:271:GLN:NE2	1:A:277:VAL:H	1.95	0.65
2:A:501:RRH:CAT	2:A:501:RRH:H15	2.27	0.65
1:A:286:GLN:NE2	1:A:465:LEU:HD12	2.12	0.64
1:B:325:ILE:HD12	1:B:388:ILE:HG23	1.80	0.64
1:A:430:GLN:HG3	3:A:656:HOH:O	1.99	0.63
1:B:358:LYS:HB2	1:B:359:PRO:HD2	1.81	0.63
1:B:358:LYS:HB2	1:B:359:PRO:CD	2.29	0.63
1:A:456:ILE:HG21	1:A:463:MET:HE1	1.81	0.63
1:B:321:GLY:O	1:B:325:ILE:HG12	1.99	0.62
1:A:287:PHE:CE1	1:A:291:GLU:OE2	2.53	0.62
3:A:656:HOH:O	1:B:414:LEU:HB3	1.98	0.62
1:B:256:MET:HA	1:B:269:PRO:HB3	1.81	0.61
1:B:212:ARG:NH1	1:B:212:ARG:HB3	2.14	0.61
1:A:320:TYR:HB3	1:A:397:ARG:NH1	2.13	0.61
1:B:466:HIS:N	1:B:467:PRO:CD	2.58	0.61
2:A:501:RRH:CAJ	2:A:501:RRH:OAD	2.49	0.61
1:A:419:LEU:HA	1:A:422:LYS:CE	2.30	0.61
1:B:267:ILE:HG12	1:B:268:THR:H	1.65	0.61
1:A:271:GLN:NE2	1:A:276:GLU:HB2	2.17	0.60
1:A:279:ILE:HD13	1:A:360:PHE:CZ	2.37	0.60
1:A:320:TYR:HB2	1:A:397:ARG:HD2	1.83	0.60
1:B:220:ASP:O	1:B:224:LYS:HG2	2.00	0.60
1:B:338:GLY:HA3	1:B:347:PHE:CZ	2.37	0.60
1:A:268:THR:HB	1:A:269:PRO:CD	2.32	0.59
1:A:325:ILE:HD11	1:A:392:ILE:HG13	1.85	0.59
1:B:466:HIS:H	1:B:467:PRO:HD2	1.64	0.59
1:A:430:GLN:HB2	1:B:411:ASP:OD1	2.03	0.59
1:A:448:GLU:HB3	3:A:643:HOH:O	2.03	0.59
1:A:364:MET:HE1	2:A:501:RRH:H9	1.85	0.59
1:A:288:ARG:CD	2:A:501:RRH:H3	2.32	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:341:ILE:HG22	2:A:501:RRH:H5	1.85	0.58
1:A:270:LEU:HD22	1:A:271:GLN:H	1.69	0.58
1:A:242:THR:O	1:A:242:THR:HG22	2.04	0.58
1:A:268:THR:HB	1:A:269:PRO:HD3	1.86	0.57
1:A:271:GLN:C	1:A:276:GLU:HA	2.25	0.57
1:A:370:PHE:HB2	1:A:445:ILE:HD11	1.86	0.57
1:B:460:GLU:O	1:B:461:THR:HG23	2.05	0.57
1:A:359:PRO:HG2	1:A:360:PHE:CD1	2.40	0.56
1:A:419:LEU:HA	1:A:422:LYS:HE3	1.88	0.56
1:A:267:ILE:O	1:A:280:ARG:NH2	2.38	0.55
1:B:234:ARG:NH2	1:B:334:MET:O	2.38	0.55
2:A:501:RRH:H19	2:A:501:RRH:CAN	2.36	0.55
1:A:271:GLN:HB2	1:A:276:GLU:CA	2.33	0.55
1:A:293:VAL:HG11	1:A:468:LEU:HD11	1.87	0.55
1:B:358:LYS:HZ3	1:B:358:LYS:HA	1.71	0.55
1:A:358:LYS:HB2	1:A:359:PRO:HD3	1.89	0.55
1:B:269:PRO:HA	1:B:280:ARG:NH2	2.20	0.55
1:B:351:GLU:HG3	3:B:544:HOH:O	2.06	0.55
1:B:235:ALA:HB1	1:B:241:THR:HG21	1.88	0.55
1:A:404:LYS:N	1:A:405:PRO:HD2	2.22	0.54
1:A:407:GLU:HG3	3:A:633:HOH:O	2.07	0.54
3:A:638:HOH:O	1:B:430:GLN:HB2	2.06	0.54
1:B:252:MET:HB2	3:B:525:HOH:O	2.08	0.54
1:A:287:PHE:CE1	2:A:501:RRH:CAF	2.91	0.54
1:A:433:ALA:O	1:A:437:GLN:HG3	2.08	0.54
1:A:271:GLN:HE21	1:A:277:VAL:N	2.02	0.54
1:A:259:GLU:OE2	1:A:266:HIS:HB2	2.08	0.54
1:A:263:LYS:HB3	3:A:626:HOH:O	2.07	0.53
1:B:220:ASP:O	1:B:224:LYS:HE2	2.08	0.53
1:B:290:VAL:HG21	1:B:473:TYR:CD1	2.44	0.53
1:B:217:HIS:HE1	1:B:302:SER:O	1.91	0.53
1:A:238:THR:O	1:A:240:LYS:N	2.37	0.53
1:B:267:ILE:HD13	1:B:280:ARG:HG2	1.90	0.53
1:B:386:ILE:HB	1:B:417:LEU:HD13	1.90	0.53
1:B:324:GLU:HG3	1:B:446:VAL:HG21	1.89	0.53
1:A:288:ARG:HD3	2:A:501:RRH:H3	1.89	0.53
1:A:293:VAL:HG22	1:A:322:VAL:HG11	1.91	0.53
1:A:307:VAL:HA	1:A:314:GLN:OE1	2.08	0.53
1:A:342:SER:HB2	2:A:501:RRH:OAC	2.09	0.53
2:A:501:RRH:CAZ	2:A:501:RRH:CAP	2.67	0.53
1:B:258:GLY:O	1:B:262:ILE:HG22	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:358:LYS:HB2	1:A:359:PRO:CD	2.39	0.52
1:A:325:ILE:HG23	1:A:388:ILE:CD1	2.33	0.52
1:B:358:LYS:CB	1:B:359:PRO:CD	2.86	0.52
1:B:451:GLN:O	1:B:455:VAL:HG23	2.09	0.52
1:A:456:ILE:HG21	1:A:463:MET:CE	2.39	0.52
1:B:270:LEU:HB2	3:B:552:HOH:O	2.09	0.52
1:A:271:GLN:HG3	1:A:272:GLU:H	1.74	0.52
1:A:288:ARG:NH2	1:A:295:GLU:OE2	2.43	0.52
1:B:310:ASP:OD2	1:B:312:ASN:HB2	2.10	0.52
1:B:275:LYS:CE	1:B:275:LYS:HA	2.29	0.51
1:B:368:PHE:O	1:B:372:VAL:HG23	2.10	0.51
1:B:326:ILE:HB	3:B:546:HOH:O	2.10	0.51
1:A:271:GLN:HB2	1:A:277:VAL:H	1.74	0.51
1:B:316:THR:HG21	1:B:400:LEU:HD23	1.93	0.51
1:B:216:LYS:HD2	3:B:570:HOH:O	2.11	0.51
1:A:288:ARG:HH21	1:A:291:GLU:HB3	1.76	0.51
1:A:467:PRO:HA	3:A:620:HOH:O	2.11	0.51
1:B:380:ASP:HB2	3:B:510:HOH:O	2.10	0.51
1:A:320:TYR:CB	1:A:397:ARG:HD2	2.41	0.50
1:A:268:THR:N	1:A:269:PRO:HD2	2.13	0.50
1:B:267:ILE:HG12	1:B:268:THR:N	2.26	0.50
1:B:417:LEU:O	1:B:421:LEU:HG	2.10	0.50
1:A:277:VAL:HG13	1:A:278:ALA:N	2.27	0.50
1:A:271:GLN:HB2	1:A:277:VAL:N	2.27	0.50
1:A:266:HIS:NE2	2:A:501:RRH:CAK	2.74	0.50
1:A:271:GLN:CB	1:A:276:GLU:HA	2.37	0.49
1:A:321:GLY:O	1:A:325:ILE:HG13	2.12	0.49
1:A:357:ARG:HG2	1:A:358:LYS:N	2.26	0.49
1:A:440:THR:HG23	1:A:441:ASP:N	2.27	0.49
1:B:425:HIS:HB3	1:B:428:SER:HB3	1.93	0.49
1:A:271:GLN:CG	1:A:272:GLU:H	2.25	0.49
1:B:354:LYS:HD3	1:B:365:GLU:CG	2.41	0.49
1:A:457:LYS:HG3	3:A:664:HOH:O	2.12	0.49
1:A:419:LEU:HD12	1:A:422:LYS:HE3	1.95	0.49
1:A:395:GLY:HA2	1:A:400:LEU:HD13	1.95	0.49
1:A:363:PHE:CZ	1:A:452:LEU:HD22	2.46	0.49
1:A:357:ARG:HH12	1:A:460:GLU:CD	2.16	0.48
2:A:501:RRH:H15	2:A:501:RRH:OAC	2.13	0.48
1:A:271:GLN:HE22	1:A:277:VAL:HG12	1.75	0.48
1:A:264:PHE:HZ	1:A:341:ILE:CD1	2.26	0.48
1:A:230:LYS:O	1:A:234:ARG:HG2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:364:MET:CE	2:A:501:RRH:H9	2.44	0.48
1:B:359:PRO:O	1:B:362:ASP:OD2	2.29	0.48
1:B:403:VAL:HG12	1:B:407:GLU:HG3	1.95	0.48
1:A:419:LEU:HA	1:A:422:LYS:HE2	1.94	0.48
1:B:330:LEU:HB3	3:B:502:HOH:O	2.13	0.48
1:B:442:LEU:O	1:B:446:VAL:HG23	2.13	0.48
1:A:325:ILE:HD11	1:A:392:ILE:CG1	2.44	0.48
1:B:365:GLU:N	1:B:366:PRO:HD2	2.29	0.48
1:A:286:GLN:NE2	1:A:465:LEU:CD1	2.77	0.47
1:A:265:LYS:HZ2	1:A:265:LYS:HB3	1.78	0.47
1:B:210:ASP:HB3	3:B:541:HOH:O	2.14	0.47
1:B:237:LEU:O	1:B:239:GLY:N	2.46	0.47
1:B:216:LYS:HD3	1:B:220:ASP:OD2	2.15	0.47
1:A:320:TYR:OH	1:A:398:PRO:HB2	2.14	0.47
1:A:474:LYS:HD2	3:A:658:HOH:O	2.15	0.47
1:A:267:ILE:HG22	1:A:268:THR:N	2.30	0.47
1:B:290:VAL:HG21	1:B:473:TYR:CE1	2.51	0.46
1:A:311:LEU:HD23	1:A:311:LEU:C	2.36	0.46
2:A:501:RRH:H12	2:A:501:RRH:H11	1.67	0.46
1:B:455:VAL:HA	1:B:458:LYS:HE2	1.97	0.46
1:A:264:PHE:HZ	1:A:341:ILE:HD11	1.81	0.46
1:A:427:GLU:H	1:A:427:GLU:CD	2.19	0.46
1:B:273:GLN:OE1	1:B:273:GLN:N	2.48	0.46
1:A:410:GLN:HE22	1:B:437:GLN:HE22	1.63	0.46
1:A:430:GLN:OE1	1:B:415:GLN:HG2	2.16	0.46
1:B:279:ILE:O	1:B:283:GLN:HG3	2.15	0.46
1:B:212:ARG:CB	1:B:212:ARG:HH11	2.29	0.46
1:B:379:LEU:HD21	1:B:435:LEU:HD13	1.98	0.46
1:A:250:TYR:CD2	1:A:250:TYR:N	2.84	0.45
1:A:436:LEU:O	1:A:439:MET:HB2	2.16	0.45
1:B:354:LYS:HD3	1:B:365:GLU:HG3	1.98	0.45
1:B:418:GLU:O	1:B:422:LYS:HG3	2.17	0.45
1:A:395:GLY:HA2	1:A:400:LEU:CD1	2.46	0.45
1:A:415:GLN:HG3	3:A:638:HOH:O	2.17	0.45
1:A:370:PHE:CZ	1:A:442:LEU:HD21	2.52	0.45
1:A:254:SER:O	1:A:258:GLY:N	2.48	0.45
1:B:212:ARG:CA	1:B:212:ARG:HH11	2.30	0.45
1:A:394:SER:HB2	1:A:397:ARG:HG2	1.97	0.45
1:A:207:GLU:HG3	1:A:209:ALA:N	2.31	0.45
1:A:403:VAL:HG13	3:A:633:HOH:O	2.16	0.45
1:B:216:LYS:CD	1:B:220:ASP:OD2	2.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:334:MET:HE2	1:B:368:PHE:HA	1.98	0.44
1:A:262:ILE:HG22	1:A:263:LYS:N	2.32	0.44
1:A:267:ILE:HB	1:A:280:ARG:HD2	1.99	0.44
1:B:427:GLU:HA	1:B:427:GLU:OE2	2.17	0.44
1:A:266:HIS:CE1	2:A:501:RRH:CAK	2.90	0.44
1:B:212:ARG:HB3	1:B:212:ARG:HH11	1.83	0.44
1:B:448:GLU:O	1:B:451:GLN:HB3	2.17	0.44
1:A:293:VAL:HG22	1:A:322:VAL:CG1	2.47	0.43
1:A:271:GLN:NE2	1:A:272:GLU:OE2	2.51	0.43
1:A:349:THR:HG22	1:A:351:GLU:H	1.82	0.43
1:B:268:THR:HB	1:B:269:PRO:CD	2.45	0.43
1:B:271:GLN:CD	1:B:277:VAL:HG23	2.38	0.43
1:A:288:ARG:HH21	1:A:291:GLU:CB	2.31	0.43
1:A:237:LEU:HD22	1:A:335:ASN:HD22	1.84	0.43
2:A:501:RRH:H14	2:A:501:RRH:CAB	2.45	0.43
1:B:318:LEU:HD12	1:B:318:LEU:HA	1.83	0.43
1:B:253:ASN:HA	1:B:253:ASN:HD22	1.60	0.43
1:B:415:GLN:HB3	3:B:521:HOH:O	2.17	0.43
1:A:238:THR:C	1:A:240:LYS:H	2.22	0.43
1:B:237:LEU:O	1:B:239:GLY:O	2.37	0.43
1:B:454:GLN:O	1:B:457:LYS:HB3	2.19	0.43
1:B:474:LYS:HE2	1:B:474:LYS:HB2	1.78	0.43
1:A:219:TYR:CD1	1:A:382:SER:HA	2.54	0.42
1:B:393:LEU:O	1:B:410:GLN:HB2	2.19	0.42
1:B:228:LEU:HD22	1:B:233:ALA:HB2	2.01	0.42
1:B:345:GLN:OE1	1:B:345:GLN:HA	2.19	0.42
1:B:456:ILE:C	1:B:458:LYS:H	2.21	0.42
1:A:440:THR:CG2	1:A:441:ASP:N	2.83	0.42
1:A:269:PRO:HB2	1:A:270:LEU:H	1.67	0.42
1:A:265:LYS:HZ3	1:A:265:LYS:HB3	1.80	0.42
1:A:259:GLU:HG3	1:A:268:THR:HA	2.02	0.42
1:A:310:ASP:OD2	1:A:312:ASN:HB2	2.20	0.42
1:B:311:LEU:H	1:B:311:LEU:HD12	1.85	0.42
1:A:469:LEU:O	1:A:473:TYR:CD2	2.73	0.41
1:B:262:ILE:HG13	1:B:263:LYS:N	2.35	0.41
1:A:395:GLY:HA3	3:A:633:HOH:O	2.19	0.41
1:A:435:LEU:O	1:A:438:LYS:HB2	2.21	0.41
1:B:341:ILE:HG23	1:B:342:SER:N	2.35	0.41
1:B:369:GLU:HB2	3:B:557:HOH:O	2.21	0.41
2:A:501:RRH:CAR	2:A:501:RRH:CAN	2.94	0.41
1:A:259:GLU:OE1	1:A:266:HIS:O	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:216:LYS:O	1:B:216:LYS:HD3	2.21	0.41
1:B:237:LEU:HB3	1:B:238:THR:H	1.65	0.41
1:B:224:LYS:HD3	1:B:224:LYS:N	2.36	0.41
1:A:288:ARG:O	1:A:291:GLU:HB2	2.21	0.41
1:A:388:ILE:HD13	1:A:388:ILE:HA	1.79	0.41
1:A:403:VAL:O	1:A:407:GLU:HG3	2.21	0.41
1:B:343:GLU:HG3	1:B:343:GLU:O	2.21	0.41
1:A:335:ASN:OD1	1:A:337:ASP:N	2.50	0.40
1:B:237:LEU:O	1:B:238:THR:C	2.59	0.40
1:B:434:LYS:HD3	3:B:555:HOH:O	2.21	0.40
1:A:335:ASN:C	1:A:335:ASN:OD1	2.59	0.40
1:A:468:LEU:O	1:A:472:ILE:HG13	2.22	0.40
1:B:358:LYS:HZ2	1:B:358:LYS:HA	1.83	0.40
1:A:219:TYR:O	1:A:222:TYR:HB3	2.21	0.40
1:B:240:LYS:O	1:B:241:THR:C	2.59	0.40
1:A:357:ARG:HD2	1:A:359:PRO:HD2	2.04	0.40
1:B:223:ILE:HD13	1:B:223:ILE:HA	1.91	0.40
1:B:430:GLN:NE2	3:B:556:HOH:O	2.54	0.40
1:A:268:THR:N	1:A:269:PRO:CD	2.82	0.40
1:A:255:LEU:CD2	1:A:277:VAL:HG23	2.51	0.40
1:A:409:ILE:O	1:A:412:ASN:HB2	2.21	0.40
1:B:336:LYS:HG3	3:B:536:HOH:O	2.21	0.40

There are no symmetry-related clashes.

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	266/287 (93%)	244 (92%)	13 (5%)	9 (3%)	3	5
1	B	266/287 (93%)	229 (86%)	22 (8%)	15 (6%)	2	1
All	All	532/574 (93%)	473 (89%)	35 (7%)	24 (4%)	2	3

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	266	HIS
1	A	269	PRO
1	B	237	LEU
1	B	244	LYS
1	B	261	LYS
1	B	357	ARG
1	B	394	SER
1	A	239	GLY
1	A	272	GLU
1	B	238	THR
1	B	240	LYS
1	B	266	HIS
1	B	272	GLU
1	A	359	PRO
1	B	258	GLY
1	A	244	LYS
1	A	336	LYS
1	B	259	GLU
1	B	461	THR
1	A	268	THR
1	B	275	LYS
1	B	358	LYS
1	B	467	PRO
1	A	358	LYS

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	241/258 (93%)	227 (94%)	14 (6%)	20	38
1	B	241/258 (93%)	225 (93%)	16 (7%)	16	32
All	All	482/516 (93%)	452 (94%)	30 (6%)	18	35

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	216	LYS
1	A	221	SER
1	A	271	GLN
1	A	287	PHE
1	A	288	ARG
1	A	322	VAL
1	A	363	PHE
1	A	396	ASP
1	A	402	ASN
1	A	404	LYS
1	A	427	GLU
1	A	441	ASP
1	A	452	LEU
1	A	460	GLU
1	B	207	GLU
1	B	253	ASN
1	B	254	SER
1	B	272	GLU
1	B	275	LYS
1	B	294	GLN
1	B	318	LEU
1	B	322	VAL
1	B	330	LEU
1	B	335	ASN
1	B	358	LYS
1	B	379	LEU
1	B	412	ASN
1	B	443	ARG
1	B	461	THR
1	B	469	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	271	GLN
1	A	283	GLN
1	A	286	GLN
1	A	454	GLN
1	A	470	GLN
1	B	217	HIS
1	B	253	ASN
1	B	271	GLN
1	B	410	GLN

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Mol	Chain	Res	Type
1	B	412	ASN
1	B	437	GLN
1	B	444	GLN
1	B	451	GLN
1	B	466	HIS
1	B	470	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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](#)

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	RRH	A	501	-	26,29,29	1.16	1 (3%)	33,39,39	1.07	1 (3%)

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	RRH	A	501	-	-	5/16/20/20	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	RRH	CAX-CAW	-5.26	1.39	1.49

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	RRH	CAV-OAS-CBA	-4.72	115.47	118.62

There are no chirality outliers.

All (5) torsion outliers are listed below:

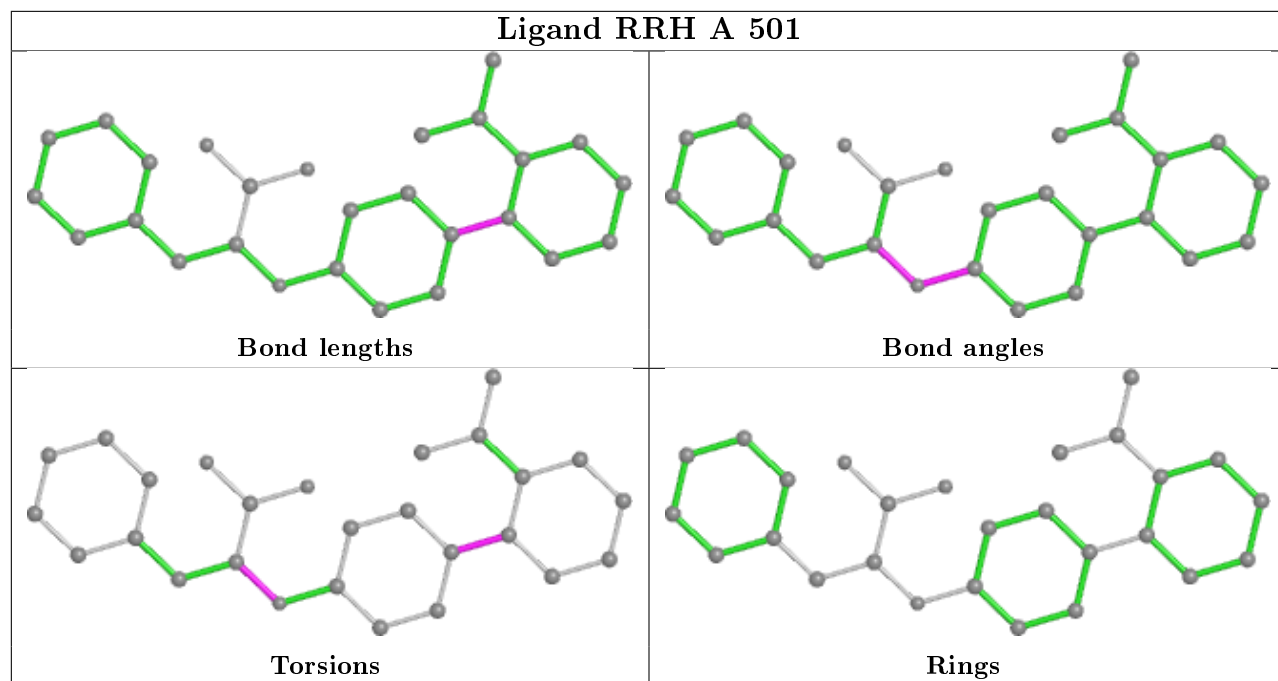
Mol	Chain	Res	Type	Atoms
2	A	501	RRH	CAR-CBA-OAS-CAV
2	A	501	RRH	CAQ-CAW-CAX-CAY
2	A	501	RRH	CAP-CAW-CAX-CAY
2	A	501	RRH	CAP-CAW-CAX-CAL
2	A	501	RRH	CAQ-CAW-CAX-CAL

There are no ring outliers.

1 monomer is involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	RRH	23	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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, 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	268/287 (93%)	0.60	24 (8%) 9 9	29, 49, 98, 100	1 (0%)
1	B	265/287 (92%)	1.10	46 (17%) 1 1	26, 50, 100, 100	0
All	All	533/574 (92%)	0.85	70 (13%) 3 3	26, 49, 100, 100	1 (0%)

All (70) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	268	THR	13.2
1	B	464	SER	12.9
1	B	270	LEU	12.8
1	A	269	PRO	12.3
1	B	269	PRO	11.2
1	B	268	THR	10.2
1	A	267	ILE	8.1
1	B	271	GLN	7.9
1	B	267	ILE	7.6
1	B	462	ASP	7.5
1	B	459	THR	7.1
1	B	238	THR	7.0
1	A	273	GLN	6.9
1	B	272	GLU	6.3
1	B	463	MET	6.0
1	B	261	LYS	5.5
1	A	239	GLY	5.2
1	B	273	GLN	5.2
1	B	465	LEU	5.2
1	A	264	PHE	4.9
1	B	240	LYS	4.7
1	B	360	PHE	4.7
1	B	461	THR	4.6
1	B	264	PHE	4.6

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Mol	Chain	Res	Type	RSRZ
1	A	270	LEU	4.1
1	B	274	SER	4.1
1	A	272	GLU	4.1
1	B	474	LYS	4.1
1	B	263	LYS	4.0
1	B	257	MET	4.0
1	A	265	LYS	3.9
1	B	242	THR	3.9
1	B	356	LEU	3.8
1	B	452	LEU	3.6
1	B	266	HIS	3.5
1	B	250	TYR	3.5
1	B	456	ILE	3.4
1	B	243	ASP	3.3
1	A	266	HIS	3.3
1	A	274	SER	3.2
1	A	279	ILE	3.2
1	B	362	ASP	3.1
1	A	241	THR	3.1
1	B	469	LEU	3.1
1	B	239	GLY	3.1
1	A	271	GLN	2.9
1	B	256	MET	2.9
1	B	427	GLU	2.8
1	A	263	LYS	2.8
1	B	275	LYS	2.7
1	B	241	THR	2.6
1	B	276	GLU	2.6
1	B	207	GLU	2.5
1	A	261	LYS	2.5
1	B	265	LYS	2.4
1	B	277	VAL	2.4
1	B	352	PHE	2.4
1	A	360	PHE	2.3
1	B	355	SER	2.3
1	A	252	MET	2.2
1	A	363	PHE	2.2
1	A	256	MET	2.1
1	A	473	TYR	2.1
1	A	242	THR	2.1
1	A	262	ILE	2.1
1	B	451	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	455	VAL	2.1
1	B	473	TYR	2.1
1	B	245	SER	2.1
1	A	336	LYS	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](#)

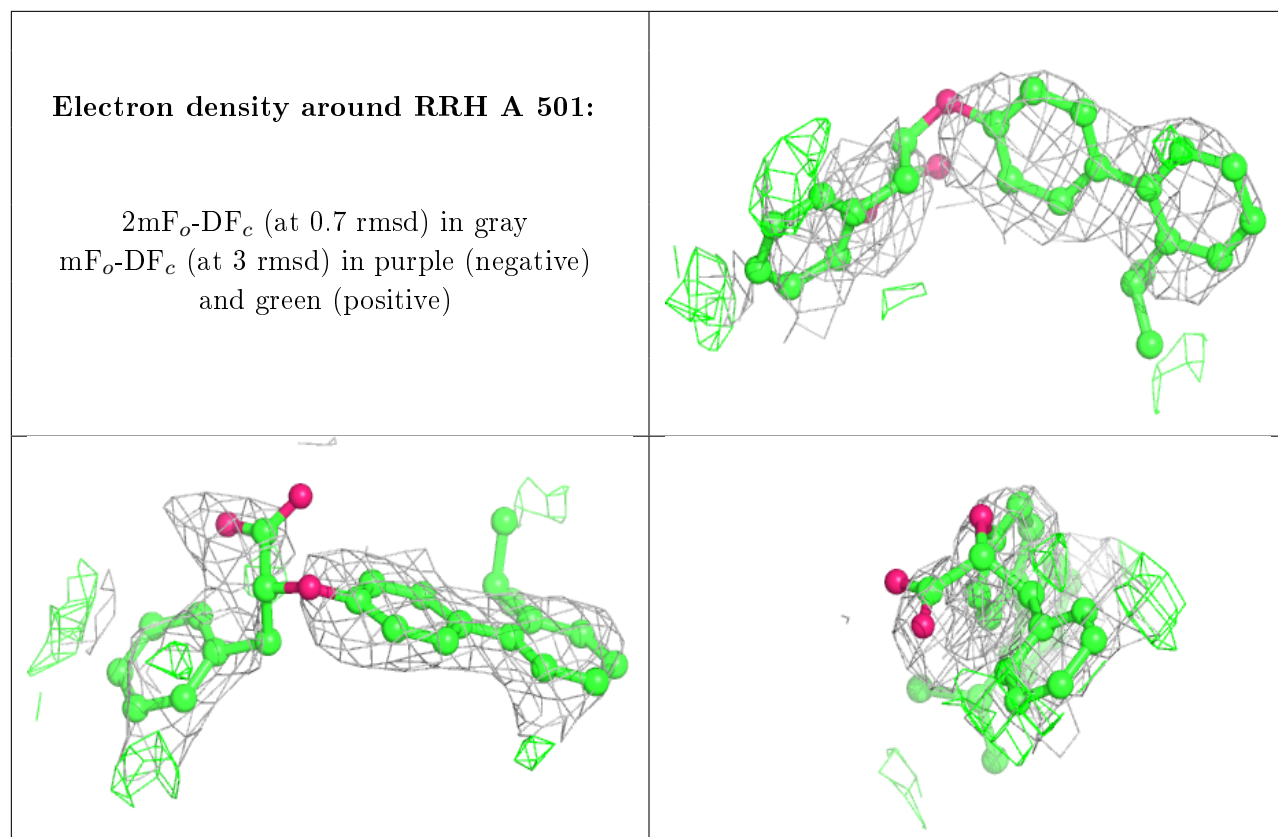
There are no carbohydrates in this entry.

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. 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	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	RRH	A	501	27/27	0.72	0.38	92,94,100,100	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers [i](#)

There are no such residues in this entry.