



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 04:46 AM UTC

PDB ID : 6JNO / pdb_00006jno
Title : RXRa structure complexed with CU-6PMN
Authors : Kawasaki, M.; Nakano, S.; Motoyama, T.; Yamada, S.; Watanabe, M.; Takamura, Y.; Fujihara, M.; Tokiwa, H.; Kakuta, H.; Ito, S.
Deposited on : 2019-03-17
Resolution : 2.65 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

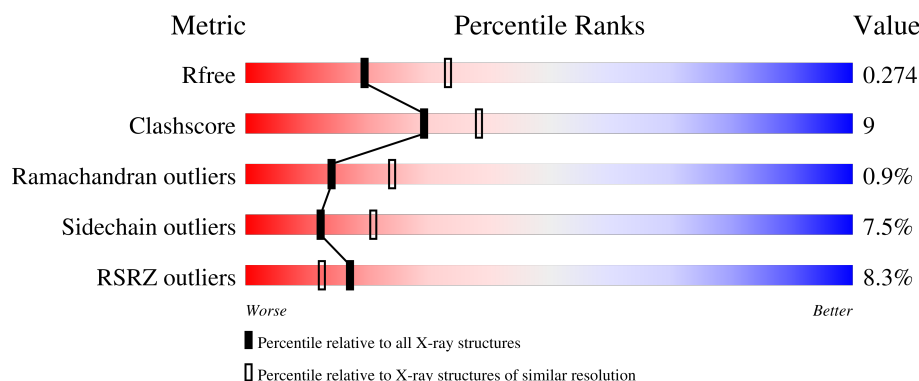
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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}	180053	1110 (2.66-2.66)
Clashscore	190562	1141 (2.66-2.66)
Ramachandran outliers	187476	1126 (2.66-2.66)
Sidechain outliers	187428	1126 (2.66-2.66)
RSRZ outliers	180081	1110 (2.66-2.66)

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 of 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	243	5% 64% 15% • 20%
1	B	243	8% 66% 13% • 21%
1	C	243	6% 62% 16% • 18%
1	D	243	8% 63% 18% • 16%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6349 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.

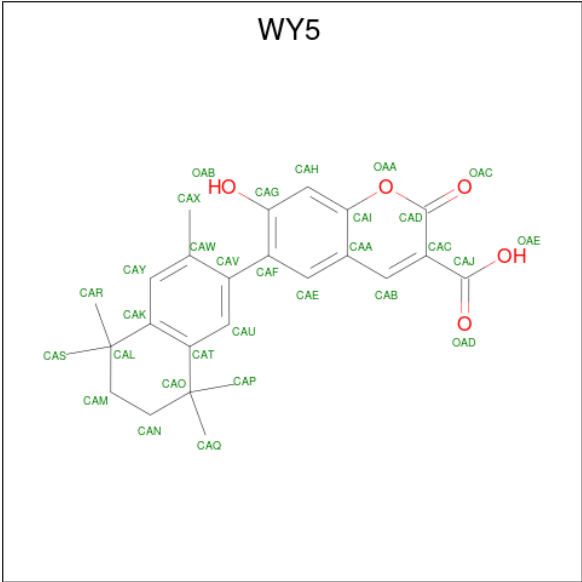
- Molecule 1 is a protein called Retinoic acid receptor RXR-alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	195	Total	C	N	O	S	0	0	0
			1539	992	266	272	9			
1	B	193	Total	C	N	O	S	0	0	0
			1527	985	264	269	9			
1	C	200	Total	C	N	O	S	0	0	0
			1588	1025	274	280	9			
1	D	203	Total	C	N	O	S	0	0	0
			1608	1035	278	286	9			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	220	GLY	-	expression tag	UNP P19793
A	221	SER	-	expression tag	UNP P19793
A	222	SER	-	expression tag	UNP P19793
A	223	HIS	-	expression tag	UNP P19793
B	220	GLY	-	expression tag	UNP P19793
B	221	SER	-	expression tag	UNP P19793
B	222	SER	-	expression tag	UNP P19793
B	223	HIS	-	expression tag	UNP P19793
C	220	GLY	-	expression tag	UNP P19793
C	221	SER	-	expression tag	UNP P19793
C	222	SER	-	expression tag	UNP P19793
C	223	HIS	-	expression tag	UNP P19793
D	220	GLY	-	expression tag	UNP P19793
D	221	SER	-	expression tag	UNP P19793
D	222	SER	-	expression tag	UNP P19793
D	223	HIS	-	expression tag	UNP P19793

- Molecule 2 is 7-oxidanyl-2-oxidanylidene-6-(3,5,5,8,8-pentamethyl-6,7-dihydronaphthalen-2-yl)chromene-3-carboxylic acid (CCD ID: WY5) (formula: C₂₅H₂₆O₅) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			30	25	5		

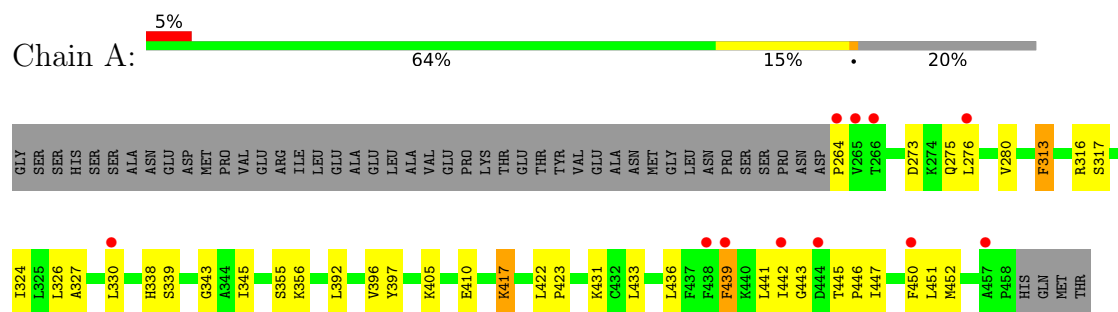
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	18	Total	O	0	0
			18	18		
3	B	11	Total	O	0	0
			11	11		
3	C	14	Total	O	0	0
			14	14		
3	D	14	Total	O	0	0
			14	14		

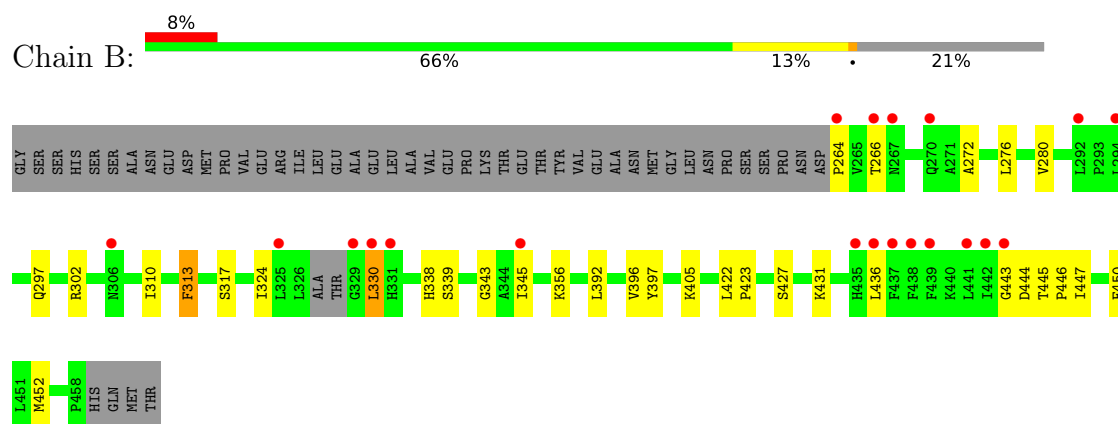
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

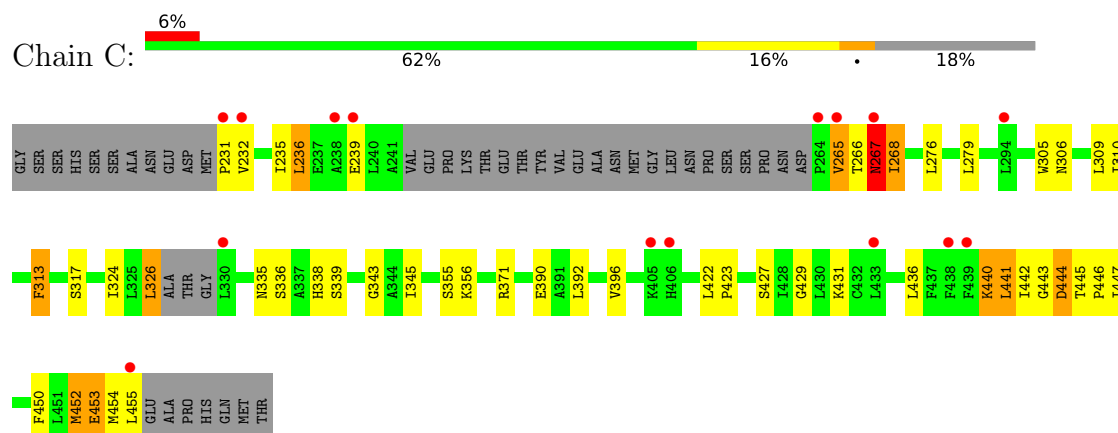
• Molecule 1: Retinoic acid receptor RXR-alpha



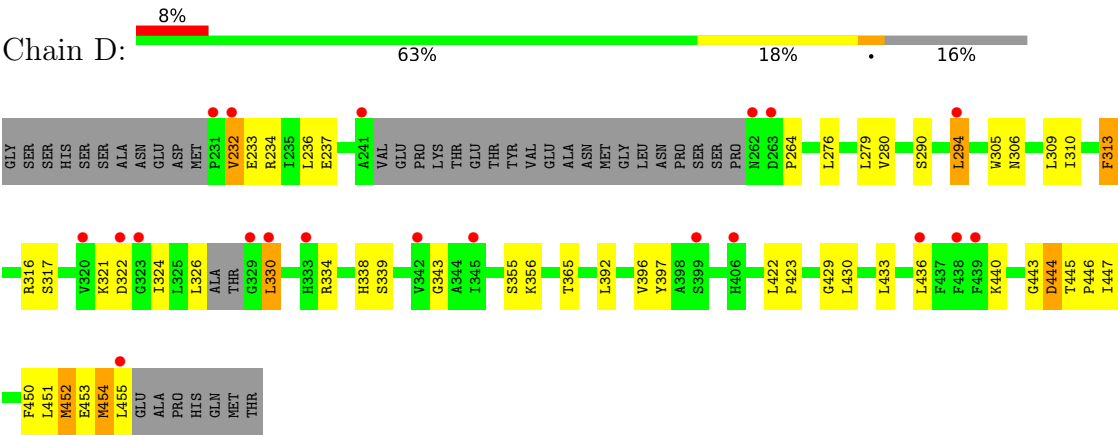
• Molecule 1: Retinoic acid receptor RXR-alpha



• Molecule 1: Retinoic acid receptor RXR-alpha



● Molecule 1: Retinoic acid receptor RXR-alpha



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	46.62Å 99.39Å 110.16Å 90.00° 99.42° 90.00°	Depositor
Resolution (Å)	46.00 – 2.65 46.00 – 2.65	Depositor EDS
% Data completeness (in resolution range)	99.7 (46.00-2.65) 99.7 (46.00-2.65)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.70 (at 2.65Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.223 , 0.274 0.228 , 0.274	Depositor DCC
R_{free} test set	1425 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	46.8	Xtriage
Anisotropy	0.044	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 55.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.031 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6349	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.58% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: WY5

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	0.96	0/1572	1.52	1/2125 (0.0%)
1	B	0.97	0/1559	1.53	0/2105
1	C	0.97	0/1619	1.52	0/2184
1	D	0.96	0/1639	1.53	0/2212
All	All	0.96	0/6389	1.53	1/8626 (0.0%)

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	C	0	2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	264	PRO	CA-N-CD	-6.37	103.08	112.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	267	ASN	Peptide
1	C	452	MET	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	1539	0	1581	28	0
1	B	1527	0	1568	19	1
1	C	1588	0	1637	37	1
1	D	1608	0	1649	39	0
2	A	30	0	0	3	0
3	A	18	0	0	2	0
3	B	11	0	0	0	0
3	C	14	0	0	1	0
3	D	14	0	0	0	0
All	All	6349	0	6435	109	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 (109) 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:410:GLU:HG3	3:A:611:HOH:O	1.48	1.11
1:A:273:ASP:OD1	1:D:264:PRO:HD2	1.57	1.04
2:A:501:WY5:CAR	1:D:305:TRP:HE1	1.83	0.90
1:C:239:GLU:OE2	1:C:371:ARG:NH1	2.09	0.86
1:D:440:LYS:O	1:D:444:ASP:HB2	1.75	0.86
1:A:417:LYS:NZ	1:C:390:GLU:OE2	2.13	0.82
1:C:440:LYS:O	1:C:444:ASP:HB2	1.80	0.80
1:C:445:THR:OG1	1:C:446:PRO:HD3	1.87	0.75
1:A:273:ASP:OD1	1:D:264:PRO:CD	2.36	0.73
1:D:232:VAL:HG22	1:D:232:VAL:O	1.90	0.71
1:D:233:GLU:O	1:D:237:GLU:HB2	1.95	0.66
1:A:439:PHE:CE2	2:A:501:WY5:CAP	2.79	0.65
2:A:501:WY5:CAR	1:D:305:TRP:NE1	2.59	0.64
1:A:436:LEU:HD21	1:D:436:LEU:HD21	1.80	0.64
1:D:232:VAL:O	1:D:232:VAL:CG2	2.46	0.64
1:C:236:LEU:HD22	1:C:236:LEU:O	1.98	0.63
1:C:265:VAL:HG21	1:C:450:PHE:CG	2.34	0.61
1:C:267:ASN:HD22	1:C:267:ASN:N	1.97	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:232:VAL:CG2	1:D:365:THR:CG2	2.79	0.61
1:D:232:VAL:HG22	1:D:365:THR:HG23	1.83	0.60
1:C:306:ASN:ND2	1:C:429:GLY:O	2.35	0.60
1:D:316:ARG:HH11	1:D:326:LEU:HA	1.67	0.59
1:D:453:GLU:O	1:D:453:GLU:HG3	2.02	0.59
1:A:410:GLU:CG	3:A:611:HOH:O	2.24	0.59
1:D:232:VAL:HG22	1:D:365:THR:CG2	2.34	0.57
1:A:439:PHE:C	1:A:439:PHE:CD2	2.83	0.56
1:C:236:LEU:HD22	1:C:236:LEU:C	2.31	0.56
1:C:236:LEU:O	1:C:236:LEU:CD2	2.54	0.56
1:A:317:SER:OG	1:A:324:ILE:HA	2.05	0.55
1:D:306:ASN:ND2	1:D:429:GLY:O	2.39	0.55
1:D:450:PHE:O	1:D:453:GLU:HG2	2.06	0.55
1:B:436:LEU:HD21	1:C:436:LEU:HD21	1.89	0.54
1:D:317:SER:OG	1:D:324:ILE:HA	2.08	0.54
1:C:236:LEU:C	1:C:236:LEU:CD2	2.81	0.53
1:D:232:VAL:CG2	1:D:365:THR:HG23	2.38	0.53
1:B:317:SER:OG	1:B:324:ILE:HA	2.09	0.52
1:C:317:SER:OG	1:C:324:ILE:HA	2.09	0.52
1:D:392:LEU:O	1:D:396:VAL:HG23	2.10	0.52
1:A:436:LEU:CD2	1:D:436:LEU:HD21	2.40	0.51
1:A:451:LEU:HD21	1:D:276:LEU:HD21	1.93	0.51
1:B:445:THR:N	1:B:446:PRO:HD2	2.26	0.50
1:D:236:LEU:O	1:D:236:LEU:HD12	2.11	0.50
1:C:392:LEU:O	1:C:396:VAL:HG23	2.11	0.50
1:D:445:THR:N	1:D:446:PRO:HD2	2.27	0.49
1:B:392:LEU:O	1:B:396:VAL:HG23	2.13	0.49
1:A:417:LYS:CE	1:C:390:GLU:OE2	2.60	0.48
1:A:445:THR:N	1:A:446:PRO:HD2	2.29	0.48
1:C:231:PRO:O	1:C:235:ILE:HD12	2.13	0.48
1:A:443:GLY:O	1:A:447:ILE:HG12	2.14	0.48
1:B:443:GLY:O	1:B:447:ILE:HG12	2.14	0.48
1:B:276:LEU:O	1:B:280:VAL:HG23	2.14	0.47
1:A:275:GLN:HE22	1:A:327:ALA:HB3	1.79	0.47
1:B:272:ALA:HB3	1:C:266:THR:HG21	1.96	0.47
1:A:316:ARG:NH2	1:A:327:ALA:HB2	2.30	0.47
1:B:445:THR:N	1:B:446:PRO:CD	2.77	0.47
1:C:279:LEU:HD21	1:C:305:TRP:HA	1.97	0.47
1:B:345:ILE:HD13	1:B:431:LYS:HB3	1.97	0.47
1:A:276:LEU:O	1:A:280:VAL:HG23	2.15	0.47
1:C:443:GLY:O	1:C:447:ILE:HG12	2.15	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:265:VAL:CG2	1:C:450:PHE:CG	2.98	0.46
1:D:445:THR:N	1:D:446:PRO:CD	2.78	0.46
1:C:453:GLU:O	1:C:453:GLU:CG	2.63	0.46
1:C:445:THR:N	1:C:446:PRO:HD2	2.30	0.46
1:B:338:HIS:ND1	1:B:343:GLY:HA3	2.31	0.46
1:A:392:LEU:O	1:A:396:VAL:HG23	2.16	0.46
1:A:330:LEU:HG	1:A:330:LEU:O	2.16	0.46
1:A:445:THR:N	1:A:446:PRO:CD	2.79	0.46
1:D:279:LEU:HD21	1:D:305:TRP:HA	1.97	0.46
1:A:422:LEU:N	1:A:423:PRO:CD	2.78	0.46
1:C:441:LEU:HD22	1:C:441:LEU:HA	1.80	0.46
1:B:427:SER:HB3	1:D:430:LEU:HD11	1.99	0.45
1:D:322:ASP:OD2	1:D:334:ARG:HD3	2.15	0.45
1:C:338:HIS:ND1	1:C:343:GLY:HA3	2.32	0.45
1:D:264:PRO:HG3	1:D:450:PHE:CG	2.52	0.45
1:C:345:ILE:HD13	1:C:431:LYS:HB3	1.99	0.45
1:C:268:ILE:HD11	1:C:443:GLY:HA2	1.98	0.45
1:A:313:PHE:C	1:A:313:PHE:CD1	2.95	0.45
1:A:338:HIS:ND1	1:A:343:GLY:HA3	2.32	0.45
1:C:442:ILE:O	1:C:446:PRO:HG2	2.17	0.44
1:D:443:GLY:O	1:D:447:ILE:HG12	2.18	0.44
1:B:422:LEU:N	1:B:423:PRO:CD	2.80	0.44
1:D:422:LEU:N	1:D:423:PRO:CD	2.81	0.44
1:C:422:LEU:N	1:C:423:PRO:CD	2.81	0.44
1:B:313:PHE:C	1:B:313:PHE:CD1	2.95	0.44
1:C:445:THR:N	1:C:446:PRO:CD	2.80	0.44
1:D:313:PHE:CD1	1:D:313:PHE:C	2.95	0.44
1:D:330:LEU:O	1:D:330:LEU:HG	2.17	0.43
1:D:453:GLU:O	1:D:453:GLU:CG	2.61	0.43
1:D:451:LEU:O	1:D:454:MET:HG2	2.18	0.43
1:B:330:LEU:O	1:B:330:LEU:HG	2.18	0.43
1:B:272:ALA:CB	1:C:266:THR:HG21	2.48	0.43
1:C:313:PHE:C	1:C:313:PHE:CD1	2.96	0.43
1:C:326:LEU:C	3:C:513:HOH:O	2.62	0.43
1:D:310:ILE:HA	1:D:313:PHE:CE2	2.54	0.43
1:D:338:HIS:ND1	1:D:343:GLY:HA3	2.34	0.42
1:C:310:ILE:HA	1:C:313:PHE:CE2	2.54	0.42
1:C:345:ILE:HD13	1:C:431:LYS:CB	2.50	0.42
1:B:297:GLN:HB2	1:C:454:MET:HE3	2.02	0.42
1:A:433:LEU:HD23	1:A:433:LEU:HA	1.90	0.41
1:A:345:ILE:HD13	1:A:431:LYS:HB3	2.01	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:264:PRO:HB2	1:B:446:PRO:HB3	2.02	0.41
1:D:276:LEU:O	1:D:280:VAL:HG23	2.21	0.41
1:A:452:MET:HG2	1:D:294:LEU:HD23	2.01	0.41
1:B:310:ILE:HA	1:B:313:PHE:CE2	2.56	0.41
1:B:436:LEU:CD2	1:C:436:LEU:HD21	2.50	0.41
1:C:276:LEU:O	1:C:279:LEU:HB3	2.22	0.40
1:D:433:LEU:HD23	1:D:433:LEU:HA	1.85	0.40
1:A:441:LEU:HA	1:A:441:LEU:HD23	1.83	0.40
1:A:442:ILE:O	1:A:446:PRO:HG2	2.21	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)
1:B:338:HIS:ND1	1:C:335:ASN:ND2[1_455]	2.07	0.13

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	193/243 (79%)	187 (97%)	6 (3%)	0	100	100
1	B	189/243 (78%)	182 (96%)	6 (3%)	1 (0%)	24	39
1	C	194/243 (80%)	184 (95%)	6 (3%)	4 (2%)	5	9
1	D	197/243 (81%)	187 (95%)	8 (4%)	2 (1%)	12	20
All	All	773/972 (80%)	740 (96%)	26 (3%)	7 (1%)	14	24

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	444	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	267	ASN
1	C	444	ASP
1	C	452	MET
1	D	444	ASP
1	D	452	MET
1	C	268	ILE

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	167/209 (80%)	157 (94%)	10 (6%)	17	30
1	B	166/209 (79%)	156 (94%)	10 (6%)	17	30
1	C	173/209 (83%)	157 (91%)	16 (9%)	8	14
1	D	175/209 (84%)	160 (91%)	15 (9%)	10	16
All	All	681/836 (82%)	630 (92%)	51 (8%)	12	21

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	313	PHE
1	A	326	LEU
1	A	339	SER
1	A	355	SER
1	A	356	LYS
1	A	397	TYR
1	A	405	LYS
1	A	417	LYS
1	A	439	PHE
1	A	450	PHE
1	B	266	THR
1	B	302	ARG
1	B	313	PHE
1	B	330	LEU
1	B	339	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	356	LYS
1	B	397	TYR
1	B	405	LYS
1	B	450	PHE
1	B	452	MET
1	C	232	VAL
1	C	236	LEU
1	C	265	VAL
1	C	267	ASN
1	C	309	LEU
1	C	313	PHE
1	C	326	LEU
1	C	336	SER
1	C	339	SER
1	C	355	SER
1	C	356	LYS
1	C	427	SER
1	C	440	LYS
1	C	441	LEU
1	C	453	GLU
1	C	455	LEU
1	D	232	VAL
1	D	234	ARG
1	D	290	SER
1	D	294	LEU
1	D	309	LEU
1	D	313	PHE
1	D	321	LYS
1	D	330	LEU
1	D	339	SER
1	D	355	SER
1	D	356	LYS
1	D	397	TYR
1	D	452	MET
1	D	454	MET
1	D	455	LEU

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

Mol	Chain	Res	Type
1	A	267	ASN
1	A	275	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	297	GLN
1	B	297	GLN
1	C	267	ASN
1	C	297	GLN
1	C	335	ASN
1	D	270	GLN
1	D	297	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 ⓘ

There are no oligosaccharides 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	WY5	A	501	-	33,33,33	0.68	1 (3%)	53,53,53	0.67	1 (1%)

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	WY5	A	501	-	-	4/8/27/27	0/4/4/4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	WY5	OAE-CAJ	-2.15	1.24	1.30

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	WY5	OAD-CAJ-CAC	-2.38	117.75	122.67

There are no chirality outliers.

All (4) torsion outliers are listed below:

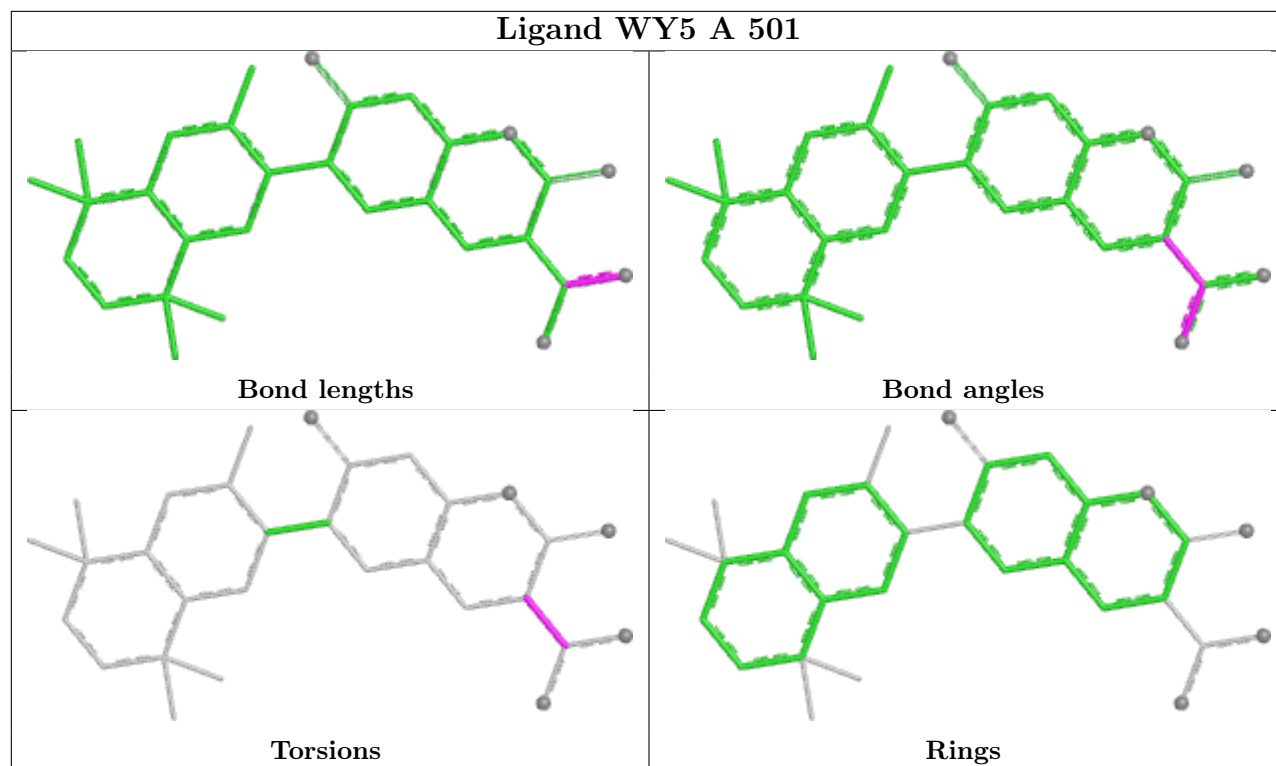
Mol	Chain	Res	Type	Atoms
2	A	501	WY5	CAD-CAC-CAJ-OAD
2	A	501	WY5	CAD-CAC-CAJ-OAE
2	A	501	WY5	CAB-CAC-CAJ-OAD
2	A	501	WY5	CAB-CAC-CAJ-OAE

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	WY5	3	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	195/243 (80%)	0.26	11 (5%) 30 24	20, 43, 75, 101	0
1	B	193/243 (79%)	0.69	20 (10%) 11 9	31, 53, 93, 106	0
1	C	200/243 (82%)	0.51	15 (7%) 20 15	22, 50, 82, 105	0
1	D	203/243 (83%)	0.75	20 (9%) 13 10	31, 53, 106, 132	0
All	All	791/972 (81%)	0.56	66 (8%) 17 12	20, 50, 88, 132	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	231	PRO	6.3
1	D	231	PRO	5.7
1	D	329	GLY	4.9
1	D	455	LEU	4.5
1	B	329	GLY	4.4
1	D	322	ASP	4.3
1	B	264	PRO	4.3
1	D	330	LEU	4.0
1	A	442	ILE	3.9
1	C	405	LYS	3.7
1	B	438	PHE	3.7
1	D	320	VAL	3.7
1	B	442	ILE	3.6
1	B	330	LEU	3.5
1	D	241	ALA	3.5
1	D	232	VAL	3.3
1	A	444	ASP	3.3
1	B	436	LEU	3.3
1	C	264	PRO	3.2
1	A	330	LEU	3.2
1	C	455	LEU	3.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	333	HIS	3.1
1	D	406	HIS	3.1
1	D	345	ILE	3.1
1	C	439	PHE	3.1
1	B	331	HIS	2.9
1	B	439	PHE	2.9
1	D	439	PHE	2.9
1	A	439	PHE	2.9
1	C	238	ALA	2.8
1	D	294	LEU	2.8
1	B	267	ASN	2.8
1	C	330	LEU	2.8
1	A	265	VAL	2.7
1	D	436	LEU	2.7
1	D	438	PHE	2.6
1	C	406	HIS	2.5
1	C	265	VAL	2.4
1	A	438	PHE	2.4
1	A	264	PRO	2.4
1	B	345	ILE	2.4
1	C	267	ASN	2.4
1	D	263	ASP	2.4
1	B	266	THR	2.3
1	B	270	GLN	2.3
1	B	306	ASN	2.3
1	C	232	VAL	2.3
1	B	294	LEU	2.3
1	C	294	LEU	2.3
1	C	239	GLU	2.2
1	B	443	GLY	2.2
1	A	276	LEU	2.2
1	C	438	PHE	2.2
1	B	441	LEU	2.2
1	D	342	VAL	2.2
1	B	325	LEU	2.2
1	A	266	THR	2.2
1	B	435	HIS	2.2
1	A	450	PHE	2.2
1	B	292	LEU	2.1
1	C	433	LEU	2.1
1	D	262	ASN	2.1
1	A	457	ALA	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	399	SER	2.1
1	B	437	PHE	2.0
1	D	323	GLY	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](#)

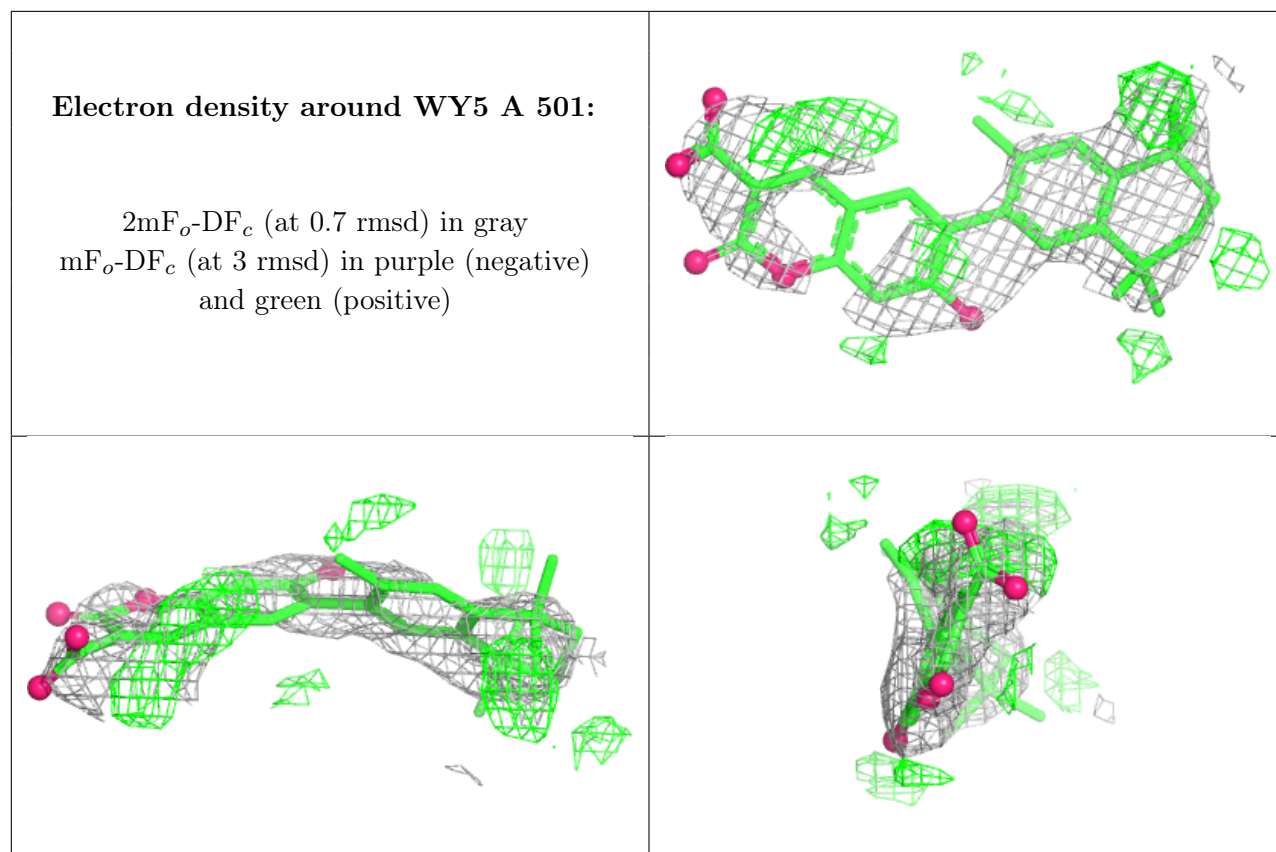
There are no oligosaccharides in this entry.

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($\text{\AA}^2$)	Q<0.9
2	WY5	A	501	30/30	0.73	0.34	52,61,66,67	30

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.