



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 11:50 PM UTC

PDB ID : 2NV7 / pdb_00002nv7
Title : Crystal Structure of Estrogen Receptor Beta Complexed with WAY-555
Authors : Mewshaw, R.E.; Bowen, M.S.; Harris, H.A.; Xu, Z.B.; Manas, E.S.; Cohn, S.T.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on : 2006-11-10
Resolution : 2.10 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

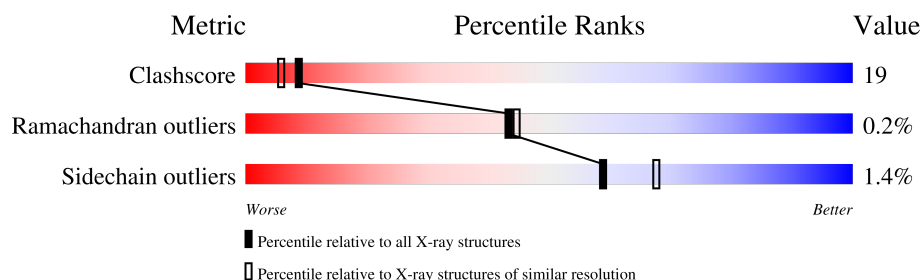
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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))
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	238	 68% 27% . .
1	B	238	 62% 29% . 5%
2	C	10	 80% 20%
2	D	10	 60% 30% 10%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4017 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.

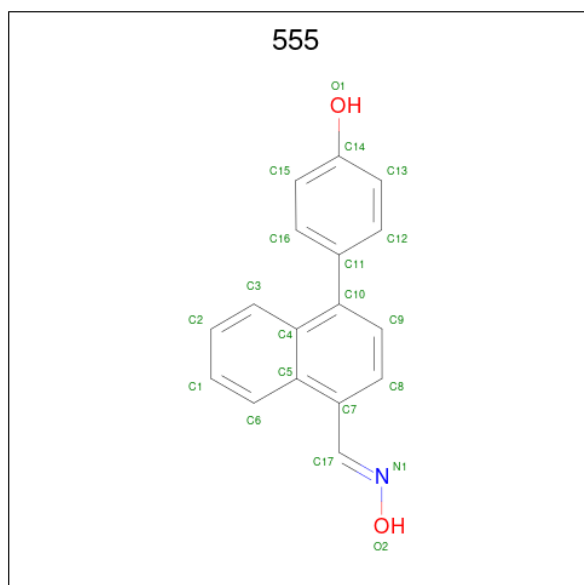
- Molecule 1 is a protein called Estrogen receptor beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	228	Total	C	N	O	S	0	0	0
			1797	1157	304	316	20			
1	B	225	Total	C	N	O	S	0	0	0
			1772	1140	299	313	20			

- Molecule 2 is a protein called Nuclear receptor coactivator 1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	10	Total	C	N	O	0	0	0
			81	52	14	15			
2	D	10	Total	C	N	O	0	0	0
			81	52	14	15			

- Molecule 3 is 4-(4-HYDROXYPHENYL)-1-NAPHTHALDEHYDE OXIME (CCD ID: 555) (formula: C₁₇H₁₃NO₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			20	17	1	2		
3	B	1	Total	C	N	O	0	0
			20	17	1	2		

- Molecule 4 is water.

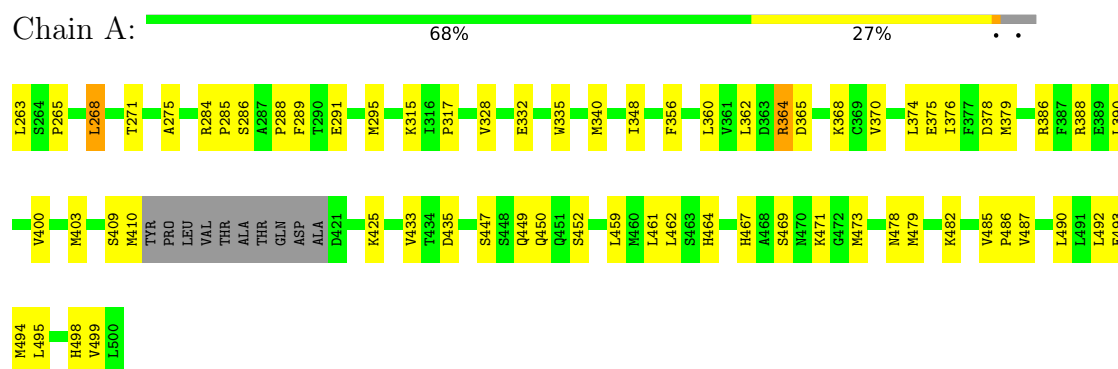
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	145	Total	O	0	0
			145	145		
4	B	93	Total	O	0	0
			93	93		
4	C	4	Total	O	0	0
			4	4		
4	D	4	Total	O	0	0
			4	4		

3 Residue-property plots [i](#)

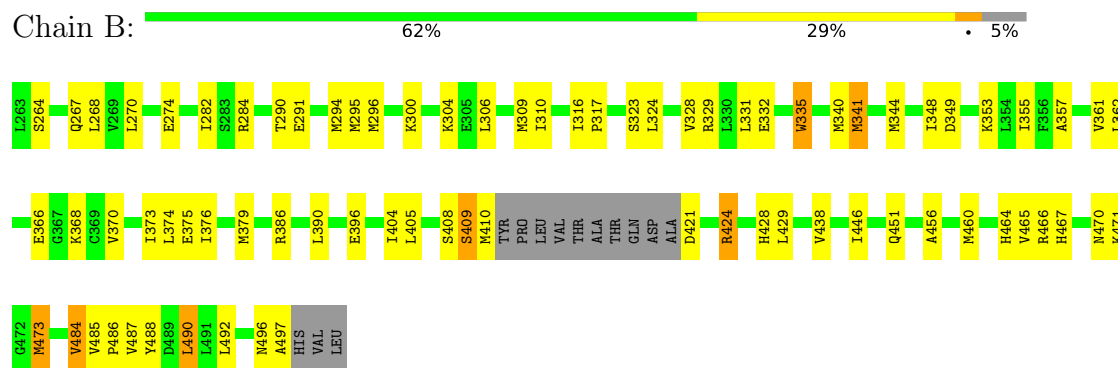
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

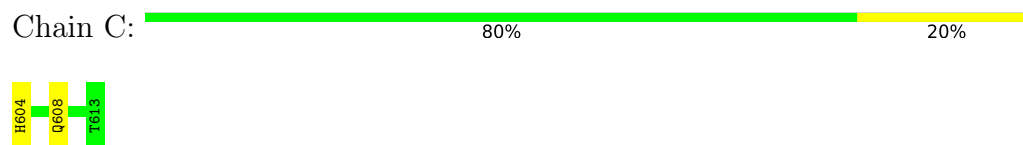
- Molecule 1: Estrogen receptor beta



- Molecule 1: Estrogen receptor beta



- Molecule 2: Nuclear receptor coactivator 1



- Molecule 2: Nuclear receptor coactivator 1





4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	52.13Å 88.68Å 100.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.99 – 2.10	Depositor
% Data completeness (in resolution range)	98.2 (19.99-2.10)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.211 , 0.265	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4017	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 555

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	0.56	0/1829	0.99	8/2469 (0.3%)
1	B	0.55	2/1803 (0.1%)	0.94	5/2433 (0.2%)
2	C	0.61	0/81	0.83	0/108
2	D	0.58	0/81	1.04	0/108
All	All	0.56	2/3794 (0.1%)	0.96	13/5118 (0.3%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	473	MET	SD-CE	-5.30	1.66	1.79
1	B	341	MET	SD-CE	-5.04	1.67	1.79

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	364	ARG	N-CA-C	12.77	125.28	111.36
1	B	424	ARG	N-CA-C	-7.60	102.94	111.14
1	A	268	LEU	N-CA-C	-6.63	104.13	111.36
1	B	396	GLU	N-CA-C	-6.00	104.31	111.69
1	B	290	THR	N-CA-C	-5.92	100.50	109.85
1	A	335	TRP	N-CA-C	5.83	118.10	111.11
1	A	485	VAL	CA-C-N	-5.68	113.93	119.90
1	A	485	VAL	C-N-CA	-5.68	113.93	119.90
1	B	335	TRP	N-CA-C	5.45	117.65	111.11
1	A	486	PRO	CA-C-N	-5.38	116.27	122.95
1	A	486	PRO	C-N-CA	-5.38	116.27	122.95
1	A	348	ILE	N-CA-C	5.28	116.64	110.62
1	B	484	VAL	N-CA-C	-5.01	106.48	113.00

There are no chirality outliers.

There are no planarity outliers.

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	1797	0	1877	71	0
1	B	1772	0	1850	76	0
2	C	81	0	90	1	0
2	D	81	0	90	4	0
3	A	20	0	12	1	0
3	B	20	0	13	1	0
4	A	145	0	0	18	1
4	B	93	0	0	7	0
4	C	4	0	0	0	0
4	D	4	0	0	2	0
All	All	4017	0	3932	144	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 19.

All (144) 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:291:GLU:HG3	1:A:370:VAL:HG22	1.26	1.13
1:A:271:THR:HB	4:A:227:HOH:O	1.64	0.96
1:B:341:MET:HE3	1:B:404:ILE:HD11	1.49	0.94
1:A:268:LEU:O	1:A:271:THR:HG22	1.68	0.94
4:A:232:HOH:O	1:B:438:VAL:HG11	1.68	0.93
1:A:386:ARG:HG2	1:A:461:LEU:HD21	1.52	0.92
1:B:410:MET:HE3	1:B:466:ARG:HH22	1.36	0.91
2:D:604:HIS:HB2	4:D:161:HOH:O	1.71	0.90
1:A:487:VAL:HG21	1:A:492:LEU:HD13	1.54	0.89
1:B:341:MET:HE1	1:B:465:VAL:HG21	1.54	0.89
1:A:365:ASP:HA	1:A:368:LYS:HE2	1.59	0.82
1:A:364:ARG:NH2	4:A:226:HOH:O	2.05	0.79
1:A:365:ASP:CA	1:A:368:LYS:HE2	2.15	0.77
1:B:274:GLU:HG2	4:B:231:HOH:O	1.85	0.75

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:488:TYR:HA	1:B:492:LEU:CB	2.16	0.75
1:B:408:SER:C	1:B:410:MET:H	1.95	0.73
1:B:428:HIS:HB2	4:B:74:HOH:O	1.88	0.73
1:B:309:MET:SD	4:B:194:HOH:O	2.47	0.73
1:B:485:VAL:HG23	1:B:486:PRO:HD2	1.71	0.73
1:A:400:VAL:HG13	1:A:462:LEU:HD21	1.72	0.72
1:A:464:HIS:HA	1:B:410:MET:HE1	1.72	0.72
1:A:425:LYS:HG2	4:A:49:HOH:O	1.90	0.71
1:B:294:MET:HE2	1:B:362:LEU:HD13	1.72	0.70
1:B:488:TYR:HA	1:B:492:LEU:HB2	1.74	0.68
1:A:452:SER:HB2	4:A:232:HOH:O	1.93	0.67
2:C:604:HIS:O	2:C:608:GLN:HG3	1.95	0.67
1:A:375:GLU:HG2	1:A:379:MET:HE2	1.78	0.66
1:B:295:MET:HE3	1:B:370:VAL:HG21	1.77	0.66
1:B:341:MET:HE2	1:B:465:VAL:HG11	1.79	0.65
1:B:379:MET:HE1	1:B:467:HIS:ND1	2.12	0.65
1:B:344:MET:HE1	1:B:465:VAL:HG22	1.80	0.64
1:A:479:MET:HE3	4:A:241:HOH:O	1.98	0.64
1:B:408:SER:O	1:B:410:MET:N	2.25	0.63
1:B:296:MET:HE2	4:B:174:HOH:O	1.97	0.63
1:B:353:LYS:HG2	1:B:361:VAL:CG1	2.30	0.61
1:A:473:MET:HE2	1:A:498:HIS:ND1	2.15	0.61
1:A:388:ARG:NH1	4:A:109:HOH:O	2.32	0.61
1:A:487:VAL:CG2	1:A:492:LEU:HD13	2.28	0.61
1:B:421:ASP:CB	1:B:424:ARG:HD2	2.30	0.60
1:B:488:TYR:HA	1:B:492:LEU:HB3	1.83	0.60
1:B:487:VAL:O	1:B:492:LEU:HB2	2.00	0.60
1:B:300:LYS:HG2	4:B:174:HOH:O	2.02	0.60
1:A:487:VAL:HG23	1:A:492:LEU:HB2	1.85	0.58
1:B:456:ALA:O	1:B:460:MET:HG3	2.03	0.58
1:A:364:ARG:HG3	1:A:374:LEU:HD11	1.84	0.58
1:A:271:THR:HG21	1:A:317:PRO:HG2	1.86	0.58
1:A:467:HIS:CD2	1:A:471:LYS:HE2	2.38	0.57
1:A:386:ARG:HG2	1:A:461:LEU:CD2	2.30	0.57
1:A:449:GLN:NE2	4:A:232:HOH:O	2.37	0.57
1:A:364:ARG:CG	1:A:374:LEU:HD11	2.34	0.57
1:B:335:TRP:CZ2	1:B:473:MET:HE1	2.39	0.57
1:B:353:LYS:HG2	1:B:361:VAL:HG12	1.86	0.57
1:B:492:LEU:HD11	1:B:496:ASN:HD21	1.68	0.57
1:A:490:LEU:O	1:A:494:MET:HG2	2.04	0.56
1:B:408:SER:C	1:B:410:MET:N	2.60	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:495:LEU:O	1:A:499:VAL:HG23	2.06	0.55
1:A:410:MET:HG2	1:B:467:HIS:CG	2.42	0.55
1:A:268:LEU:O	1:A:271:THR:CG2	2.50	0.54
1:A:479:MET:HG3	4:A:68:HOH:O	2.06	0.54
1:B:296:MET:HE1	1:B:486:PRO:HG2	1.89	0.54
1:A:473:MET:HG3	4:A:202:HOH:O	2.07	0.54
1:A:386:ARG:NE	4:A:93:HOH:O	2.32	0.54
1:A:390:LEU:HG	4:A:93:HOH:O	2.08	0.53
1:A:403:MET:HE1	1:A:459:LEU:HD21	1.89	0.53
1:B:370:VAL:HB	1:B:373:ILE:CG1	2.38	0.53
1:B:296:MET:HG3	4:B:29:HOH:O	2.08	0.53
1:B:355:ILE:HD13	1:B:361:VAL:HG13	1.90	0.53
1:B:355:ILE:CD1	1:B:361:VAL:HG13	2.39	0.53
1:A:376:ILE:HA	1:A:379:MET:HE3	1.91	0.52
1:B:370:VAL:HB	1:B:373:ILE:HG13	1.91	0.52
1:B:485:VAL:CG2	1:B:486:PRO:HD2	2.39	0.51
1:A:364:ARG:HG2	1:A:364:ARG:NH1	2.26	0.51
1:A:487:VAL:HG23	1:A:487:VAL:O	2.10	0.51
1:A:364:ARG:HD2	1:A:378:ASP:OD1	2.11	0.51
1:B:264:SER:OG	1:B:267:GLN:HG3	2.10	0.51
1:B:328:VAL:O	1:B:332:GLU:HG3	2.11	0.51
1:B:410:MET:HE3	1:B:466:ARG:NH2	2.17	0.50
1:B:284:ARG:NH1	1:B:366:GLU:OE1	2.44	0.50
2:D:607:VAL:HG23	4:D:161:HOH:O	2.10	0.50
1:A:403:MET:HE3	1:B:460:MET:SD	2.52	0.50
1:A:340:MET:SD	1:A:469:SER:HA	2.52	0.49
2:D:604:HIS:O	2:D:608:GLN:HG3	2.12	0.49
1:B:370:VAL:CG1	1:B:373:ILE:HG12	2.41	0.49
1:A:410:MET:HG3	1:B:379:MET:HE3	1.94	0.49
1:A:471:LYS:HE3	4:A:89:HOH:O	2.13	0.49
1:A:467:HIS:ND1	1:B:410:MET:SD	2.84	0.49
1:B:353:LYS:CG	1:B:361:VAL:HG12	2.42	0.49
1:B:324:LEU:O	1:B:324:LEU:HG	2.10	0.49
1:B:386:ARG:NH2	1:B:390:LEU:HD21	2.28	0.49
1:B:340:MET:O	1:B:344:MET:HG3	2.13	0.49
1:B:341:MET:CE	1:B:465:VAL:HG21	2.34	0.49
1:A:379:MET:HE1	1:A:471:LYS:HG3	1.95	0.49
1:B:375:GLU:O	1:B:379:MET:HG3	2.13	0.49
1:A:365:ASP:CB	1:A:368:LYS:HE2	2.43	0.48
1:A:493:GLU:HG2	4:A:115:HOH:O	2.13	0.48
1:A:364:ARG:HG3	1:A:374:LEU:CD1	2.43	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:376:ILE:CD1	1:B:471:LYS:HB3	2.44	0.48
1:B:268:LEU:HD12	1:B:317:PRO:HG2	1.96	0.48
1:A:265:PRO:HG3	1:A:435:ASP:OD2	2.13	0.48
1:B:306:LEU:HB3	1:B:490:LEU:HD13	1.96	0.47
1:A:364:ARG:HG2	1:A:364:ARG:HH11	1.78	0.47
1:A:467:HIS:NE2	1:A:471:LYS:HE2	2.30	0.47
1:A:478:ASN:OD1	1:A:482:LYS:HE2	2.14	0.47
1:B:294:MET:HE2	1:B:362:LEU:CD1	2.42	0.47
1:A:328:VAL:O	1:A:332:GLU:HG3	2.15	0.47
1:A:447:SER:OG	1:A:450:GLN:HG2	2.15	0.47
1:B:295:MET:HA	1:B:295:MET:HE2	1.97	0.46
1:A:285:PRO:O	1:A:286:SER:C	2.57	0.46
1:A:409:SER:O	1:B:464:HIS:CE1	2.69	0.46
1:B:310:ILE:HD12	1:B:331:LEU:HD13	1.99	0.45
1:B:410:MET:CE	1:B:466:ARG:HH22	2.20	0.45
1:B:496:ASN:O	1:B:497:ALA:HB3	2.17	0.45
1:B:316:ILE:HD12	1:B:405:LEU:HD23	1.99	0.44
1:A:386:ARG:HG3	1:A:461:LEU:HD11	1.99	0.44
1:B:268:LEU:CD1	1:B:317:PRO:HG2	2.48	0.44
1:A:473:MET:CG	4:A:202:HOH:O	2.65	0.44
1:A:263:LEU:N	4:A:156:HOH:O	2.51	0.43
1:A:365:ASP:HB3	1:A:368:LYS:HE2	2.01	0.43
1:A:410:MET:HG2	1:B:467:HIS:CD2	2.53	0.43
1:A:464:HIS:CA	1:B:410:MET:HE1	2.43	0.43
1:A:356:PHE:HB2	1:A:360:LEU:HG	2.01	0.43
1:A:360:LEU:HD11	1:A:362:LEU:HD11	2.00	0.43
1:B:446:ILE:HG13	1:B:451:GLN:HG3	2.02	0.42
1:B:304:LYS:NZ	4:B:136:HOH:O	2.44	0.42
1:A:403:MET:HG3	1:A:433:VAL:CG1	2.50	0.42
1:B:309:MET:HE1	1:B:335:TRP:CB	2.49	0.42
1:B:348:ILE:HG23	1:B:349:ASP:N	2.34	0.42
1:B:329:ARG:HH12	1:B:409:SER:HA	1.84	0.41
1:B:368:LYS:HD3	1:B:374:LEU:CD1	2.50	0.41
1:A:284:ARG:CZ	1:A:289:PHE:CE1	3.03	0.41
1:A:295:MET:HE1	3:A:501:555:N1	2.35	0.41
1:A:403:MET:HG3	1:A:433:VAL:HG12	2.02	0.41
1:A:482:LYS:HE3	4:A:191:HOH:O	2.18	0.41
1:A:275:ALA:HA	1:A:315:LYS:HD2	2.03	0.41
1:B:309:MET:HE1	1:B:335:TRP:HB2	2.03	0.41
1:B:484:VAL:O	1:B:484:VAL:HG12	2.21	0.41
1:B:282:ILE:HG22	1:B:357:ALA:CB	2.51	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:291:GLU:HG3	1:B:370:VAL:HA	2.02	0.41
2:D:612:THR:O	2:D:612:THR:CG2	2.68	0.41
1:A:425:LYS:CG	4:A:49:HOH:O	2.57	0.41
1:A:364:ARG:CD	1:A:378:ASP:OD1	2.69	0.40
1:A:409:SER:O	1:B:464:HIS:HE1	2.04	0.40
1:B:470:ASN:HD22	1:B:470:ASN:HA	1.75	0.40
3:B:501:555:H6	3:B:501:555:N1	2.37	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:27:HOH:O	4:A:148:HOH:O[4_456]	2.06	0.14

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	224/238 (94%)	217 (97%)	7 (3%)	0	100	100
1	B	221/238 (93%)	214 (97%)	6 (3%)	1 (0%)	24	22
2	C	8/10 (80%)	8 (100%)	0	0	100	100
2	D	8/10 (80%)	8 (100%)	0	0	100	100
All	All	461/496 (93%)	447 (97%)	13 (3%)	1 (0%)	43	44

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	409	SER

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	204/214 (95%)	203 (100%)	1 (0%)	81	88
1	B	201/214 (94%)	197 (98%)	4 (2%)	48	56
2	C	10/10 (100%)	10 (100%)	0	100	100
2	D	10/10 (100%)	9 (90%)	1 (10%)	7	5
All	All	425/448 (95%)	419 (99%)	6 (1%)	59	67

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	288	PRO
1	B	270	LEU
1	B	323	SER
1	B	429	LEU
1	B	490	LEU
2	D	612	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	350	HIS
1	A	407	ASN
1	A	428	HIS
1	A	450	GLN
1	A	470	ASN
1	B	327	GLN
1	B	407	ASN
1	B	428	HIS
1	B	470	ASN
1	B	478	ASN
1	B	496	ASN

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 ⓘ

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	555	A	501	-	22,22,22	2.04	8 (36%)	30,30,30	1.17	2 (6%)
3	555	B	501	-	22,22,22	1.91	8 (36%)	30,30,30	1.36	3 (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
3	555	A	501	-	-	2/7/7/7	0/3/3/3
3	555	B	501	-	-	0/7/7/7	0/3/3/3

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	501	555	C16-C11	3.48	1.46	1.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	501	555	C9-C10	3.28	1.44	1.38
3	B	501	555	C16-C11	3.21	1.45	1.39
3	B	501	555	C10-C4	3.13	1.49	1.42
3	A	501	555	C5-C4	2.85	1.48	1.43
3	B	501	555	C9-C10	2.80	1.43	1.38
3	A	501	555	C3-C4	2.74	1.47	1.42
3	A	501	555	C10-C4	2.70	1.48	1.42
3	A	501	555	C12-C11	2.49	1.44	1.39
3	B	501	555	C5-C4	2.46	1.48	1.43
3	B	501	555	C3-C4	2.23	1.46	1.42
3	A	501	555	C7-C17	2.20	1.51	1.47
3	A	501	555	C10-C11	2.18	1.53	1.49
3	B	501	555	C7-C5	2.10	1.48	1.43
3	B	501	555	C1-C6	2.09	1.41	1.36
3	B	501	555	C12-C11	2.01	1.43	1.39

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	501	555	C7-C17-N1	4.17	125.65	119.65
3	A	501	555	C7-C17-N1	3.29	124.39	119.65
3	B	501	555	C11-C10-C4	2.81	126.82	122.03
3	A	501	555	C11-C10-C4	2.78	126.77	122.03
3	B	501	555	O2-N1-C17	-2.12	108.17	111.83

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	501	555	N1-C17-C7-C8
3	A	501	555	N1-C17-C7-C5

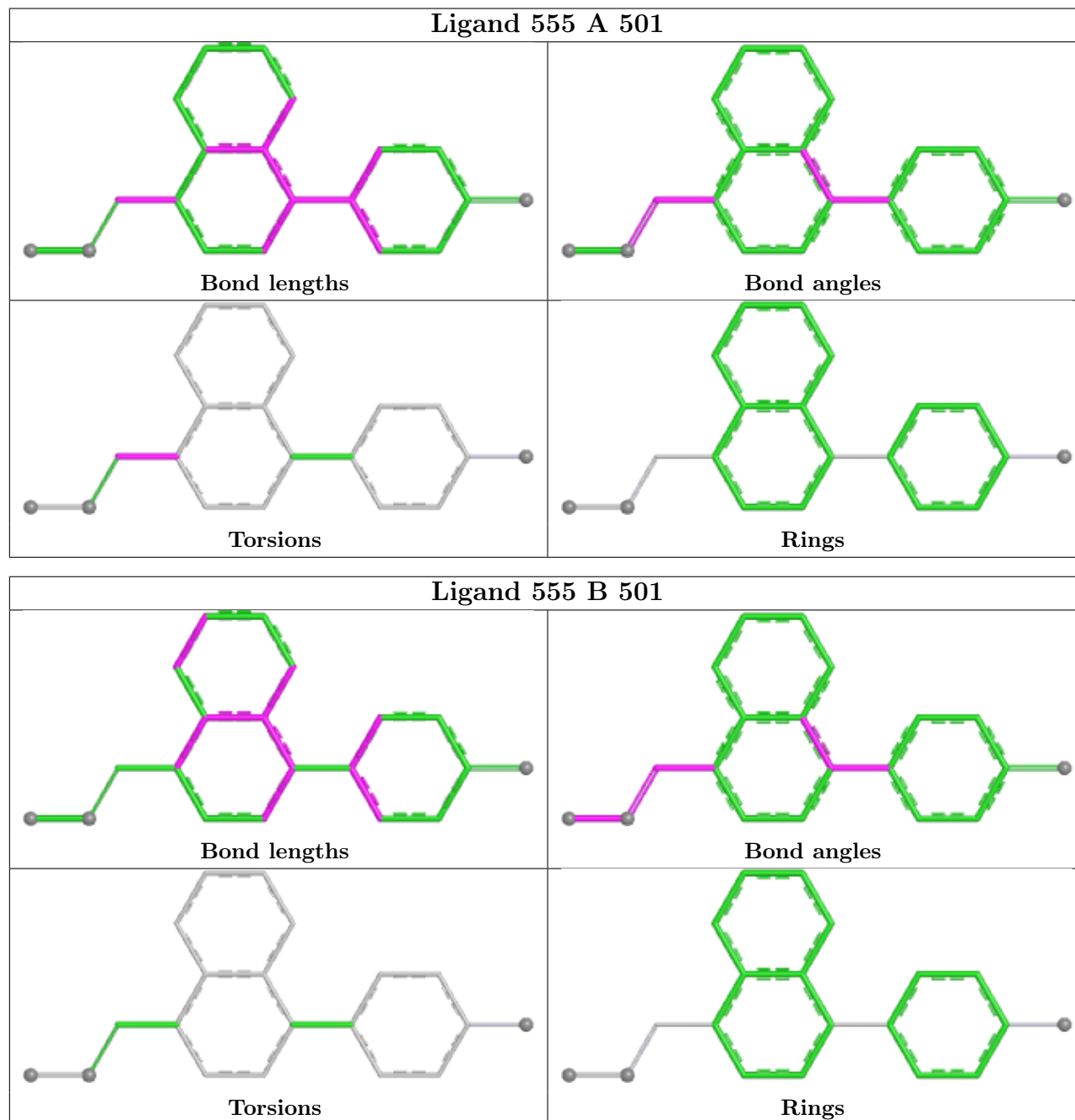
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	501	555	1	0
3	B	501	555	1	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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.