



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:21 PM UTC

PDB ID : 1OSV / pdb_00001osv
Title : STRUCTURAL BASIS FOR BILE ACID BINDING AND ACTIVATION OF
THE NUCLEAR RECEPTOR FXR
Authors : Mi, L.Z.; Devarakonda, S.; Harp, J.M.; Han, Q.; Pellicciari, R.; Willson, T.M.;
Khorasanizadeh, S.; Rastinejad, F.
Deposited on : 2003-03-20
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 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:

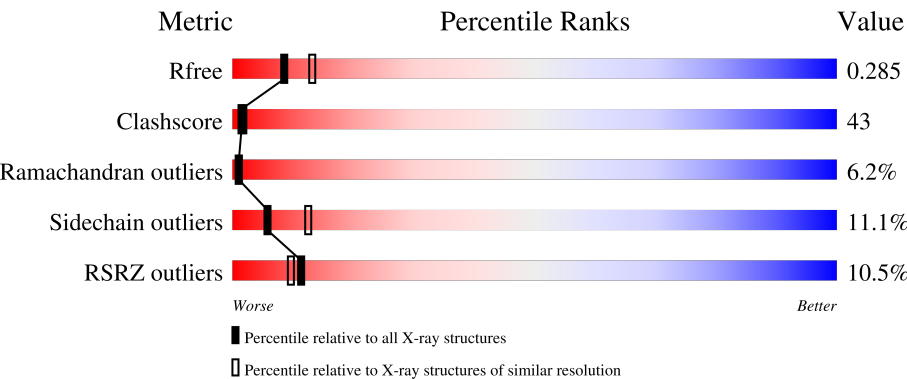
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 i

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}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (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 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	230	11% 42% 45% 12% .
1	B	230	10% 40% 46% 10% .
2	C	12	17% 67% 17% 17%
2	D	12	8% 25% 50% 25%

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Mol	Chain	Length	Quality of chain
2	E	12	8% 58% 25% 17%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4265 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 Bile acid receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	229	Total	C	N	O	S	0	0	0
			1875	1201	311	352	11			
1	B	229	Total	C	N	O	S	0	0	0
			1875	1201	311	352	11			

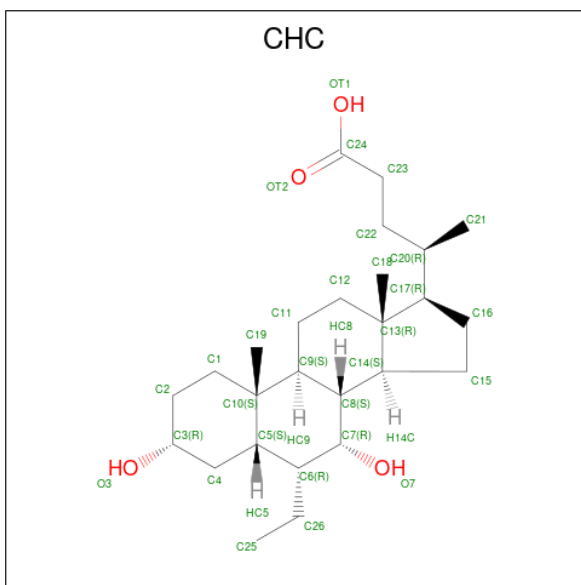
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	240	ALA	-	cloning artifact	UNP Q62735
B	240	ALA	-	cloning artifact	UNP Q62735

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	12	Total	C	N	O	0	0	0
			100	64	17	19			
2	D	12	Total	C	N	O	0	0	0
			103	65	17	21			
2	E	12	Total	C	N	O	0	0	0
			100	64	17	19			

- Molecule 3 is 6-ETHYL-CHENODEOXYCHOLIC ACID (CCD ID: CHC) (formula: C₂₆H₄₄O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			30	26	4		
3	B	1	Total	C	O	0	0
			30	26	4		

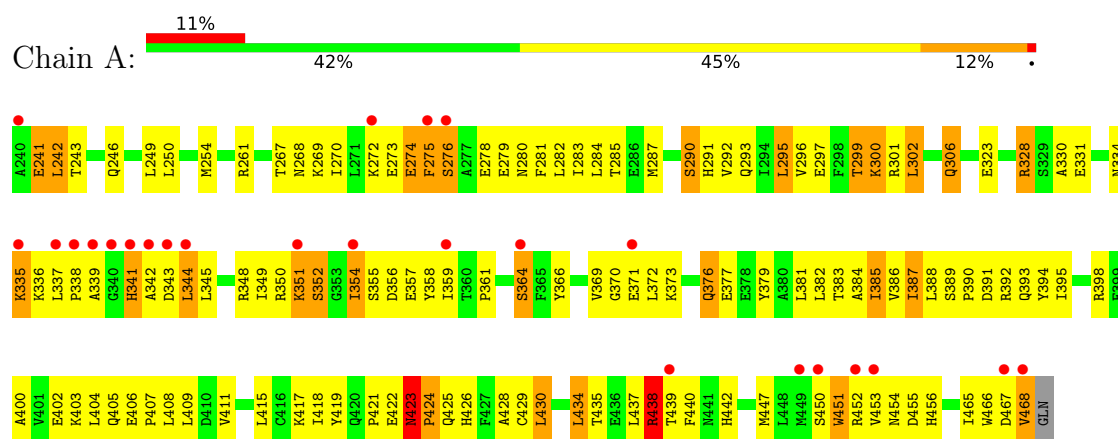
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	68	Total O 68 68	0	0
4	B	71	Total O 71 71	0	0
4	C	3	Total O 3 3	0	0
4	D	3	Total O 3 3	0	0
4	E	7	Total O 7 7	0	0

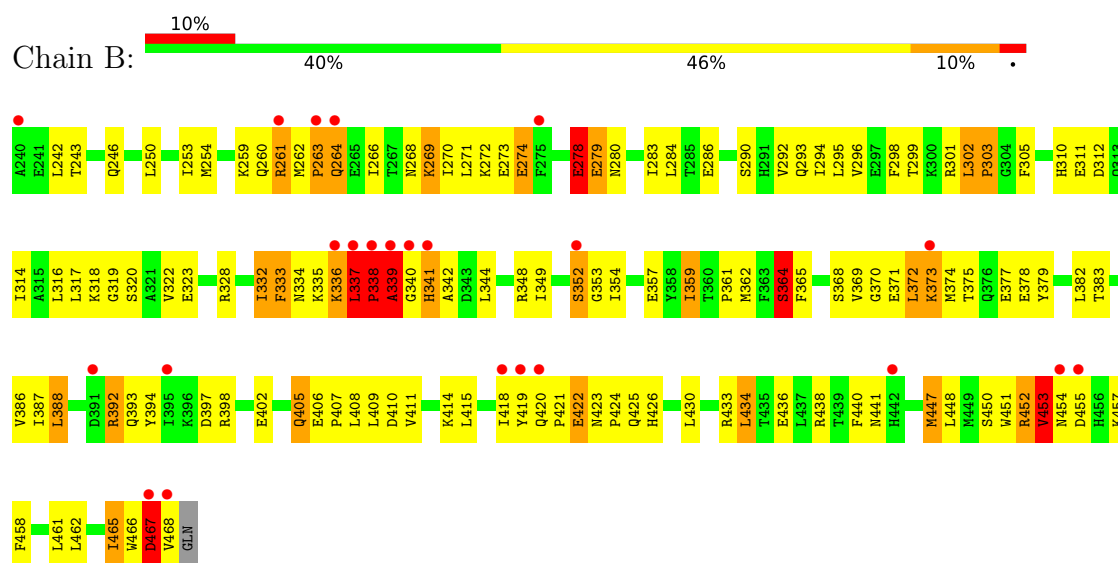
3 Residue-property plots

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: Bile acid receptor



• Molecule 1: Bile acid receptor

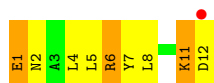


• Molecule 2: Nuclear receptor coactivator 2

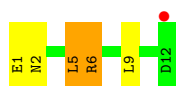




- Molecule 2: Nuclear receptor coactivator 2



- Molecule 2: Nuclear receptor coactivator 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	98.97Å 108.52Å 69.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.88 – 2.50 19.88 – 2.50	Depositor EDS
% Data completeness (in resolution range)	91.4 (19.88-2.50) 92.9 (19.88-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.98 (at 2.34Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.242 , 0.276 0.253 , 0.285	Depositor DCC
R_{free} test set	1874 reflections (6.72%)	wwPDB-VP
Wilson B-factor (Å ²)	42.3	Xtriage
Anisotropy	0.710	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 55.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4265	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.53% 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: CHC

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	0.50	0/1913	1.12	16/2584 (0.6%)
1	B	0.48	0/1913	1.02	14/2584 (0.5%)
2	C	0.42	0/100	1.08	1/132 (0.8%)
2	D	0.42	0/103	0.74	0/136
2	E	0.37	0/100	0.69	0/132
All	All	0.49	0/4129	1.05	31/5568 (0.6%)

There are no bond length outliers.

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	450	SER	CA-C-N	-12.01	105.00	122.77
1	A	450	SER	C-N-CA	-12.01	105.00	122.77
1	A	451	TRP	CA-C-N	-11.20	104.84	122.87
1	A	451	TRP	C-N-CA	-11.20	104.84	122.87
2	C	10	ASP	N-CA-C	-8.48	98.65	110.35
1	A	450	SER	N-CA-C	-8.22	101.41	112.26
1	B	342	ALA	N-CA-C	-8.20	102.43	111.36
1	B	392	ARG	N-CA-C	-7.72	99.61	110.50
1	B	364	SER	N-CA-C	-7.61	103.06	111.36
1	B	333	PHE	N-CA-C	-7.49	100.62	110.43
1	B	359	ILE	N-CA-C	6.95	117.09	110.42
1	B	305	PHE	N-CA-C	6.92	119.42	111.11
1	A	352	SER	N-CA-C	-6.83	101.99	112.99
1	B	341	HIS	N-CA-C	6.72	120.91	111.30
1	B	279	GLU	N-CA-C	-6.71	104.82	112.87
1	B	278	GLU	N-CA-C	-6.31	105.34	113.16
1	B	339	ALA	N-CA-C	-6.06	97.89	110.80
1	A	274	GLU	N-CA-C	5.96	118.23	109.24
1	A	343	ASP	N-CA-C	-5.92	104.77	112.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	372	LEU	N-CA-C	-5.91	106.42	113.21
1	A	393	GLN	N-CA-C	5.90	123.37	110.80
1	A	438	ARG	N-CA-C	-5.77	105.13	111.82
1	A	302	LEU	N-CA-C	-5.73	102.56	109.72
1	A	364	SER	N-CA-C	-5.60	104.80	111.69
1	A	418	ILE	N-CA-C	5.56	115.70	110.30
1	B	352	SER	N-CA-C	-5.54	100.99	109.41
1	A	394	TYR	N-CA-C	5.54	121.91	113.61
1	A	280	ASN	N-CA-C	-5.23	105.47	111.07
1	B	274	GLU	N-CA-C	5.04	117.36	110.55
1	B	357	GLU	N-CA-C	-5.04	105.79	111.28
1	A	290	SER	N-CA-C	-5.01	105.47	111.03

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	1875	0	1879	154	0
1	B	1875	0	1879	190	0
2	C	100	0	104	3	0
2	D	103	0	106	14	0
2	E	100	0	104	11	0
3	A	30	0	43	0	0
3	B	30	0	43	2	0
4	A	68	0	0	11	0
4	B	71	0	0	7	0
4	C	3	0	0	0	0
4	D	3	0	0	0	0
4	E	7	0	0	0	0
All	All	4265	0	4158	359	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 43.

All (359) 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:B:270:ILE:HG23	1:B:274:GLU:HG3	1.34	1.09
1:B:405:GLN:HE21	1:B:409:LEU:HD11	1.18	1.06
1:A:335:LYS:HE3	1:A:373:LYS:HA	1.41	0.99
1:A:402:GLU:HA	4:A:149:HOH:O	1.61	0.98
1:B:374:MET:HE1	1:B:382:LEU:HD11	1.45	0.97
1:B:332:ILE:O	1:B:335:LYS:HB2	1.65	0.96
1:A:302:LEU:HD23	1:A:388:LEU:HD21	1.47	0.95
1:A:297:GLU:O	1:A:300:LYS:HG3	1.67	0.93
1:B:261:ARG:HA	1:B:261:ARG:HH11	1.32	0.91
1:A:355:SER:HB3	1:A:357:GLU:HG2	1.53	0.89
1:B:447:MET:HE3	1:B:451:TRP:HB2	1.51	0.89
1:B:271:LEU:O	1:B:271:LEU:HD13	1.73	0.88
1:B:405:GLN:NE2	1:B:409:LEU:HD11	1.91	0.85
1:A:337:LEU:HB3	4:A:143:HOH:O	1.77	0.85
1:B:299:THR:HA	1:B:302:LEU:CD2	2.04	0.85
1:A:405:GLN:HB3	4:A:149:HOH:O	1.76	0.85
1:B:374:MET:HE1	1:B:382:LEU:CD1	2.07	0.84
1:B:263:PRO:HD2	1:B:294:ILE:HD11	1.60	0.84
1:B:263:PRO:HD2	1:B:294:ILE:CD1	2.08	0.83
1:A:335:LYS:NZ	1:A:373:LYS:HG2	1.94	0.83
1:A:423:ASN:HB2	1:A:424:PRO:O	1.79	0.82
2:D:6:ARG:HB3	2:D:6:ARG:NH1	1.94	0.82
1:B:336:LYS:HG3	1:B:338:PRO:HD2	1.58	0.82
1:B:262:MET:HG3	1:B:268:ASN:HD21	1.42	0.82
1:B:299:THR:HG22	1:B:387:ILE:HD13	1.61	0.81
1:A:295:LEU:O	1:A:299:THR:HG23	1.80	0.81
1:A:423:ASN:HD22	1:A:424:PRO:HA	1.45	0.80
1:A:383:THR:O	1:A:387:ILE:HD12	1.82	0.79
1:B:452:ARG:CZ	1:B:453:VAL:H	1.96	0.79
1:A:423:ASN:ND2	1:A:424:PRO:HA	1.98	0.78
1:B:466:TRP:O	1:B:467:ASP:HB2	1.84	0.77
1:B:374:MET:HE3	1:B:430:LEU:HD22	1.67	0.76
1:A:424:PRO:HG2	1:A:425:GLN:H	1.50	0.76
1:A:435:THR:HG23	4:A:98:HOH:O	1.85	0.76
1:B:447:MET:HE2	1:B:447:MET:C	2.11	0.75
1:A:451:TRP:O	1:A:452:ARG:HD3	1.86	0.75
1:B:262:MET:CG	1:B:268:ASN:HD21	1.99	0.75
1:A:389:SER:HB2	1:A:392:ARG:HH11	1.51	0.75
1:B:295:LEU:O	1:B:299:THR:HG23	1.87	0.75
1:A:377:GLU:HG2	4:A:63:HOH:O	1.86	0.75
1:A:283:ILE:CD1	1:A:348:ARG:HH21	2.00	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:389:SER:CB	1:A:392:ARG:HH11	2.00	0.74
1:A:330:ALA:HB1	1:A:369:VAL:HG21	1.68	0.74
1:B:293:GLN:HE22	2:E:5:LEU:HG	1.53	0.73
2:D:6:ARG:HB3	2:D:6:ARG:HH11	1.52	0.73
1:A:390:PRO:O	1:A:395:ILE:HD11	1.88	0.73
1:A:422:GLU:CD	1:A:422:GLU:H	1.96	0.73
1:A:323:GLU:HG3	4:A:33:HOH:O	1.88	0.72
1:B:253:ILE:HD12	1:B:254:MET:N	2.04	0.72
1:A:351:LYS:HZ3	1:A:351:LYS:H	1.36	0.72
1:A:395:ILE:HD11	1:A:398:ARG:HG2	1.70	0.72
1:B:261:ARG:HD3	1:B:328:ARG:HH12	1.54	0.71
1:A:424:PRO:C	1:A:426:HIS:H	1.98	0.71
1:B:266:ILE:O	1:B:270:ILE:HG13	1.91	0.71
1:A:350:ARG:HD3	1:A:359:ILE:HD12	1.71	0.70
1:B:461:LEU:HD13	2:D:4:LEU:HD22	1.73	0.70
1:B:264:GLN:HG3	2:E:5:LEU:HD12	1.73	0.70
1:A:351:LYS:H	1:A:351:LYS:NZ	1.90	0.69
1:B:334:ASN:ND2	1:B:370:GLY:HA3	2.08	0.68
1:B:270:ILE:HG23	1:B:274:GLU:CG	2.18	0.68
2:E:6:ARG:HG3	2:E:6:ARG:HH11	1.59	0.68
1:A:385:ILE:HD11	1:A:434:LEU:CD2	2.24	0.68
1:A:276:SER:HB2	1:A:279:GLU:HB3	1.75	0.67
1:B:422:GLU:CD	1:B:422:GLU:H	2.02	0.67
1:B:336:LYS:O	1:B:337:LEU:HB2	1.93	0.67
1:B:270:ILE:HG22	1:B:283:ILE:HG12	1.75	0.67
1:A:254:MET:HE1	1:A:376:GLN:HB3	1.75	0.67
2:C:10:ASP:O	2:C:11:LYS:C	2.37	0.67
1:A:465:ILE:HG13	1:A:466:TRP:N	2.09	0.67
1:A:351:LYS:HZ3	1:A:351:LYS:N	1.92	0.66
1:A:400:ALA:O	1:A:404:LEU:HD13	1.95	0.66
1:A:292:VAL:HG21	1:A:465:ILE:HD13	1.77	0.66
1:B:263:PRO:O	1:B:264:GLN:HB2	1.95	0.66
1:A:381:LEU:O	1:A:385:ILE:HG23	1.96	0.65
1:B:262:MET:HB2	3:B:201:CHC:OT1	1.96	0.65
1:A:334:ASN:ND2	1:A:370:GLY:HA2	2.11	0.65
1:B:284:LEU:HD11	1:B:349:ILE:HA	1.77	0.65
1:B:447:MET:HE1	1:B:451:TRP:CE3	2.32	0.65
1:A:270:ILE:HD11	1:A:341:HIS:HB2	1.78	0.65
1:A:423:ASN:HB2	1:A:424:PRO:C	2.21	0.65
1:B:447:MET:HE1	1:B:451:TRP:HE3	1.62	0.65
1:A:300:LYS:NZ	1:A:301:ARG:HH11	1.94	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:320:SER:HA	1:B:392:ARG:NH2	2.12	0.64
1:A:292:VAL:HG21	1:A:465:ILE:CD1	2.28	0.63
1:B:264:GLN:HB2	4:B:115:HOH:O	1.98	0.63
1:A:366:TYR:O	1:A:369:VAL:HG22	1.99	0.62
1:A:348:ARG:O	1:A:352:SER:HB3	1.98	0.62
1:B:299:THR:HA	1:B:302:LEU:HD23	1.80	0.62
1:B:457:LYS:N	1:B:457:LYS:HD2	2.14	0.62
1:A:283:ILE:HD13	1:A:348:ARG:HH21	1.64	0.62
2:E:6:ARG:HG3	2:E:6:ARG:NH1	2.15	0.62
1:A:467:ASP:O	1:A:468:VAL:HG13	2.00	0.62
1:B:296:VAL:HG11	2:D:8:LEU:HB3	1.81	0.61
1:A:387:ILE:HG22	1:A:388:LEU:HD22	1.82	0.61
1:B:272:LYS:HG2	1:B:344:LEU:HD23	1.81	0.61
1:A:323:GLU:HB3	1:A:437:LEU:HD13	1.82	0.61
1:B:386:VAL:HG22	1:B:434:LEU:HD21	1.82	0.61
1:B:447:MET:HE2	1:B:448:LEU:HA	1.83	0.61
1:B:333:PHE:C	1:B:335:LYS:H	2.09	0.61
1:B:375:THR:OG1	1:B:377:GLU:HG2	2.01	0.61
1:A:344:LEU:N	1:A:344:LEU:HD23	2.15	0.61
1:A:306:GLN:HE21	1:A:306:GLN:N	1.97	0.61
1:B:407:PRO:O	1:B:411:VAL:HG23	2.01	0.61
1:B:457:LYS:HD2	1:B:457:LYS:H	1.66	0.61
1:A:356:ASP:HA	1:A:359:ILE:HG12	1.83	0.61
1:A:372:LEU:HD13	1:A:430:LEU:CD2	2.30	0.61
1:A:335:LYS:HZ1	1:A:373:LYS:HG2	1.64	0.60
1:A:276:SER:HB2	1:A:279:GLU:CB	2.32	0.60
1:B:336:LYS:HE2	1:B:338:PRO:HB2	1.82	0.60
1:B:335:LYS:O	1:B:337:LEU:N	2.35	0.60
1:B:374:MET:CE	1:B:430:LEU:HD22	2.31	0.60
1:B:270:ILE:CG2	1:B:283:ILE:HG12	2.31	0.60
2:D:7:TYR:O	2:D:11:LYS:HB2	2.02	0.60
1:A:250:LEU:HD21	4:A:63:HOH:O	2.01	0.60
1:B:286:GLU:HG2	2:E:9:LEU:HD22	1.84	0.60
1:A:278:GLU:HB2	1:A:456:HIS:NE2	2.18	0.59
1:A:415:LEU:HG	1:A:419:TYR:CE2	2.38	0.59
1:B:243:THR:OG1	1:B:246:GLN:HG3	2.03	0.59
1:B:323:GLU:OE1	1:B:438:ARG:HG3	2.02	0.59
1:A:384:ALA:O	1:A:388:LEU:HD23	2.03	0.59
1:A:323:GLU:HB3	1:A:437:LEU:CD1	2.32	0.59
1:B:461:LEU:HD13	2:D:4:LEU:CD2	2.33	0.59
1:B:322:VAL:HG21	1:B:441:ASN:OD1	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:452:ARG:NE	1:B:453:VAL:H	2.01	0.59
1:A:341:HIS:HA	1:A:344:LEU:HG	1.84	0.59
1:A:423:ASN:HB2	1:A:424:PRO:CA	2.31	0.58
1:B:318:LYS:HD2	2:D:2:ASN:ND2	2.18	0.58
1:B:374:MET:HE3	1:B:430:LEU:CD2	2.33	0.58
1:B:261:ARG:HD3	1:B:328:ARG:NH1	2.19	0.58
1:A:372:LEU:HD13	1:A:430:LEU:HD23	1.85	0.58
1:A:351:LYS:NZ	1:A:351:LYS:N	2.51	0.58
1:B:334:ASN:CG	1:B:370:GLY:HA3	2.29	0.58
1:B:447:MET:HE2	1:B:448:LEU:N	2.18	0.58
1:B:466:TRP:O	1:B:467:ASP:CB	2.52	0.58
2:D:4:LEU:O	2:D:4:LEU:HD23	2.03	0.57
1:B:405:GLN:HE21	1:B:409:LEU:CD1	2.06	0.57
1:B:423:ASN:C	1:B:425:GLN:H	2.13	0.57
1:B:264:GLN:HE22	2:E:1:GLU:HB3	1.69	0.57
1:A:447:MET:SD	1:A:447:MET:C	2.87	0.57
2:D:4:LEU:HD23	2:D:4:LEU:C	2.29	0.57
1:A:282:LEU:HA	1:A:285:THR:HG22	1.87	0.57
1:B:372:LEU:O	1:B:373:LYS:C	2.48	0.57
1:A:292:VAL:O	1:A:296:VAL:HG23	2.05	0.56
1:A:278:GLU:HB2	1:A:456:HIS:CD2	2.41	0.56
1:B:250:LEU:HD12	1:B:253:ILE:HD11	1.86	0.56
1:A:335:LYS:HZ2	1:A:373:LYS:HG2	1.69	0.56
1:B:293:GLN:NE2	2:E:5:LEU:HG	2.19	0.56
1:A:241:GLU:O	1:A:242:LEU:HB2	2.06	0.56
1:B:319:GLY:O	1:B:392:ARG:NH2	2.38	0.56
1:B:362:MET:HE1	1:B:440:PHE:HB3	1.87	0.56
1:A:438:ARG:HD2	4:A:41:HOH:O	2.07	0.55
1:B:434:LEU:O	1:B:438:ARG:HD2	2.06	0.55
1:A:300:LYS:HZ2	1:A:301:ARG:HH11	1.54	0.55
1:B:335:LYS:C	1:B:337:LEU:N	2.63	0.55
1:A:241:GLU:O	1:A:242:LEU:CB	2.54	0.55
1:A:281:PHE:CG	1:A:453:VAL:HG21	2.40	0.55
1:B:397:ASP:HB3	4:B:20:HOH:O	2.06	0.55
1:B:393:GLN:O	1:B:394:TYR:HB2	2.07	0.55
1:A:389:SER:HB2	1:A:392:ARG:NH1	2.21	0.54
1:B:263:PRO:HD2	1:B:294:ILE:HD13	1.89	0.54
1:A:423:ASN:HD22	1:A:424:PRO:CA	2.18	0.54
1:A:300:LYS:O	1:A:306:GLN:NE2	2.37	0.54
1:B:332:ILE:O	1:B:335:LYS:CB	2.48	0.54
1:B:335:LYS:HG3	1:B:336:LYS:HG2	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:390:PRO:HG3	4:A:149:HOH:O	2.08	0.54
1:A:407:PRO:O	1:A:411:VAL:HG23	2.06	0.54
1:A:437:LEU:HD12	1:A:437:LEU:C	2.33	0.54
1:B:280:ASN:OD1	1:B:348:ARG:HD3	2.08	0.53
1:B:462:LEU:HD23	1:B:465:ILE:HD11	1.90	0.53
1:A:354:ILE:HD13	1:A:355:SER:N	2.23	0.53
1:B:354:ILE:HD11	1:B:359:ILE:HD11	1.89	0.53
1:B:447:MET:HE3	1:B:451:TRP:CB	2.31	0.53
1:A:385:ILE:HD11	1:A:434:LEU:HD21	1.90	0.53
1:B:339:ALA:O	1:B:341:HIS:CD2	2.62	0.53
1:B:453:VAL:O	1:B:453:VAL:HG13	2.09	0.53
1:B:335:LYS:HE3	1:B:336:LYS:NZ	2.24	0.52
1:A:337:LEU:C	1:A:339:ALA:H	2.17	0.52
1:A:355:SER:C	1:A:357:GLU:H	2.16	0.52
1:A:355:SER:CB	1:A:357:GLU:HG2	2.34	0.52
1:B:338:PRO:O	1:B:339:ALA:CB	2.56	0.52
1:B:278:GLU:C	1:B:278:GLU:OE1	2.53	0.52
1:A:354:ILE:HG12	1:A:447:MET:CE	2.40	0.52
1:B:436:GLU:HB2	4:B:39:HOH:O	2.08	0.52
1:B:438:ARG:HH11	1:B:438:ARG:HG2	1.75	0.52
1:B:418:ILE:HG22	1:B:419:TYR:CD2	2.45	0.51
1:B:264:GLN:NE2	2:E:2:ASN:HB2	2.25	0.51
1:B:337:LEU:O	1:B:338:PRO:C	2.52	0.51
1:B:383:THR:O	1:B:387:ILE:HG13	2.10	0.51
1:B:336:LYS:O	1:B:337:LEU:CB	2.56	0.51
1:B:388:LEU:O	1:B:405:GLN:OE1	2.27	0.51
1:A:302:LEU:CD2	1:A:388:LEU:HD21	2.32	0.51
1:B:269:LYS:HB2	1:B:269:LYS:NZ	2.26	0.51
2:D:11:LYS:O	2:D:12:ASP:CG	2.53	0.51
1:B:261:ARG:HB2	4:B:125:HOH:O	2.11	0.51
1:B:371:GLU:C	1:B:373:LYS:H	2.19	0.51
1:B:278:GLU:OE1	1:B:279:GLU:N	2.43	0.51
1:A:282:LEU:O	1:A:285:THR:HG22	2.10	0.51
1:A:243:THR:OG1	1:A:246:GLN:HG3	2.11	0.50
1:B:334:ASN:HD21	1:B:370:GLY:HA3	1.74	0.50
1:B:374:MET:HB2	1:B:379:TYR:CE1	2.46	0.50
1:B:261:ARG:O	1:B:262:MET:C	2.54	0.50
1:B:278:GLU:O	1:B:278:GLU:HG2	2.12	0.50
1:B:339:ALA:HB1	1:B:341:HIS:CE1	2.47	0.50
1:B:452:ARG:HG3	1:B:452:ARG:HH11	1.76	0.50
1:A:389:SER:CB	1:A:392:ARG:NH1	2.72	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:318:LYS:NZ	2:D:2:ASN:HD21	2.10	0.49
1:A:395:ILE:CD1	1:A:398:ARG:HG2	2.39	0.49
1:B:292:VAL:O	1:B:295:LEU:N	2.45	0.49
1:B:299:THR:HA	1:B:302:LEU:HD22	1.89	0.49
1:B:398:ARG:HH12	1:B:402:GLU:CD	2.21	0.49
1:A:354:ILE:HD12	1:A:359:ILE:HG23	1.95	0.49
1:B:278:GLU:C	1:B:280:ASN:N	2.70	0.49
1:B:335:LYS:O	1:B:336:LYS:C	2.56	0.49
1:B:338:PRO:O	1:B:339:ALA:HB3	2.12	0.49
1:B:352:SER:O	1:B:354:ILE:N	2.43	0.49
1:A:424:PRO:C	1:A:426:HIS:N	2.67	0.49
1:A:354:ILE:CD1	1:A:358:TYR:HB3	2.42	0.49
1:B:365:PHE:O	1:B:369:VAL:HG23	2.13	0.49
1:A:281:PHE:CD1	1:A:281:PHE:C	2.91	0.49
1:A:424:PRO:HG2	1:A:425:GLN:N	2.24	0.49
1:B:392:ARG:HD2	4:B:43:HOH:O	2.12	0.49
1:A:241:GLU:H	1:A:241:GLU:CD	2.21	0.48
1:A:287:MET:O	1:A:290:SER:HB3	2.13	0.48
1:B:259:LYS:HE3	1:B:301:ARG:CZ	2.43	0.48
1:B:319:GLY:C	1:B:392:ARG:HD3	2.37	0.48
1:A:372:LEU:HD21	1:A:429:CYS:SG	2.53	0.48
1:A:281:PHE:CD2	1:A:453:VAL:HG21	2.49	0.48
1:B:260:GLN:HB2	1:B:294:ILE:HG23	1.96	0.48
1:B:447:MET:HE2	1:B:448:LEU:CA	2.42	0.48
2:E:2:ASN:HB3	2:E:5:LEU:HB2	1.96	0.48
1:A:465:ILE:HG13	1:A:466:TRP:H	1.77	0.48
1:B:298:PHE:O	1:B:302:LEU:HD22	2.14	0.48
1:B:420:GLN:N	1:B:421:PRO:HD3	2.28	0.48
1:B:262:MET:HG3	1:B:268:ASN:ND2	2.21	0.48
1:A:437:LEU:HA	1:A:440:PHE:HD2	1.79	0.47
1:A:275:PHE:O	1:A:279:GLU:HB3	2.14	0.47
1:B:333:PHE:O	1:B:334:ASN:CB	2.59	0.47
1:A:355:SER:C	1:A:357:GLU:N	2.72	0.47
1:A:351:LYS:HA	1:A:351:LYS:HZ2	1.79	0.47
1:A:415:LEU:HG	1:A:419:TYR:HE2	1.79	0.47
1:A:423:ASN:HD22	1:A:424:PRO:C	2.22	0.47
1:B:261:ARG:N	1:B:263:PRO:HD3	2.29	0.47
1:B:320:SER:OG	1:B:386:VAL:HG12	2.15	0.46
1:B:311:GLU:N	1:B:311:GLU:CD	2.73	0.46
1:B:322:VAL:CG2	1:B:441:ASN:OD1	2.63	0.46
1:A:267:THR:C	1:A:269:LYS:H	2.22	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:437:LEU:HA	1:A:440:PHE:HB2	1.96	0.46
1:B:264:GLN:HE22	2:E:1:GLU:CB	2.26	0.46
1:B:312:ASP:O	1:B:316:LEU:HG	2.14	0.46
1:A:272:LYS:C	1:A:273:GLU:O	2.56	0.46
1:A:423:ASN:CB	1:A:424:PRO:CA	2.93	0.46
1:B:272:LYS:HZ3	1:B:272:LYS:HB2	1.81	0.46
1:B:328:ARG:HE	3:B:201:CHC:C24	2.29	0.46
1:A:344:LEU:O	1:A:348:ARG:HG2	2.16	0.46
1:A:403:LYS:HE2	4:A:83:HOH:O	2.15	0.46
1:A:452:ARG:HD3	1:A:452:ARG:HA	1.69	0.46
1:A:282:LEU:C	1:A:285:THR:HG22	2.41	0.45
1:B:333:PHE:C	1:B:335:LYS:N	2.72	0.45
1:A:331:GLU:HA	1:A:379:TYR:CZ	2.51	0.45
1:B:335:LYS:HE3	1:B:336:LYS:HZ2	1.80	0.45
1:A:388:LEU:HD22	1:A:388:LEU:N	2.31	0.45
1:B:254:MET:SD	1:B:377:GLU:HA	2.56	0.45
1:B:337:LEU:HB3	1:B:338:PRO:HD3	1.98	0.45
1:B:426:HIS:CE1	1:B:430:LEU:HD21	2.51	0.45
1:A:361:PRO:O	1:A:364:SER:HB3	2.17	0.45
1:B:426:HIS:O	1:B:430:LEU:HG	2.16	0.45
1:A:291:HIS:NE2	1:A:328:ARG:HG3	2.32	0.45
1:A:354:ILE:HD11	1:A:358:TYR:HB3	1.99	0.45
1:B:320:SER:OG	1:B:387:ILE:HA	2.17	0.45
1:A:467:ASP:C	1:A:468:VAL:HG22	2.42	0.45
1:B:278:GLU:C	1:B:280:ASN:H	2.25	0.45
1:B:374:MET:HA	1:B:378:GLU:OE2	2.17	0.45
1:A:354:ILE:HG12	1:A:447:MET:HE1	1.99	0.45
1:A:447:MET:HA	4:A:126:HOH:O	2.15	0.44
1:B:450:SER:O	1:B:452:ARG:HG3	2.17	0.44
1:B:278:GLU:HG3	1:B:453:VAL:HG22	1.99	0.44
2:D:7:TYR:CZ	2:D:11:LYS:HG3	2.52	0.44
1:A:275:PHE:O	1:A:276:SER:HB2	2.17	0.44
1:B:262:MET:O	1:B:263:PRO:O	2.34	0.44
1:B:311:GLU:CD	1:B:311:GLU:H	2.26	0.44
1:B:319:GLY:C	1:B:392:ARG:HH21	2.25	0.44
1:B:310:HIS:CE1	2:D:6:ARG:HD3	2.53	0.44
1:B:361:PRO:HA	1:B:364:SER:OG	2.17	0.44
1:A:354:ILE:HD12	1:A:359:ILE:CG2	2.47	0.44
1:B:338:PRO:C	1:B:340:GLY:H	2.23	0.44
2:C:6:ARG:HE	2:C:6:ARG:HB2	1.50	0.44
2:E:5:LEU:HD22	2:E:9:LEU:HG	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:273:GLU:C	1:A:274:GLU:HG3	2.43	0.44
1:A:453:VAL:HG23	1:A:453:VAL:O	2.17	0.44
1:B:335:LYS:C	1:B:337:LEU:H	2.26	0.44
1:B:388:LEU:HD23	1:B:408:LEU:CD1	2.48	0.44
1:A:282:LEU:CA	1:A:285:THR:HG22	2.48	0.43
1:B:262:MET:C	1:B:263:PRO:O	2.61	0.43
1:B:320:SER:HB2	4:B:43:HOH:O	2.17	0.43
1:A:290:SER:O	1:A:291:HIS:C	2.59	0.43
1:A:335:LYS:HA	1:A:335:LYS:HD3	1.75	0.43
1:B:319:GLY:HA3	1:B:392:ARG:HD3	1.99	0.43
1:B:268:ASN:O	1:B:271:LEU:HB3	2.18	0.43
1:B:269:LYS:NZ	1:B:269:LYS:CB	2.81	0.43
1:A:249:LEU:HD21	1:A:408:LEU:HD23	2.01	0.43
1:A:270:ILE:HG21	1:A:287:MET:HE1	2.00	0.43
1:A:275:PHE:HB3	1:A:276:SER:H	1.46	0.43
1:B:320:SER:HA	1:B:392:ARG:HH22	1.82	0.43
1:A:290:SER:O	1:A:293:GLN:N	2.52	0.43
1:B:246:GLN:OE1	1:B:414:LYS:HD3	2.19	0.43
1:B:423:ASN:O	1:B:425:GLN:N	2.52	0.43
1:A:345:LEU:O	1:A:349:ILE:HG13	2.18	0.43
1:A:422:GLU:OE2	1:A:422:GLU:N	2.47	0.43
1:B:462:LEU:HA	1:B:465:ILE:HD11	2.01	0.43
1:A:267:THR:C	1:A:269:LYS:N	2.77	0.43
1:B:374:MET:HE2	1:B:374:MET:HB3	1.95	0.43
1:A:254:MET:SD	1:A:377:GLU:HG3	2.59	0.42
1:B:261:ARG:HA	1:B:261:ARG:NH1	2.15	0.42
1:A:391:ASP:HA	1:A:398:ARG:CZ	2.49	0.42
1:B:272:LYS:HD3	1:B:341:HIS:CD2	2.54	0.42
1:B:320:SER:CA	1:B:392:ARG:NH2	2.81	0.42
1:B:423:ASN:C	1:B:425:GLN:N	2.76	0.42
1:B:262:MET:N	1:B:263:PRO:CD	2.82	0.42
1:B:452:ARG:HG3	1:B:452:ARG:NH1	2.34	0.42
2:C:1:GLU:OE1	2:C:1:GLU:HA	2.20	0.42
1:A:417:LYS:O	1:A:421:PRO:HB3	2.19	0.42
1:B:322:VAL:HG23	1:B:323:GLU:N	2.35	0.42
2:D:1:GLU:O	2:D:1:GLU:HG2	2.19	0.42
1:B:393:GLN:HG2	1:B:394:TYR:CD2	2.54	0.42
1:A:389:SER:HA	1:A:390:PRO:HD3	1.87	0.42
1:B:368:SER:OG	1:B:433:ARG:NH2	2.49	0.42
1:A:302:LEU:HD23	1:A:388:LEU:CD2	2.33	0.42
1:A:425:GLN:O	1:A:428:ALA:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:250:LEU:O	1:B:253:ILE:HG13	2.19	0.42
1:A:391:ASP:HA	1:A:398:ARG:NH1	2.34	0.42
1:B:262:MET:HE1	1:B:290:SER:CB	2.49	0.42
1:B:269:LYS:C	1:B:271:LEU:N	2.76	0.42
1:B:392:ARG:HH11	1:B:438:ARG:NH2	2.18	0.41
1:B:377:GLU:OE1	1:B:419:TYR:HE1	2.03	0.41
1:A:334:ASN:HD22	1:A:335:LYS:HG2	1.86	0.41
1:A:439:THR:O	1:A:442:HIS:HB3	2.19	0.41
1:B:259:LYS:HD2	4:B:81:HOH:O	2.20	0.41
1:A:287:MET:O	1:A:290:SER:N	2.53	0.41
1:B:336:LYS:HG3	1:B:338:PRO:CD	2.41	0.41
1:B:292:VAL:CG1	1:B:461:LEU:HD21	2.51	0.41
1:B:262:MET:HG3	1:B:262:MET:O	2.20	0.41
1:B:406:GLU:N	1:B:407:PRO:HD2	2.36	0.41
1:A:282:LEU:HA	1:A:285:THR:CG2	2.50	0.41
1:A:385:ILE:HD11	1:A:434:LEU:HD22	2.01	0.41
1:B:335:LYS:CE	1:B:336:LYS:HZ2	2.34	0.41
1:A:267:THR:HG22	1:A:268:ASN:N	2.36	0.41
1:A:297:GLU:HA	1:A:300:LYS:HG2	2.03	0.41
1:B:365:PHE:CD2	1:B:440:PHE:HE1	2.39	0.41
1:A:382:LEU:HD22	1:A:434:LEU:CD1	2.51	0.41
1:B:458:PHE:CD1	1:B:468:VAL:HG11	2.56	0.41
1:A:389:SER:OG	1:A:392:ARG:NH1	2.54	0.40
1:A:423:ASN:CB	1:A:424:PRO:HA	2.51	0.40
1:B:354:ILE:CG1	1:B:359:ILE:HD11	2.52	0.40
1:B:465:ILE:H	1:B:465:ILE:HG13	1.62	0.40
1:B:299:THR:CG2	1:B:387:ILE:HD13	2.43	0.40
1:B:334:ASN:OD1	1:B:370:GLY:HA3	2.22	0.40
1:B:447:MET:CE	1:B:451:TRP:HB2	2.37	0.40
1:B:452:ARG:NH2	1:B:453:VAL:HA	2.36	0.40
1:A:350:ARG:CD	1:A:359:ILE:HD12	2.47	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	227/230 (99%)	188 (83%)	26 (12%)	13 (6%)	1	1
1	B	227/230 (99%)	192 (85%)	20 (9%)	15 (7%)	1	1
2	C	10/12 (83%)	9 (90%)	0	1 (10%)	0	0
2	D	10/12 (83%)	9 (90%)	0	1 (10%)	0	0
2	E	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
All	All	484/496 (98%)	407 (84%)	47 (10%)	30 (6%)	1	1

All (30) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	275	PHE
1	A	335	LYS
1	A	336	LYS
1	A	423	ASN
1	A	424	PRO
1	B	337	LEU
2	D	11	LYS
1	A	241	GLU
1	A	242	LEU
1	A	342	ALA
1	B	303	PRO
1	B	336	LYS
1	B	373	LYS
1	B	453	VAL
1	B	467	ASP
1	A	261	ARG
1	A	454	ASN
1	A	455	ASP
1	B	338	PRO
1	B	454	ASN
1	B	455	ASP
1	A	276	SER
1	B	263	PRO
1	B	339	ALA
2	C	11	LYS
1	B	424	PRO
1	A	338	PRO
1	B	264	GLN

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Mol	Chain	Res	Type
1	B	353	GLY
1	B	332	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	209/210 (100%)	187 (90%)	22 (10%)	6	14
1	B	209/210 (100%)	186 (89%)	23 (11%)	6	13
2	C	10/11 (91%)	10 (100%)	0	100	100
2	D	11/11 (100%)	8 (73%)	3 (27%)	0	1
2	E	10/11 (91%)	8 (80%)	2 (20%)	1	2
All	All	449/453 (99%)	399 (89%)	50 (11%)	6	12

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	284	LEU
1	A	295	LEU
1	A	299	THR
1	A	300	LYS
1	A	306	GLN
1	A	328	ARG
1	A	341	HIS
1	A	344	LEU
1	A	351	LYS
1	A	354	ILE
1	A	371	GLU
1	A	376	GLN
1	A	385	ILE
1	A	386	VAL
1	A	387	ILE
1	A	406	GLU
1	A	409	LEU

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Mol	Chain	Res	Type
1	A	423	ASN
1	A	430	LEU
1	A	434	LEU
1	A	438	ARG
1	A	468	VAL
1	B	242	LEU
1	B	261	ARG
1	B	269	LYS
1	B	273	GLU
1	B	278	GLU
1	B	302	LEU
1	B	303	PRO
1	B	314	ILE
1	B	317	LEU
1	B	337	LEU
1	B	338	PRO
1	B	364	SER
1	B	388	LEU
1	B	405	GLN
1	B	410	ASP
1	B	415	LEU
1	B	422	GLU
1	B	434	LEU
1	B	447	MET
1	B	452	ARG
1	B	453	VAL
1	B	465	ILE
1	B	467	ASP
2	D	1	GLU
2	D	5	LEU
2	D	6	ARG
2	E	5	LEU
2	E	6	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	264	GLN
1	A	293	GLN
1	A	306	GLN
1	A	310	HIS
1	A	376	GLN

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Mol	Chain	Res	Type
1	A	423	ASN
1	A	425	GLN
1	A	443	HIS
1	A	454	ASN
1	B	264	GLN
1	B	268	ASN
1	B	293	GLN
1	B	341	HIS
1	B	376	GLN
1	B	405	GLN
1	B	420	GLN
1	B	423	ASN
1	B	456	HIS
2	D	2	ASN
2	E	2	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	CHC	A	202	-	33,33,33	3.66	20 (60%)	52,52,52	1.86	13 (25%)
3	CHC	B	201	-	33,33,33	3.59	21 (63%)	52,52,52	1.71	9 (17%)

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	CHC	A	202	-	-	2/11/76/76	0/4/4/4
3	CHC	B	201	-	-	2/11/76/76	0/4/4/4

All (41) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	202	CHC	C10-C9	7.45	1.69	1.56
3	B	201	CHC	C10-C9	7.27	1.68	1.56
3	A	202	CHC	C6-C7	6.87	1.60	1.53
3	B	201	CHC	C6-C7	6.81	1.60	1.53
3	A	202	CHC	C10-C5	6.56	1.67	1.56
3	B	201	CHC	C18-C13	6.51	1.65	1.54
3	B	201	CHC	C10-C5	6.26	1.67	1.56
3	B	201	CHC	C4-C5	6.26	1.63	1.53
3	A	202	CHC	C18-C13	6.25	1.64	1.54
3	A	202	CHC	C4-C5	6.07	1.63	1.53
3	B	201	CHC	C4-C3	5.70	1.62	1.52
3	A	202	CHC	C4-C3	5.25	1.61	1.52
3	A	202	CHC	C8-C9	4.94	1.63	1.53
3	B	201	CHC	C8-C9	4.86	1.63	1.53
3	A	202	CHC	C13-C17	4.41	1.63	1.55
3	A	202	CHC	C20-C17	4.39	1.61	1.54
3	B	201	CHC	C13-C17	4.07	1.62	1.55
3	B	201	CHC	C20-C17	4.04	1.61	1.54
3	A	202	CHC	C2-C3	3.73	1.60	1.51
3	A	202	CHC	C21-C20	3.68	1.62	1.53
3	B	201	CHC	C8-C7	3.64	1.58	1.53
3	B	201	CHC	C1-C10	3.59	1.60	1.54
3	A	202	CHC	C6-C5	3.59	1.60	1.53
3	A	202	CHC	C8-C14	3.58	1.60	1.53
3	B	201	CHC	C2-C3	3.50	1.59	1.51
3	A	202	CHC	C8-C7	3.35	1.58	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	201	CHC	C21-C20	3.32	1.61	1.53
3	A	202	CHC	C1-C10	3.15	1.59	1.54
3	B	201	CHC	C8-C14	3.04	1.59	1.53
3	A	202	CHC	C15-C14	2.86	1.60	1.54
3	A	202	CHC	C16-C17	2.84	1.60	1.54
3	B	201	CHC	C16-C17	2.84	1.60	1.54
3	B	201	CHC	C6-C5	2.84	1.58	1.53
3	A	202	CHC	C12-C11	2.58	1.58	1.53
3	B	201	CHC	C12-C13	2.49	1.58	1.54
3	A	202	CHC	C12-C13	2.49	1.58	1.54
3	B	201	CHC	C15-C14	2.42	1.59	1.54
3	B	201	CHC	C12-C11	2.37	1.58	1.53
3	A	202	CHC	O7-C7	2.21	1.48	1.43
3	B	201	CHC	C1-C2	2.11	1.57	1.53
3	B	201	CHC	O7-C7	2.05	1.48	1.43

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	202	CHC	C26-C6-C7	-6.65	103.82	112.09
3	B	201	CHC	C26-C6-C7	-5.63	105.08	112.09
3	B	201	CHC	C19-C10-C1	-4.55	101.08	108.31
3	A	202	CHC	C19-C10-C1	-4.28	101.50	108.31
3	A	202	CHC	C25-C26-C6	3.47	121.43	114.15
3	B	201	CHC	C25-C26-C6	3.23	120.93	114.15
3	A	202	CHC	C10-C9-C8	-3.17	108.30	111.84
3	B	201	CHC	C16-C15-C14	-2.95	99.38	105.14
3	A	202	CHC	C16-C15-C14	-2.93	99.41	105.14
3	B	201	CHC	C4-C5-C10	-2.88	109.01	112.25
3	A	202	CHC	C21-C20-C17	-2.84	108.62	112.88
3	B	201	CHC	C21-C20-C17	-2.72	108.81	112.88
3	B	201	CHC	C26-C6-C5	-2.69	109.39	113.62
3	A	202	CHC	C13-C17-C20	-2.52	115.61	119.50
3	B	201	CHC	C10-C9-C8	-2.51	109.04	111.84
3	A	202	CHC	C26-C6-C5	-2.51	109.67	113.62
3	A	202	CHC	C4-C5-C10	-2.45	109.50	112.25
3	B	201	CHC	C10-C5-C6	-2.24	110.16	112.43
3	A	202	CHC	C22-C23-C24	2.22	118.41	112.49
3	A	202	CHC	C10-C5-C6	-2.18	110.21	112.43
3	A	202	CHC	C15-C16-C17	2.12	109.30	105.14
3	A	202	CHC	C18-C13-C12	-2.05	107.59	110.61

There are no chirality outliers.

All (4) torsion outliers are listed below:

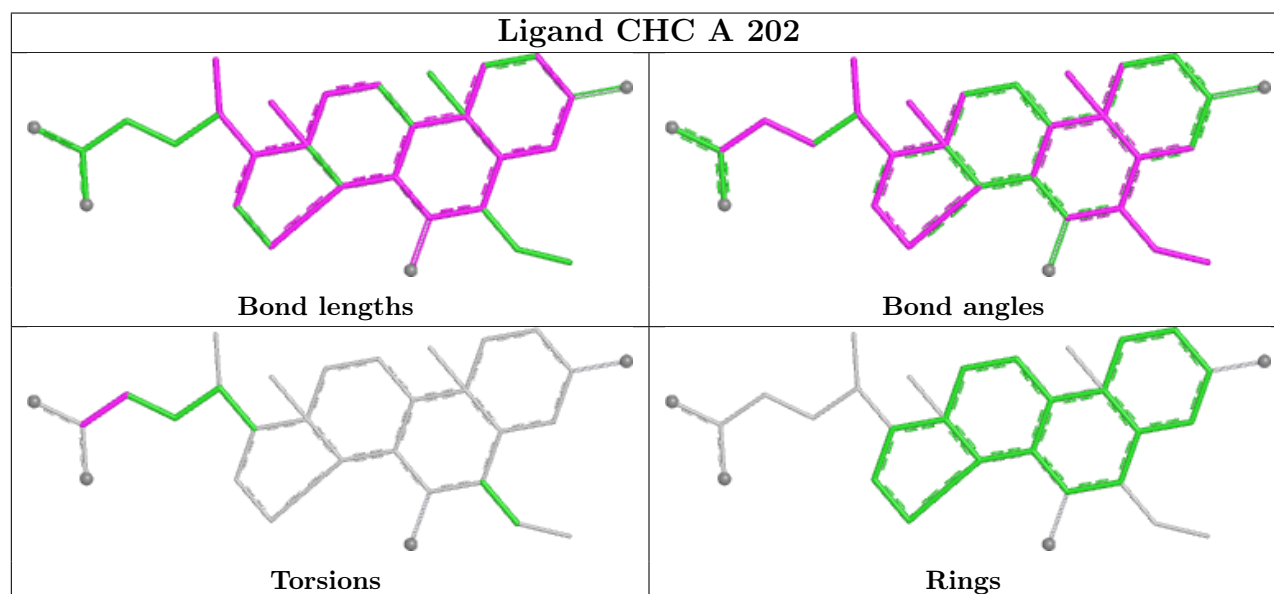
Mol	Chain	Res	Type	Atoms
3	A	202	CHC	C22-C23-C24-OT2
3	B	201	CHC	C22-C23-C24-OT1
3	A	202	CHC	C22-C23-C24-OT1
3	B	201	CHC	C22-C23-C24-OT2

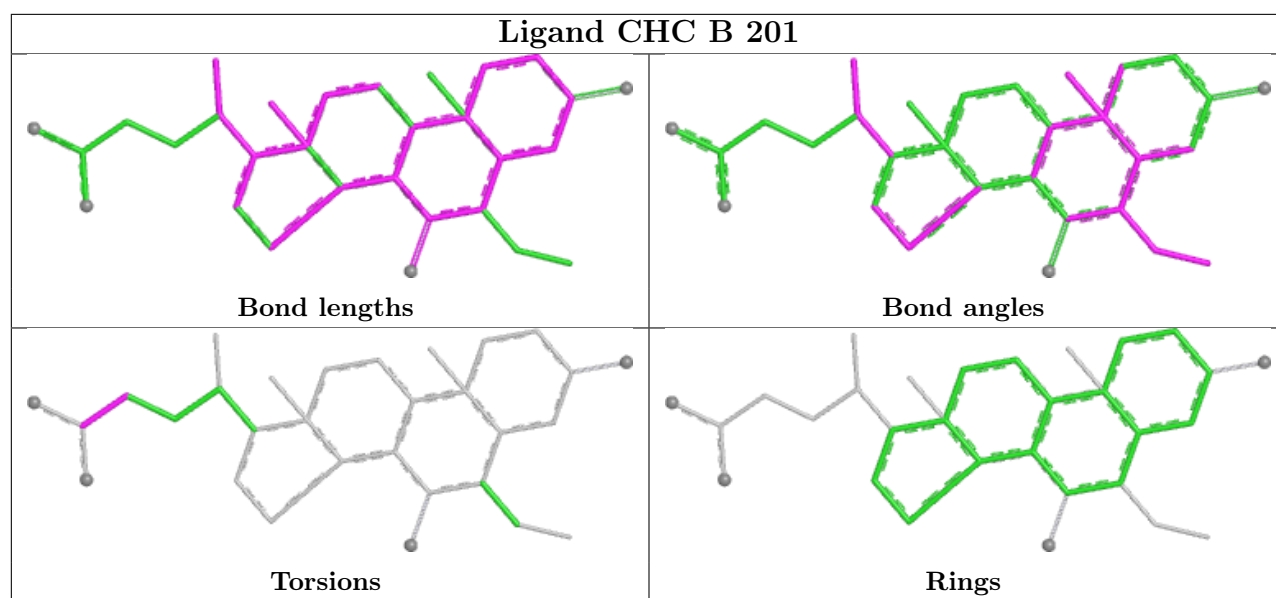
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	201	CHC	2	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	229/230 (99%)	0.68	25 (10%) 10 9	10, 50, 111, 144	1 (0%)
1	B	229/230 (99%)	0.54	23 (10%) 12 10	23, 47, 89, 119	0
2	C	12/12 (100%)	0.65	2 (16%) 4 3	37, 42, 80, 92	0
2	D	12/12 (100%)	0.49	1 (8%) 17 15	36, 42, 62, 69	0
2	E	12/12 (100%)	0.30	1 (8%) 17 15	35, 50, 82, 92	0
All	All	494/496 (99%)	0.60	52 (10%) 11 10	10, 49, 96, 144	1 (0%)

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	240	ALA	25.6
1	B	468	VAL	5.9
1	B	339	ALA	5.5
1	A	339	ALA	4.9
1	B	338	PRO	4.5
1	B	264	GLN	4.3
1	A	449	MET	4.2
1	B	261	ARG	4.0
1	A	275	PHE	4.0
1	A	342	ALA	3.7
1	B	419	TYR	3.6
1	A	453	VAL	3.5
1	A	468	VAL	3.5
1	B	340	GLY	3.5
2	C	11	LYS	3.4
2	E	12	ASP	3.3
1	A	340	GLY	3.3
1	A	359	ILE	3.3
1	B	336	LYS	3.3
1	B	352	SER	3.1

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Mol	Chain	Res	Type	RSRZ
2	C	12	ASP	3.1
1	A	338	PRO	3.0
1	B	240	ALA	2.9
1	A	354	ILE	2.9
1	B	467	ASP	2.9
1	B	395	ILE	2.9
1	A	335	LYS	2.9
1	B	341	HIS	2.8
1	B	455	ASP	2.8
1	A	439	THR	2.7
1	B	263	PRO	2.7
1	A	344	LEU	2.7
1	A	351	LYS	2.7
1	A	452	ARG	2.7
1	A	371	GLU	2.6
1	B	442	HIS	2.6
1	B	391	ASP	2.5
1	B	337	LEU	2.5
1	B	275	PHE	2.5
1	A	272	LYS	2.4
1	B	418	ILE	2.4
1	A	364	SER	2.4
1	A	343	ASP	2.4
1	A	276	SER	2.3
1	A	467	ASP	2.3
1	B	420	GLN	2.3
1	A	337	LEU	2.2
2	D	12	ASP	2.2
1	B	454	ASN	2.2
1	B	373	LYS	2.1
1	A	450	SER	2.1
1	A	341	HIS	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

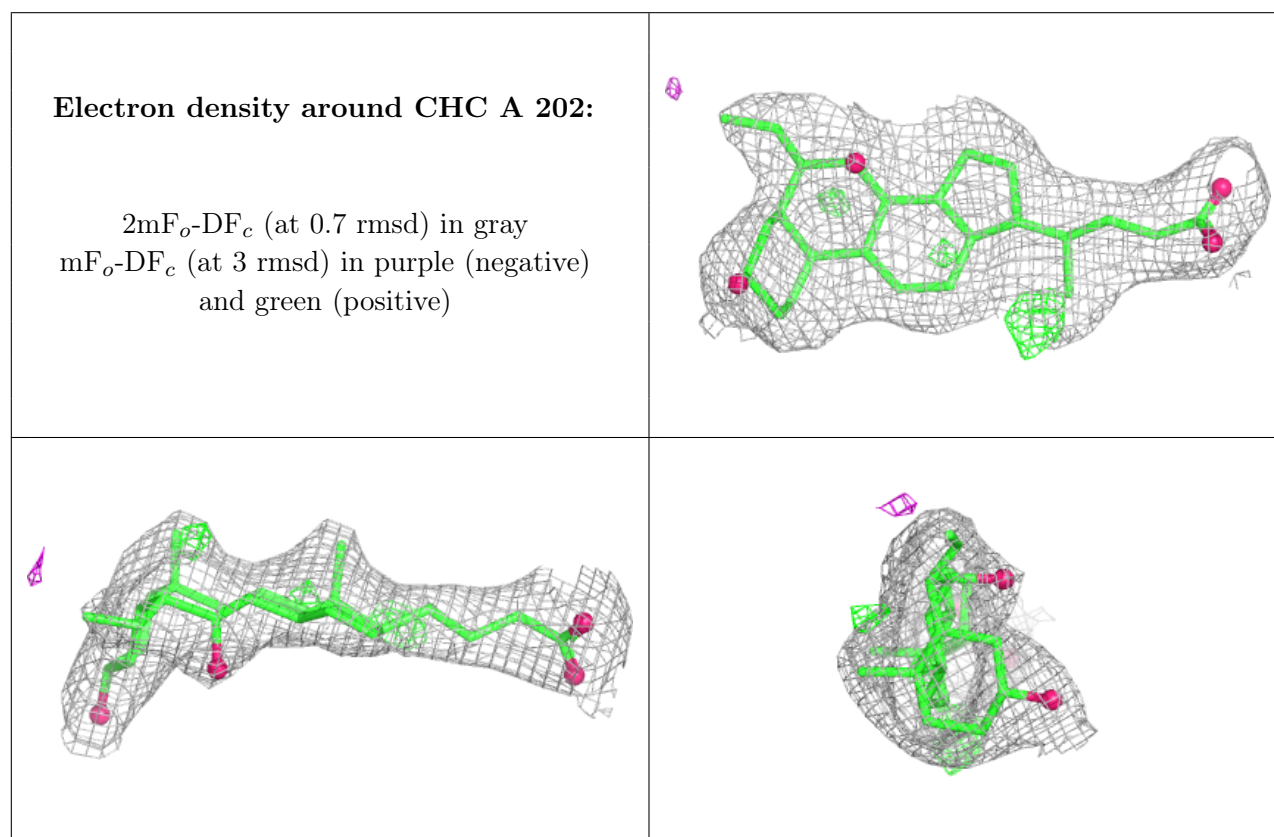
There are no oligosaccharides in this entry.

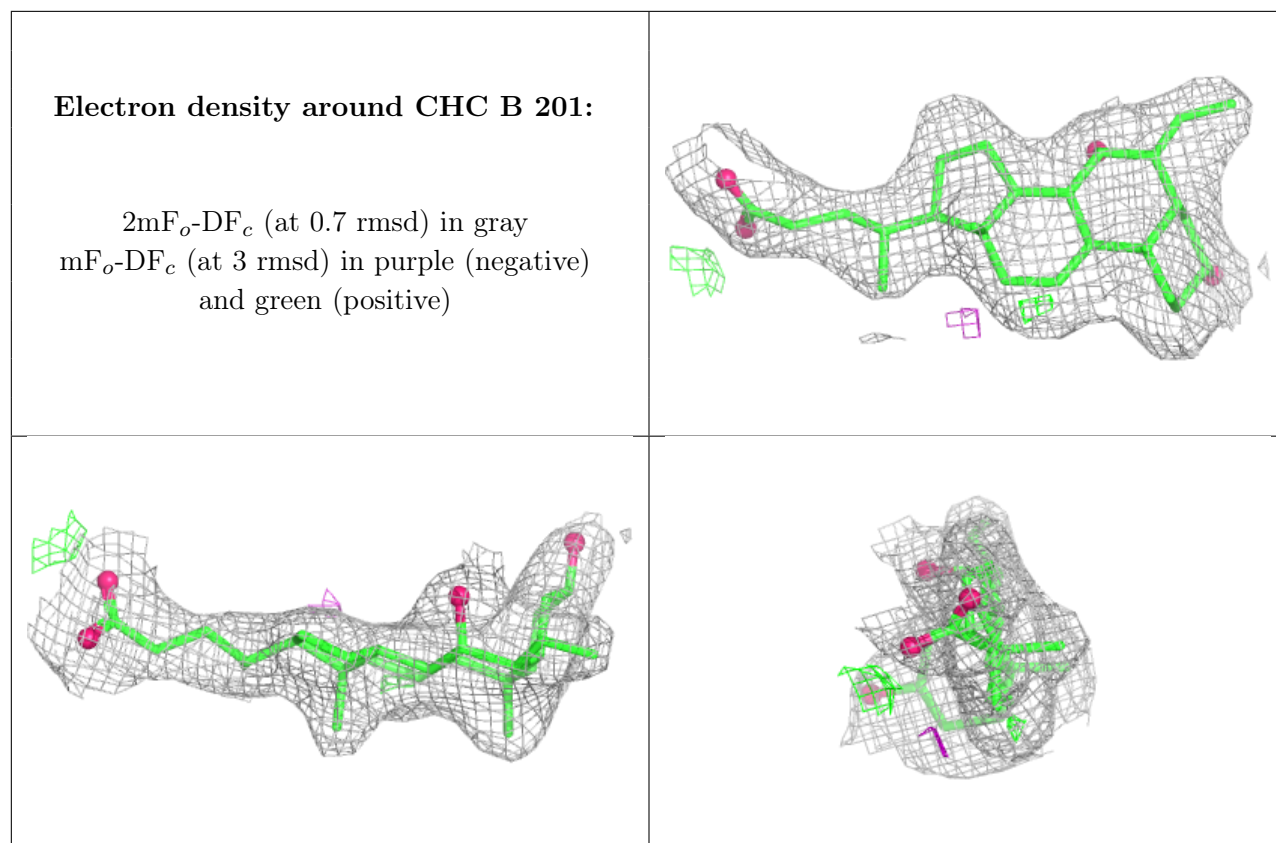
6.4 Ligands ⓘ

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. 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(Å ²)	Q<0.9
3	CHC	A	202	30/30	0.91	0.11	35,42,48,49	0
3	CHC	B	201	30/30	0.93	0.10	29,32,52,55	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 ⓘ

There are no such residues in this entry.