



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:46 PM UTC

PDB ID : 4KR8 / pdb_00004kr8
Title : Salmonella typhi OmpF complex with Daunomycin
Authors : Madhuranayaki, T.; Balasubramaniam, D.; Krishnaswamy, S.
Deposited on : 2013-05-16
Resolution : 3.10 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) : 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

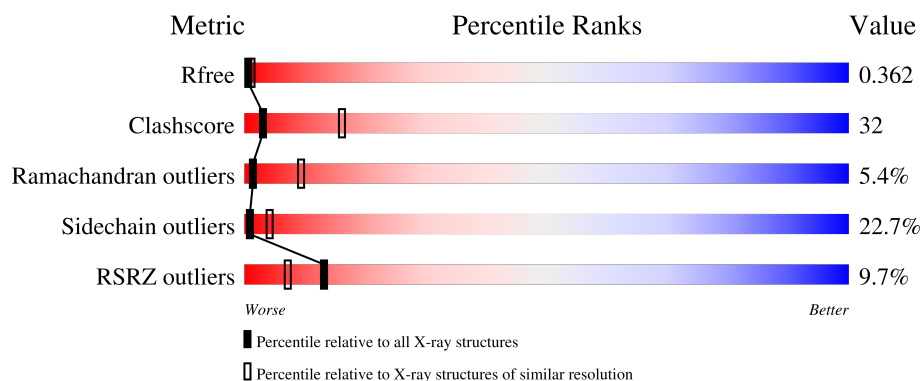
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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))
R_{free}	180053	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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 $\leq 5\%$. 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	341	6% 39% 46% 13%
1	B	341	10% 44% 43% 12%
1	C	341	13% 43% 40% 16%

2 Entry composition [i](#)

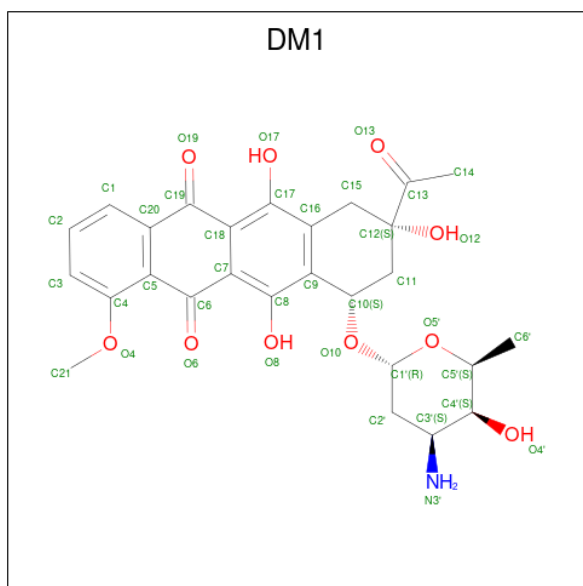
There are 2 unique types of molecules in this entry. The entry contains 7769 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Outer membrane protein F.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	340	Total	C	N	O	S	0	0	0
			2540	1584	430	519	7			
1	B	340	Total	C	N	O	S	0	0	0
			2610	1628	440	535	7			
1	C	340	Total	C	N	O	S	0	0	0
			2571	1601	433	531	6			

- Molecule 2 is DAUNOMYCIN (CCD ID: DM1) (formula: $C_{27}H_{29}NO_{10}$).

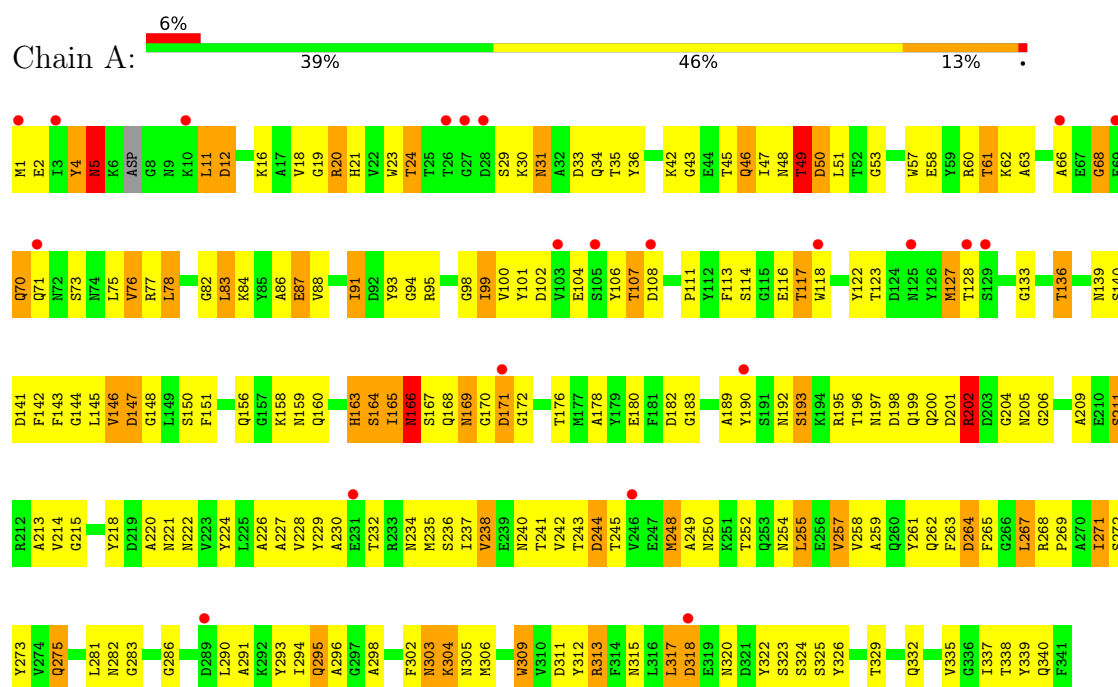


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	C	1	Total	C	N	O	0	1
			48	33	2	13		

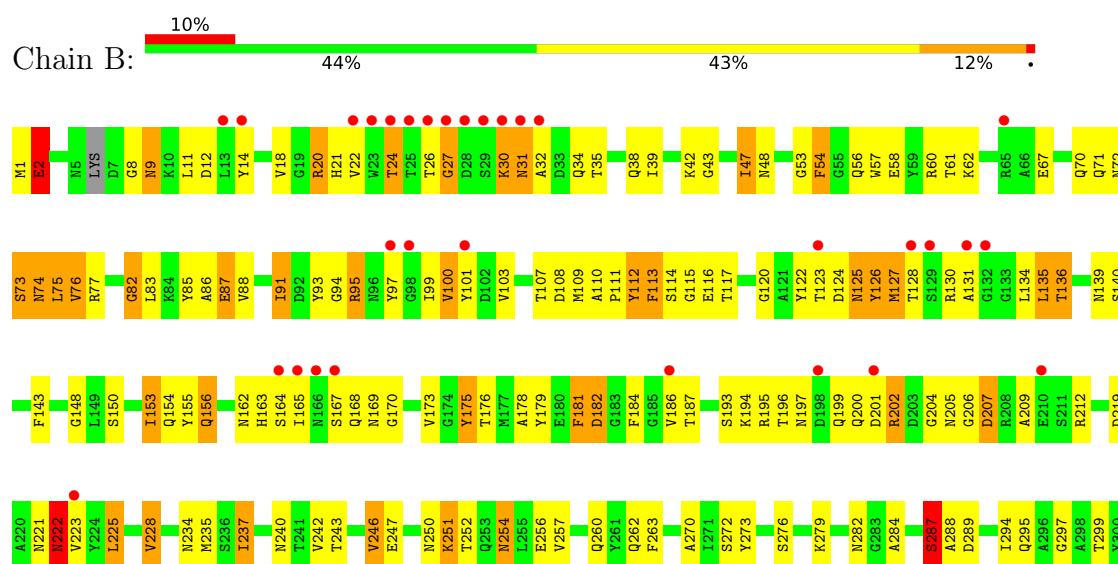
3 Residue-property plots

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: Outer membrane protein F

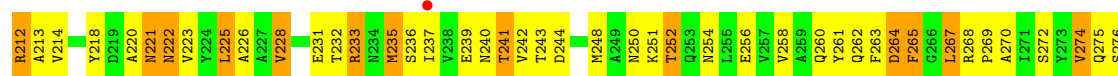
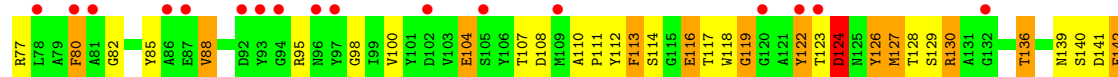
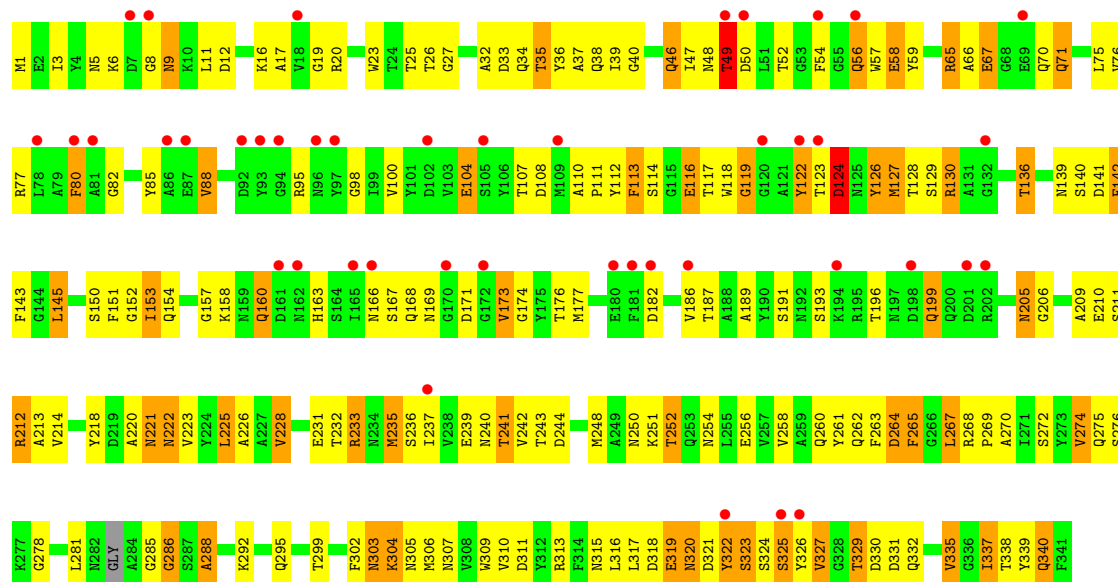
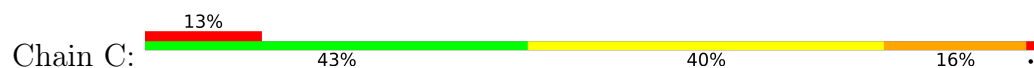


• Molecule 1: Outer membrane protein F





● Molecule 1: Outer membrane protein F



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	84.71Å 132.39Å 150.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.10 50.00 – 3.10	Depositor EDS
% Data completeness (in resolution range)	98.3 (50.00-3.10) 98.5 (50.00-3.10)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.42 (at 3.12Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.293 , 0.366 0.293 , 0.362	Depositor DCC
R_{free} test set	1559 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	75.6	Xtriage
Anisotropy	0.837	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 28.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	7769	wwPDB-VP
Average B, all atoms (Å ²)	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.10% 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: DM1

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	0.70	0/2590	1.00	3/3519 (0.1%)
1	B	0.75	0/2662	1.00	5/3609 (0.1%)
1	C	0.73	0/2623	1.02	8/3566 (0.2%)
All	All	0.73	0/7875	1.01	16/10694 (0.1%)

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	31	ASN	N-CA-C	6.94	118.73	108.60
1	B	287	SER	N-CA-C	6.67	117.04	108.24
1	B	116	GLU	N-CA-C	-6.43	105.19	113.16
1	A	136	THR	N-CA-C	6.29	118.66	108.34
1	B	82	GLY	N-CA-C	6.14	119.46	110.80
1	C	119	GLY	N-CA-C	-5.92	104.65	112.82
1	C	288	ALA	N-CA-C	5.75	118.35	110.24
1	C	54	PHE	N-CA-C	5.55	117.42	109.14
1	C	32	ALA	N-CA-C	5.51	118.43	109.06
1	C	307	ASN	N-CA-C	5.48	117.31	108.32
1	C	325	SER	N-CA-C	-5.48	106.44	113.23
1	A	78	LEU	N-CA-C	5.46	117.80	108.90
1	A	94	GLY	N-CA-C	5.38	117.18	110.29
1	C	226	ALA	N-CA-C	5.25	117.23	108.99
1	B	22	VAL	N-CA-C	5.20	115.47	107.77
1	C	82	GLY	N-CA-C	5.19	118.68	111.10

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	2540	0	2237	168	0
1	B	2610	0	2352	167	0
1	C	2571	0	2246	164	0
2	C	48	0	26	3	0
All	All	7769	0	6861	463	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 32.

All (463) 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:293:TYR:HB3	1:A:315:ASN:HD22	1.21	1.06
1:C:65:ARG:HG2	1:C:65:ARG:HH11	1.18	1.05
1:A:295:GLN:HB2	1:A:312:TYR:O	1.62	0.98
1:C:123:THR:O	1:C:124:ASP:HB2	1.66	0.95
1:A:211:SER:OG	1:A:232:THR:HA	1.67	0.94
1:B:299:THR:HG23	1:B:309:TRP:HB3	1.54	0.90
1:C:168:GLN:HB3	1:C:196:THR:HG21	1.53	0.88
1:C:16:LYS:HB3	1:C:340:GLN:HB2	1.53	0.88
1:A:57:TRP:HA	1:A:78:LEU:O	1.74	0.88
1:B:320:ASN:HD22	1:B:322:TYR:H	1.22	0.86
1:C:210:GLU:HB2	1:C:233:ARG:HB2	1.54	0.86
1:B:85:TYR:HB3	1:B:88:VAL:HB	1.58	0.85
1:B:82:GLY:HA2	1:C:337:ILE:HD11	1.57	0.85
1:B:153:ILE:HD11	1:B:155:TYR:CE2	2.11	0.85
1:A:20:ARG:HG3	1:A:34:GLN:O	1.78	0.84
1:C:8:GLY:O	1:C:9:ASN:HB2	1.78	0.83
1:A:163:HIS:HB3	1:A:167:SER:OG	1.79	0.82
1:A:165:ILE:O	1:A:166:ASN:HB2	1.77	0.82
1:C:272:SER:OG	1:C:295:GLN:CG	2.29	0.80
1:B:279:LYS:HA	1:B:287:SER:HB3	1.64	0.79
1:A:293:TYR:HB3	1:A:315:ASN:ND2	1.98	0.78
1:A:302:PHE:HB3	1:C:47:ILE:HD12	1.67	0.77
1:B:95:ARG:O	1:B:95:ARG:HG3	1.83	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1:MET:O	1:B:2:GLU:HB3	1.85	0.76
1:A:76:VAL:HG11	1:B:61:THR:HB	1.66	0.76
1:A:91:ILE:HA	1:A:136:THR:O	1.86	0.76
1:B:26:THR:HG22	1:B:27:GLY:N	2.00	0.75
1:C:113:PHE:H	2:C:401[B]:DM1:H4'	1.49	0.75
1:B:76:VAL:H	1:C:70:GLN:HE22	1.35	0.74
1:A:76:VAL:CG1	1:B:61:THR:HB	2.18	0.74
1:A:291:ALA:HA	1:A:317:LEU:HD12	1.70	0.74
1:C:127:MET:HE1	1:C:154:GLN:HG3	1.71	0.73
1:C:272:SER:OG	1:C:295:GLN:HG2	1.88	0.73
1:B:112:TYR:O	1:B:113:PHE:CG	2.41	0.73
1:C:65:ARG:HH11	1:C:65:ARG:CG	1.98	0.73
1:B:242:VAL:HG21	1:B:321:ASP:OD2	1.89	0.72
1:C:166:ASN:HD22	1:C:237:ILE:HG21	1.54	0.72
1:A:62:LYS:HB2	1:A:73:SER:HB3	1.70	0.72
1:B:320:ASN:HB3	1:B:323:SER:OG	1.89	0.72
1:A:93:TYR:OH	1:B:21:HIS:HD2	1.72	0.71
1:C:65:ARG:HG2	1:C:65:ARG:NH1	1.93	0.71
1:C:272:SER:OG	1:C:295:GLN:HG3	1.90	0.71
1:C:136:THR:HB	1:C:154:GLN:HB3	1.73	0.71
1:B:26:THR:CG2	1:B:27:GLY:N	2.54	0.70
1:B:26:THR:CG2	1:B:27:GLY:H	2.04	0.70
1:C:210:GLU:HB2	1:C:233:ARG:CB	2.21	0.70
1:C:85:TYR:HB3	1:C:88:VAL:HG13	1.74	0.69
1:C:56:GLN:HB3	1:C:80:PHE:HE1	1.58	0.69
1:B:30:LYS:HD3	1:B:31:ASN:H	1.56	0.69
1:A:33:ASP:OD1	1:A:34:GLN:N	2.26	0.68
1:C:116:GLU:OE1	2:C:401[B]:DM1:N3'	2.27	0.68
1:C:153:ILE:HA	1:C:174:GLY:O	1.92	0.68
1:C:288:ALA:HB1	1:C:320:ASN:ND2	2.09	0.67
1:A:117:THR:HG22	1:A:118:TRP:N	2.08	0.67
1:A:45:THR:OG1	1:B:303:ASN:ND2	2.27	0.67
1:A:117:THR:HG22	1:A:118:TRP:HD1	1.59	0.67
1:A:158:LYS:HA	1:A:170:GLY:HA2	1.76	0.67
1:B:120:GLY:C	1:B:122:TYR:H	2.03	0.67
1:C:123:THR:O	1:C:124:ASP:CB	2.43	0.67
1:B:53:GLY:HA3	1:C:306:MET:HG3	1.77	0.66
1:A:222:ASN:HB3	1:A:261:TYR:CE1	2.32	0.65
1:A:82:GLY:HA3	1:A:91:ILE:O	1.95	0.65
1:B:195:ARG:CZ	1:B:199:GLN:HB2	2.26	0.65
1:C:33:ASP:OD2	1:C:34:GLN:N	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:252:THR:HG22	1:C:278:GLY:HA2	1.78	0.65
1:A:2:GLU:HA	1:A:12:ASP:HB3	1.77	0.64
1:A:165:ILE:O	1:A:166:ASN:CB	2.46	0.64
1:A:303:ASN:O	1:A:306:MET:N	2.30	0.64
1:C:262:GLN:HE21	1:C:268:ARG:HH11	1.43	0.64
1:B:111:PRO:O	1:B:112:TYR:HB2	1.96	0.64
1:B:221:ASN:O	1:B:223:VAL:HG23	1.96	0.64
1:B:76:VAL:N	1:C:70:GLN:HE22	1.95	0.64
1:B:99:ILE:H	1:B:154:GLN:HE22	1.45	0.64
1:B:322:TYR:O	1:B:324:SER:N	2.31	0.64
1:B:62:LYS:HB2	1:B:73:SER:CB	2.28	0.63
1:A:11:LEU:HA	1:A:42:LYS:O	1.99	0.63
1:B:309:TRP:CE2	1:B:336:GLY:HA3	2.34	0.63
1:A:19:GLY:HA2	1:A:35:THR:HG23	1.81	0.63
1:B:257:VAL:HG12	1:B:273:TYR:HB3	1.80	0.63
1:A:150:SER:OG	1:A:178:ALA:HB3	1.99	0.63
1:B:115:GLY:O	1:B:120:GLY:HA3	1.98	0.63
1:A:281:LEU:O	1:A:286:GLY:HA2	1.99	0.63
1:A:95:ARG:HH22	1:B:67:GLU:HG3	1.63	0.62
1:A:259:ALA:O	1:A:271:ILE:HD12	1.99	0.62
1:B:125:ASN:O	1:B:126:TYR:CD2	2.52	0.62
1:B:272:SER:OG	1:B:295:GLN:HG3	1.99	0.62
1:C:193:SER:HB2	1:C:209:ALA:HB3	1.81	0.62
1:A:61:THR:OG1	1:C:76:VAL:HG11	1.99	0.62
1:A:47:ILE:HD12	1:A:51:LEU:HG	1.82	0.62
1:B:91:ILE:HA	1:B:136:THR:O	1.99	0.62
1:B:26:THR:HB	1:B:331:ASP:H	1.65	0.62
1:C:56:GLN:HB3	1:C:80:PHE:CE1	2.34	0.61
1:A:211:SER:HB2	1:A:235:MET:HE2	1.82	0.61
1:B:82:GLY:HA2	1:C:337:ILE:CD1	2.30	0.61
1:C:126:TYR:HD1	1:C:235:MET:HB3	1.65	0.61
1:C:48:ASN:O	1:C:50:ASP:N	2.34	0.61
1:A:113:PHE:HD2	1:A:311:ASP:OD1	1.84	0.61
1:C:129:SER:O	1:C:130:ARG:C	2.43	0.61
1:C:323:SER:O	1:C:324:SER:C	2.44	0.60
1:C:218:TYR:HB3	1:C:225:LEU:HD12	1.83	0.60
1:B:11:LEU:HA	1:B:43:GLY:HA2	1.83	0.60
1:A:236:SER:HB2	1:A:249:ALA:HB3	1.83	0.60
1:A:295:GLN:HB2	1:A:313:ARG:HA	1.83	0.60
1:C:220:ALA:O	1:C:221:ASN:C	2.44	0.60
1:B:178:ALA:HA	1:B:187:THR:HG22	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:18:VAL:HG22	1:A:338:THR:HG23	1.83	0.59
1:A:111:PRO:HG2	1:A:311:ASP:OD2	2.01	0.59
1:A:257:VAL:HG12	1:A:273:TYR:HB3	1.85	0.59
1:B:181:PHE:CD2	1:B:181:PHE:N	2.70	0.59
1:C:126:TYR:O	1:C:128:THR:HG23	2.02	0.59
1:B:196:THR:HG22	1:B:197:ASN:N	2.17	0.59
1:A:165:ILE:O	1:A:165:ILE:HG13	2.02	0.58
1:A:293:TYR:CB	1:A:315:ASN:HD22	2.08	0.58
1:C:20:ARG:NH1	1:C:34:GLN:HB3	2.18	0.58
1:A:117:THR:HG22	1:A:118:TRP:CD1	2.38	0.58
1:A:160:GLN:NE2	1:A:196:THR:HB	2.18	0.58
1:C:107:THR:HG21	1:C:228:VAL:HG12	1.86	0.58
1:C:117:THR:O	1:C:326:TYR:CE1	2.57	0.58
1:B:165:ILE:HA	1:B:168:GLN:HE21	1.68	0.58
1:B:38:GLN:HG3	1:B:60:ARG:HB2	1.85	0.58
1:C:118:TRP:CG	1:C:119:GLY:H	2.21	0.57
1:A:93:TYR:OH	1:B:21:HIS:CD2	2.57	0.57
1:C:288:ALA:HB1	1:C:320:ASN:HD21	1.67	0.57
1:A:159:ASN:N	1:A:169:ASN:O	2.37	0.57
1:B:21:HIS:HE1	1:B:31:ASN:ND2	2.02	0.57
1:C:315:ASN:HD22	1:C:315:ASN:C	2.13	0.57
1:C:143:PHE:HB2	1:C:145:LEU:HD22	1.87	0.57
1:C:16:LYS:CB	1:C:340:GLN:HB2	2.30	0.57
1:A:222:ASN:O	1:A:261:TYR:HD1	1.87	0.57
1:B:313:ARG:NH2	1:B:332:GLN:OE1	2.34	0.56
1:B:202:ARG:HB3	1:B:282:ASN:OD1	2.05	0.56
1:C:123:THR:O	1:C:123:THR:HG23	2.06	0.56
1:C:166:ASN:ND2	1:C:237:ILE:HG21	2.19	0.56
1:A:24:THR:HB	1:A:30:LYS:H	1.70	0.56
1:C:59:TYR:HD2	1:C:76:VAL:CG1	2.19	0.56
1:C:140:SER:O	1:C:150:SER:HB3	2.05	0.56
1:B:150:SER:OG	1:B:178:ALA:HB3	2.06	0.56
1:B:270:ALA:N	1:B:297:GLY:O	2.38	0.56
1:A:222:ASN:HB3	1:A:261:TYR:HE1	1.70	0.56
1:B:20:ARG:HD3	1:B:34:GLN:HB3	1.87	0.56
1:C:59:TYR:HD2	1:C:76:VAL:HG12	1.69	0.56
1:A:195:ARG:HH21	1:A:248:MET:HB2	1.70	0.56
1:B:117:THR:O	1:B:326:TYR:CE1	2.59	0.55
1:C:141:ASP:O	1:C:143:PHE:N	2.40	0.55
1:C:126:TYR:CD1	1:C:235:MET:HB3	2.41	0.55
1:A:183:GLY:HA3	1:A:218:TYR:CE1	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:99:ILE:HD11	1:B:176:THR:HG22	1.89	0.55
1:B:148:GLY:O	1:B:179:TYR:HA	2.06	0.55
1:C:56:GLN:HG3	1:C:57:TRP:N	2.21	0.55
1:B:54:PHE:CD1	1:B:54:PHE:C	2.85	0.55
1:B:240:ASN:HB3	1:B:243:THR:HG22	1.88	0.55
1:C:260:GLN:HB3	1:C:270:ALA:HA	1.89	0.55
1:C:11:LEU:HG	1:C:12:ASP:N	2.22	0.55
1:A:33:ASP:O	1:A:34:GLN:HG2	2.06	0.54
1:C:1:MET:C	1:C:12:ASP:OD2	2.51	0.54
1:A:142:PHE:HB3	1:A:146:VAL:HG23	1.89	0.54
1:A:47:ILE:HG23	1:B:302:PHE:HB3	1.90	0.54
1:A:242:VAL:C	1:A:244:ASP:H	2.15	0.54
1:A:238:VAL:HB	1:A:322:TYR:HD1	1.71	0.54
1:B:93:TYR:HA	1:B:134:LEU:O	2.07	0.54
1:C:111:PRO:HG2	1:C:311:ASP:OD1	2.07	0.54
1:A:43:GLY:HA3	1:B:339:TYR:CE2	2.43	0.54
1:A:263:PHE:O	1:A:265:PHE:N	2.41	0.54
1:C:264:ASP:O	1:C:265:PHE:HB3	2.06	0.54
1:C:299:THR:HG23	1:C:309:TRP:HB3	1.89	0.54
1:C:315:ASN:N	1:C:331:ASP:OD1	2.29	0.54
1:C:107:THR:CG2	1:C:228:VAL:HG12	2.38	0.53
1:A:164:SER:O	1:A:165:ILE:C	2.51	0.53
1:B:250:ASN:O	1:B:251:LYS:O	2.25	0.53
1:C:59:TYR:CD2	1:C:76:VAL:HG12	2.42	0.53
1:C:122:TYR:CZ	1:C:237:ILE:HB	2.43	0.53
1:C:160:GLN:HA	1:C:168:GLN:HG2	1.89	0.53
1:A:107:THR:OG1	1:A:228:VAL:HG22	2.08	0.53
1:B:107:THR:HG23	1:B:228:VAL:HG13	1.89	0.53
1:B:75:LEU:HD22	1:C:67:GLU:HG3	1.90	0.53
1:B:126:TYR:CE1	1:B:169:ASN:HB2	2.44	0.53
1:B:222:ASN:HB2	1:B:262:GLN:O	2.09	0.53
1:A:204:GLY:HA2	1:A:250:ASN:ND2	2.24	0.53
1:B:202:ARG:HH21	1:B:282:ASN:HB2	1.74	0.53
1:C:232:THR:HG23	1:C:235:MET:HG3	1.91	0.53
1:C:261:TYR:CE2	1:C:263:PHE:HA	2.43	0.53
1:A:313:ARG:O	1:A:313:ARG:HG3	2.08	0.53
1:C:122:TYR:CE1	1:C:237:ILE:HB	2.44	0.53
1:A:141:ASP:OD2	1:A:144:GLY:HA2	2.09	0.53
1:A:295:GLN:C	1:A:295:GLN:CD	2.77	0.53
1:B:97:TYR:HA	1:B:130:ARG:HA	1.90	0.53
1:C:95:ARG:NH2	1:C:124:ASP:OD2	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:187:THR:O	1:C:214:VAL:HA	2.09	0.53
1:B:140:SER:O	1:B:150:SER:HB3	2.09	0.52
1:C:158:LYS:HA	1:C:169:ASN:O	2.09	0.52
1:C:322:TYR:O	1:C:323:SER:C	2.51	0.52
1:A:209:ALA:HA	1:A:234:ASN:HB2	1.90	0.52
1:A:151:PHE:HB2	1:A:176:THR:O	2.09	0.52
1:A:227:ALA:HB2	1:A:257:VAL:HG23	1.92	0.52
1:B:26:THR:HG22	1:B:27:GLY:H	1.69	0.52
1:B:91:ILE:HG13	1:B:91:ILE:O	2.07	0.52
1:B:101:TYR:HB2	1:B:128:THR:O	2.10	0.52
1:A:303:ASN:O	1:A:305:ASN:N	2.43	0.52
1:B:181:PHE:O	1:B:184:PHE:HB2	2.10	0.52
1:C:163:HIS:HB3	1:C:167:SER:HB2	1.92	0.52
1:A:230:ALA:N	1:A:254:ASN:O	2.42	0.52
1:B:62:LYS:HB2	1:B:73:SER:HB2	1.90	0.52
1:B:117:THR:O	1:B:326:TYR:CZ	2.62	0.52
1:C:27:GLY:HA3	1:C:330:ASP:OD1	2.10	0.52
1:B:14:TYR:HE2	1:B:42:LYS:HG3	1.75	0.52
1:A:117:THR:CG2	1:A:118:TRP:N	2.73	0.51
1:A:205:ASN:HB3	1:A:234:ASN:HD21	1.75	0.51
1:B:303:ASN:HB3	1:B:305:ASN:H	1.76	0.51
1:C:117:THR:HG23	1:C:118:TRP:H	1.75	0.51
1:B:54:PHE:C	1:B:54:PHE:HD1	2.16	0.51
1:B:54:PHE:HD1	1:B:54:PHE:O	1.92	0.51
1:B:8:GLY:O	1:B:9:ASN:HB2	2.10	0.51
1:B:252:THR:O	1:B:254:ASN:ND2	2.43	0.51
1:C:222:ASN:HB3	1:C:262:GLN:O	2.11	0.51
1:B:99:ILE:O	1:B:100:VAL:C	2.53	0.51
1:B:168:GLN:OE1	1:B:196:THR:HG21	2.11	0.51
1:A:46:GLN:HE21	1:A:46:GLN:CA	2.24	0.51
1:C:16:LYS:HB3	1:C:340:GLN:CB	2.33	0.51
1:A:195:ARG:HD3	1:A:206:GLY:O	2.11	0.51
1:B:312:TYR:HD1	1:B:313:ARG:N	2.08	0.51
1:A:213:ALA:HB1	1:A:229:TYR:O	2.10	0.50
1:B:163:HIS:HB3	1:B:167:SER:HB2	1.93	0.50
1:B:201:ASP:O	1:B:202:ARG:C	2.53	0.50
1:C:59:TYR:CD2	1:C:76:VAL:CG1	2.94	0.50
1:C:116:GLU:HG2	2:C:401[A]:DM1:H4'	1.92	0.50
1:A:11:LEU:HG	1:A:12:ASP:N	2.27	0.50
1:A:60:ARG:NH1	1:A:77:ARG:NH1	2.59	0.50
1:A:215:GLY:HA3	1:A:228:VAL:HG12	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:23:TRP:O	1:C:332:GLN:HG3	2.12	0.50
1:A:47:ILE:CG2	1:B:302:PHE:HB3	2.42	0.50
1:A:267:LEU:HD11	1:A:298:ALA:HB1	1.94	0.50
1:B:60:ARG:O	1:B:74:ASN:HA	2.11	0.50
1:B:76:VAL:H	1:C:70:GLN:NE2	2.05	0.50
1:A:309:TRP:CD1	1:A:309:TRP:C	2.90	0.50
1:C:205:ASN:HB2	1:C:250:ASN:HD21	1.76	0.49
1:A:228:VAL:O	1:A:255:LEU:HD12	2.12	0.49
1:A:290:LEU:C	1:A:317:LEU:HD11	2.37	0.49
1:C:313:ARG:NH1	1:C:327:VAL:HG22	2.26	0.49
1:A:101:TYR:O	1:A:104:GLU:N	2.45	0.49
1:A:273:TYR:HA	1:A:294:ILE:HG23	1.93	0.49
1:B:21:HIS:HE1	1:B:31:ASN:HD21	1.60	0.49
1:A:267:LEU:HD12	1:A:269:PRO:HG3	1.95	0.49
1:B:205:ASN:O	1:B:207:ASP:N	2.46	0.49
1:A:106:TYR:HD1	1:A:106:TYR:H	1.61	0.49
1:B:140:SER:HA	1:B:150:SER:HB2	1.95	0.49
1:A:16:LYS:HE3	1:A:36:TYR:CE1	2.48	0.49
1:B:110:ALA:C	1:B:112:TYR:N	2.71	0.49
1:A:50:ASP:HB3	1:A:86:ALA:HB3	1.94	0.49
1:B:153:ILE:HD13	1:B:153:ILE:C	2.37	0.49
1:C:16:LYS:HG2	1:C:38:GLN:HB3	1.95	0.49
1:C:262:GLN:NE2	1:C:268:ARG:HH11	2.10	0.49
1:B:168:GLN:O	1:B:169:ASN:HB3	2.13	0.49
1:C:136:THR:HB	1:C:154:GLN:CB	2.42	0.49
1:A:99:ILE:H	1:A:127:MET:HE3	1.78	0.48
1:A:172:GLY:HA3	1:A:193:SER:OG	2.13	0.48
1:B:196:THR:CG2	1:B:197:ASN:N	2.76	0.48
1:C:127:MET:HE2	1:C:173:VAL:O	2.11	0.48
1:A:4:TYR:O	1:A:5:ASN:CB	2.61	0.48
1:B:204:GLY:O	1:B:205:ASN:HB2	2.12	0.48
1:A:160:GLN:HE21	1:A:196:THR:HB	1.76	0.48
1:B:26:THR:HG23	1:B:27:GLY:H	1.79	0.48
1:C:232:THR:HG21	1:C:236:SER:OG	2.14	0.48
1:A:140:SER:O	1:A:150:SER:HB3	2.12	0.48
1:C:319:GLU:HA	1:C:329:THR:HG21	1.96	0.48
1:A:146:VAL:C	1:A:148:GLY:H	2.22	0.48
1:B:87:GLU:O	1:B:143:PHE:HA	2.12	0.48
1:B:2:GLU:HA	1:B:12:ASP:OD1	2.14	0.48
1:B:110:ALA:C	1:B:112:TYR:H	2.21	0.48
1:B:320:ASN:HD22	1:B:322:TYR:N	2.01	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:20:ARG:NH1	1:B:34:GLN:HG3	2.29	0.47
1:A:262:GLN:OE1	1:A:268:ARG:NH1	2.46	0.47
1:A:142:PHE:O	1:A:142:PHE:CD2	2.67	0.47
1:C:19:GLY:HA2	1:C:35:THR:OG1	2.14	0.47
1:C:104:GLU:HG2	1:C:118:TRP:CZ2	2.48	0.47
1:C:233:ARG:O	1:C:250:ASN:HA	2.14	0.47
1:B:24:THR:OG1	1:B:30:LYS:O	2.32	0.47
1:C:152:GLY:N	1:C:176:THR:O	2.47	0.47
1:C:323:SER:O	1:C:325:SER:N	2.47	0.47
1:A:163:HIS:ND1	1:A:163:HIS:N	2.63	0.47
1:B:93:TYR:HB2	1:B:135:LEU:HD22	1.96	0.47
1:B:86:ALA:C	1:B:88:VAL:H	2.22	0.47
1:C:256:GLU:HG2	1:C:274:VAL:HB	1.95	0.47
1:A:295:GLN:CB	1:A:313:ARG:HA	2.44	0.47
1:B:57:TRP:CZ3	1:C:39:ILE:HD12	2.50	0.47
1:C:58:GLU:HG2	1:C:77:ARG:HB2	1.97	0.47
1:A:16:LYS:HE3	1:A:36:TYR:HE1	1.80	0.47
1:A:82:GLY:O	1:A:83:LEU:HD23	2.15	0.47
1:B:235:MET:O	1:B:237:ILE:HD13	2.14	0.47
1:C:98:GLY:HA3	1:C:127:MET:C	2.39	0.47
1:B:250:ASN:O	1:B:251:LYS:C	2.58	0.47
1:B:320:ASN:CB	1:B:323:SER:OG	2.60	0.47
1:A:95:ARG:NH2	1:B:67:GLU:HG3	2.29	0.46
1:A:295:GLN:CD	1:A:295:GLN:O	2.58	0.46
1:B:199:GLN:C	1:B:201:ASP:N	2.73	0.46
1:C:321:ASP:O	1:C:323:SER:N	2.48	0.46
1:A:76:VAL:HG12	1:B:61:THR:HB	1.94	0.46
1:A:93:TYR:CE1	1:A:133:GLY:HA2	2.50	0.46
1:B:100:VAL:HB	1:B:127:MET:O	2.15	0.46
1:C:240:ASN:HB3	1:C:243:THR:O	2.15	0.46
1:A:141:ASP:CG	1:A:144:GLY:HA2	2.40	0.46
1:A:303:ASN:O	1:A:304:LYS:C	2.59	0.46
1:A:165:ILE:N	1:A:168:GLN:HE21	2.14	0.46
1:C:88:VAL:O	1:C:88:VAL:HG22	2.15	0.46
1:C:241:THR:OG1	1:C:323:SER:CB	2.63	0.46
1:B:75:LEU:HA	1:C:70:GLN:NE2	2.31	0.46
1:B:320:ASN:ND2	1:B:322:TYR:H	2.02	0.46
1:C:40:GLY:HA3	1:C:57:TRP:O	2.16	0.46
1:C:88:VAL:O	1:C:88:VAL:CG2	2.64	0.46
1:A:70:GLN:NE2	1:C:76:VAL:H	2.14	0.46
1:A:147:ASP:OD1	1:A:147:ASP:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:168:GLN:C	1:A:169:ASN:CG	2.84	0.46
1:C:5:ASN:C	1:C:5:ASN:HD22	2.23	0.46
1:A:87:GLU:HB3	1:A:143:PHE:C	2.41	0.46
1:A:226:ALA:HB3	1:A:258:VAL:HG13	1.98	0.46
1:C:252:THR:CG2	1:C:278:GLY:HA2	2.46	0.46
1:A:232:THR:HG21	1:A:236:SER:OG	2.16	0.46
1:C:71:GLN:HE21	1:C:71:GLN:HB3	1.62	0.46
1:A:204:GLY:HA2	1:A:250:ASN:CG	2.41	0.45
1:C:151:PHE:HA	1:C:177:MET:HA	1.98	0.45
1:B:108:ASP:HA	1:B:114:SER:HB2	1.98	0.45
1:C:127:MET:CE	1:C:154:GLN:HG3	2.42	0.45
1:A:127:MET:HE3	1:A:127:MET:HB3	1.66	0.45
1:C:17:ALA:N	1:C:339:TYR:O	2.45	0.45
1:A:35:THR:HB	1:A:63:ALA:HB3	1.99	0.45
1:A:108:ASP:HA	1:A:114:SER:HB2	1.98	0.45
1:A:170:GLY:O	1:A:171:ASP:C	2.60	0.45
1:C:16:LYS:CB	1:C:340:GLN:CB	2.94	0.45
1:C:46:GLN:HA	1:C:52:THR:HG22	1.98	0.45
1:A:320:ASN:HB2	1:A:323:SER:OG	2.16	0.45
1:C:189:ALA:N	1:C:213:ALA:O	2.50	0.45
1:C:199:GLN:CD	1:C:199:GLN:C	2.85	0.45
1:A:113:PHE:CD2	1:A:311:ASP:OD1	2.69	0.45
1:C:262:GLN:NE2	1:C:268:ARG:HD2	2.31	0.45
1:A:295:GLN:HG2	1:A:296:ALA:O	2.16	0.45
1:B:125:ASN:O	1:B:126:TYR:HD2	1.97	0.44
1:B:99:ILE:H	1:B:154:GLN:NE2	2.14	0.44
1:B:164:SER:O	1:B:168:GLN:HG3	2.18	0.44
1:C:23:TRP:HZ3	1:C:335:VAL:HG12	1.81	0.44
1:A:51:LEU:HD12	1:A:84:LYS:O	2.16	0.44
1:A:220:ALA:O	1:A:221:ASN:C	2.59	0.44
1:C:112:TYR:O	1:C:113:PHE:HB2	2.18	0.44
1:A:98:GLY:HA3	1:A:127:MET:O	2.17	0.44
1:C:142:PHE:O	1:C:145:LEU:HB2	2.18	0.44
1:A:100:VAL:HG12	1:A:100:VAL:O	2.17	0.44
1:B:57:TRP:CD1	1:C:37:ALA:HB3	2.52	0.44
1:A:53:GLY:C	1:B:306:MET:HE3	2.43	0.44
1:A:238:VAL:HG13	1:A:325:SER:HB3	2.00	0.44
1:A:291:ALA:HA	1:A:317:LEU:CD1	2.43	0.44
1:A:128:THR:HG23	1:A:235:MET:HE3	1.98	0.44
1:A:197:ASN:C	1:A:199:GLN:H	2.25	0.44
1:A:53:GLY:HA3	1:B:306:MET:HE3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:18:VAL:O	1:B:35:THR:HG23	2.18	0.43
1:B:170:GLY:HA3	1:B:194:LYS:O	2.17	0.43
1:B:301:TYR:HD1	1:B:307:ASN:HB2	1.83	0.43
1:C:139:ASN:O	1:C:150:SER:HB2	2.18	0.43
1:C:157:GLY:O	1:C:158:LYS:C	2.60	0.43
1:C:318:ASP:O	1:C:319:GLU:C	2.60	0.43
1:A:117:THR:HG22	1:A:118:TRP:H	1.81	0.43
1:A:263:PHE:HB2	1:A:265:PHE:CD2	2.53	0.43
1:A:275:GLN:HA	1:A:291:ALA:O	2.17	0.43
1:B:306:MET:HE1	1:B:339:TYR:HB2	1.99	0.43
1:B:225:LEU:HD23	1:B:225:LEU:N	2.32	0.43
1:C:313:ARG:HH12	1:C:327:VAL:HG22	1.84	0.43
1:B:47:ILE:H	1:B:47:ILE:HG13	1.54	0.43
1:B:182:ASP:C	1:B:184:PHE:H	2.26	0.43
1:B:320:ASN:HD22	1:B:321:ASP:N	2.17	0.43
1:C:129:SER:O	1:C:130:ARG:O	2.37	0.43
1:B:93:TYR:CG	1:B:94:GLY:N	2.85	0.43
1:C:100:VAL:CG2	1:C:191:SER:HB3	2.49	0.43
1:A:305:ASN:O	1:A:306:MET:HG2	2.17	0.43
1:C:212:ARG:HE	1:C:233:ARG:HH11	1.66	0.43
1:C:113:PHE:HZ	1:C:332:GLN:HG2	1.82	0.43
1:A:21:HIS:CE1	1:A:31:ASN:HD21	2.37	0.43
1:B:270:ALA:C	1:B:295:GLN:HE22	2.27	0.43
1:C:33:ASP:OD2	1:C:35:THR:N	2.51	0.43
1:C:218:TYR:CZ	1:C:220:ALA:HB3	2.54	0.43
1:B:113:PHE:CD2	1:B:311:ASP:OD1	2.71	0.43
1:A:101:TYR:O	1:A:102:ASP:C	2.62	0.43
1:C:304:LYS:O	1:C:340:GLN:NE2	2.52	0.43
1:B:139:ASN:HD21	1:B:143:PHE:N	2.16	0.42
1:A:53:GLY:CA	1:B:306:MET:HE3	2.49	0.42
1:A:70:GLN:HE21	1:C:76:VAL:H	1.66	0.42
1:A:139:ASN:O	1:A:150:SER:HA	2.19	0.42
1:B:204:GLY:CA	1:B:250:ASN:HD21	2.32	0.42
1:C:292:LYS:HG2	1:C:316:LEU:HB2	2.01	0.42
1:A:339:TYR:CD2	1:A:339:TYR:C	2.97	0.42
1:B:131:ALA:HB3	1:B:134:LEU:HD11	2.02	0.42
1:B:262:GLN:HG3	1:B:263:PHE:N	2.34	0.42
1:C:281:LEU:HD22	1:C:286:GLY:HA2	2.01	0.42
1:A:23:TRP:NE1	1:A:31:ASN:HD22	2.18	0.42
1:A:100:VAL:HA	1:A:189:ALA:HB1	2.00	0.42
1:A:318:ASP:O	1:A:329:THR:HG23	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:62:LYS:HB2	1:B:73:SER:HB3	2.00	0.42
1:A:229:TYR:HD1	1:A:255:LEU:HB2	1.85	0.42
1:B:109:MET:HB2	1:B:260:GLN:NE2	2.35	0.42
1:B:112:TYR:O	1:B:113:PHE:CD2	2.71	0.42
1:B:311:ASP:OD2	1:B:311:ASP:C	2.62	0.42
1:C:151:PHE:HA	1:C:176:THR:O	2.19	0.42
1:B:221:ASN:C	1:B:223:VAL:H	2.28	0.42
1:B:83:LEU:HD21	1:C:302:PHE:CE2	2.54	0.42
1:B:219:ASP:O	1:B:219:ASP:OD1	2.38	0.42
1:A:242:VAL:HG23	1:A:243:THR:H	1.85	0.41
1:A:232:THR:HB	1:A:252:THR:HB	2.03	0.41
1:B:148:GLY:C	1:B:179:TYR:HD1	2.29	0.41
1:B:156:GLN:HE21	1:B:156:GLN:HB3	1.61	0.41
1:B:205:ASN:HD22	1:B:205:ASN:HA	1.69	0.41
1:C:320:ASN:OD1	1:C:320:ASN:C	2.62	0.41
1:A:45:THR:HG21	1:B:306:MET:HB2	2.03	0.41
1:A:117:THR:O	1:A:326:TYR:CZ	2.73	0.41
1:B:18:VAL:HG13	1:B:338:THR:HB	2.01	0.41
1:B:209:ALA:CB	1:B:234:ASN:HB3	2.51	0.41
1:B:257:VAL:CG1	1:B:273:TYR:HB3	2.49	0.41
1:C:23:TRP:CZ3	1:C:335:VAL:HG12	2.55	0.41
1:C:211:SER:HB3	1:C:235:MET:SD	2.61	0.41
1:C:303:ASN:O	1:C:305:ASN:N	2.53	0.41
1:A:240:ASN:HD22	1:A:241:THR:N	2.18	0.41
1:B:75:LEU:CB	1:C:70:GLN:NE2	2.83	0.41
1:B:175:TYR:N	1:B:175:TYR:CD2	2.88	0.41
1:C:20:ARG:NH1	1:C:36:TYR:CD2	2.89	0.41
1:C:254:ASN:ND2	1:C:276:SER:OG	2.53	0.41
1:A:150:SER:O	1:A:178:ALA:N	2.53	0.41
1:B:14:TYR:CD1	1:B:14:TYR:C	2.98	0.41
1:A:313:ARG:HD2	1:A:315:ASN:HB2	2.02	0.41
1:B:75:LEU:CA	1:C:70:GLN:NE2	2.84	0.41
1:C:48:ASN:O	1:C:49:THR:C	2.63	0.41
1:A:66:ALA:HB2	1:C:163:HIS:HD2	1.85	0.41
1:A:68:GLY:HA2	1:C:75:LEU:HD21	2.02	0.41
1:B:61:THR:HG22	1:B:74:ASN:HB3	2.02	0.41
1:B:86:ALA:O	1:B:88:VAL:N	2.51	0.41
1:A:48:ASN:O	1:A:49:THR:C	2.64	0.41
1:A:77:ARG:O	1:A:95:ARG:HG2	2.20	0.41
1:A:139:ASN:OD1	1:A:142:PHE:HA	2.21	0.41
1:A:195:ARG:HH21	1:A:248:MET:CB	2.33	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:281:LEU:N	1:A:286:GLY:O	2.47	0.41
1:A:302:PHE:HB3	1:C:47:ILE:HG23	2.02	0.41
1:A:313:ARG:NH2	1:A:332:GLN:OE1	2.53	0.41
1:B:47:ILE:O	1:B:48:ASN:HB3	2.20	0.41
1:B:108:ASP:OD1	1:B:114:SER:OG	2.24	0.41
1:B:124:ASP:HB2	1:C:66:ALA:HB1	2.03	0.41
1:B:237:ILE:HG22	1:B:246:VAL:HG12	2.02	0.41
1:C:261:TYR:HE2	1:C:263:PHE:CD2	2.39	0.41
1:A:261:TYR:O	1:A:269:PRO:HD2	2.21	0.41
1:B:42:LYS:HG2	1:B:56:GLN:CD	2.46	0.41
1:C:107:THR:O	1:C:258:VAL:HG21	2.21	0.41
1:B:301:TYR:HD1	1:B:307:ASN:CB	2.34	0.40
1:C:267:LEU:HD12	1:C:269:PRO:HD3	2.04	0.40
1:A:46:GLN:NE2	1:A:46:GLN:HA	2.36	0.40
1:B:58:GLU:HB3	1:B:77:ARG:HB2	2.04	0.40
1:B:294:ILE:HB	1:B:314:PHE:HB2	2.04	0.40
1:A:122:TYR:CE2	1:A:237:ILE:HB	2.56	0.40
1:A:165:ILE:H	1:A:168:GLN:HE21	1.68	0.40
1:B:120:GLY:C	1:B:122:TYR:N	2.72	0.40
1:B:288:ALA:HB1	1:B:320:ASN:HD21	1.86	0.40
1:C:108:ASP:HA	1:C:114:SER:HB2	2.03	0.40
1:C:110:ALA:O	1:C:111:PRO:C	2.64	0.40
1:C:231:GLU:OE2	1:C:233:ARG:NH1	2.54	0.40
1:A:202:ARG:HD3	1:A:202:ARG:HA	1.93	0.40
1:A:224:TYR:O	1:A:259:ALA:HA	2.22	0.40
1:A:306:MET:HE1	1:A:337:ILE:HD11	2.04	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	336/341 (98%)	266 (79%)	52 (16%)	18 (5%)	1	9
1	B	336/341 (98%)	271 (81%)	49 (15%)	16 (5%)	2	11
1	C	336/341 (98%)	271 (81%)	45 (13%)	20 (6%)	1	7
All	All	1008/1023 (98%)	808 (80%)	146 (14%)	54 (5%)	1	9

All (54) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	29	SER
1	A	165	ILE
1	A	202	ARG
1	B	9	ASN
1	B	112	TYR
1	B	113	PHE
1	B	126	TYR
1	B	251	LYS
1	B	323	SER
1	C	9	ASN
1	C	49	THR
1	C	113	PHE
1	C	124	ASP
1	C	142	PHE
1	C	251	LYS
1	C	265	PHE
1	C	304	LYS
1	A	5	ASN
1	A	166	ASN
1	A	182	ASP
1	A	264	ASP
1	A	304	LYS
1	A	318	ASP
1	B	2	GLU
1	B	27	GLY
1	B	202	ARG
1	B	206	GLY
1	B	284	ALA
1	C	6	LYS
1	C	35	THR
1	C	122	TYR
1	C	285	GLY
1	A	4	TYR
1	A	171	ASP

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Mol	Chain	Res	Type
1	A	303	ASN
1	B	32	ALA
1	B	87	GLU
1	B	207	ASP
1	C	126	TYR
1	C	130	ARG
1	C	221	ASN
1	A	49	THR
1	A	68	GLY
1	B	222	ASN
1	C	182	ASP
1	C	323	SER
1	A	283	GLY
1	C	244	ASP
1	A	198	ASP
1	A	244	ASP
1	C	206	GLY
1	C	286	GLY
1	A	88	VAL
1	B	100	VAL

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	237/272 (87%)	177 (75%)	60 (25%)	0	2
1	B	254/272 (93%)	201 (79%)	53 (21%)	1	5
1	C	239/272 (88%)	186 (78%)	53 (22%)	1	4
All	All	730/816 (90%)	564 (77%)	166 (23%)	1	4

All (166) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	5	ASN

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Mol	Chain	Res	Type
1	A	11	LEU
1	A	12	ASP
1	A	20	ARG
1	A	24	THR
1	A	31	ASN
1	A	46	GLN
1	A	49	THR
1	A	50	ASP
1	A	58	GLU
1	A	61	THR
1	A	70	GLN
1	A	71	GLN
1	A	75	LEU
1	A	76	VAL
1	A	83	LEU
1	A	87	GLU
1	A	91	ILE
1	A	99	ILE
1	A	107	THR
1	A	116	GLU
1	A	117	THR
1	A	123	THR
1	A	127	MET
1	A	145	LEU
1	A	146	VAL
1	A	147	ASP
1	A	156	GLN
1	A	163	HIS
1	A	164	SER
1	A	166	ASN
1	A	169	ASN
1	A	180	GLU
1	A	190	TYR
1	A	192	ASN
1	A	193	SER
1	A	200	GLN
1	A	201	ASP
1	A	202	ARG
1	A	211	SER
1	A	214	VAL
1	A	238	VAL
1	A	245	THR

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Mol	Chain	Res	Type
1	A	248	MET
1	A	255	LEU
1	A	257	VAL
1	A	264	ASP
1	A	267	LEU
1	A	271	ILE
1	A	272	SER
1	A	275	GLN
1	A	282	ASN
1	A	295	GLN
1	A	309	TRP
1	A	313	ARG
1	A	317	LEU
1	A	324	SER
1	A	335	VAL
1	A	340	GLN
1	B	2	GLU
1	B	20	ARG
1	B	24	THR
1	B	30	LYS
1	B	39	ILE
1	B	47	ILE
1	B	54	PHE
1	B	70	GLN
1	B	71	GLN
1	B	72	ASN
1	B	73	SER
1	B	74	ASN
1	B	75	LEU
1	B	76	VAL
1	B	91	ILE
1	B	95	ARG
1	B	103	VAL
1	B	123	THR
1	B	125	ASN
1	B	127	MET
1	B	135	LEU
1	B	136	THR
1	B	153	ILE
1	B	156	GLN
1	B	162	ASN
1	B	173	VAL

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Mol	Chain	Res	Type
1	B	175	TYR
1	B	181	PHE
1	B	182	ASP
1	B	186	VAL
1	B	193	SER
1	B	200	GLN
1	B	212	ARG
1	B	222	ASN
1	B	225	LEU
1	B	228	VAL
1	B	237	ILE
1	B	246	VAL
1	B	247	GLU
1	B	254	ASN
1	B	256	GLU
1	B	276	SER
1	B	287	SER
1	B	289	ASP
1	B	310	VAL
1	B	311	ASP
1	B	315	ASN
1	B	317	LEU
1	B	318	ASP
1	B	320	ASN
1	B	327	VAL
1	B	329	THR
1	B	337	ILE
1	C	3	ILE
1	C	25	THR
1	C	26	THR
1	C	46	GLN
1	C	49	THR
1	C	56	GLN
1	C	58	GLU
1	C	65	ARG
1	C	67	GLU
1	C	71	GLN
1	C	80	PHE
1	C	88	VAL
1	C	104	GLU
1	C	116	GLU
1	C	124	ASP

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Mol	Chain	Res	Type
1	C	127	MET
1	C	136	THR
1	C	145	LEU
1	C	153	ILE
1	C	160	GLN
1	C	171	ASP
1	C	173	VAL
1	C	186	VAL
1	C	199	GLN
1	C	205	ASN
1	C	212	ARG
1	C	222	ASN
1	C	223	VAL
1	C	225	LEU
1	C	228	VAL
1	C	233	ARG
1	C	235	MET
1	C	239	GLU
1	C	241	THR
1	C	242	VAL
1	C	248	MET
1	C	252	THR
1	C	264	ASP
1	C	267	LEU
1	C	274	VAL
1	C	275	GLN
1	C	303	ASN
1	C	310	VAL
1	C	317	LEU
1	C	319	GLU
1	C	320	ASN
1	C	322	TYR
1	C	327	VAL
1	C	329	THR
1	C	335	VAL
1	C	337	ILE
1	C	338	THR
1	C	340	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (48) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	31	ASN
1	A	46	GLN
1	A	70	GLN
1	A	71	GLN
1	A	160	GLN
1	A	168	GLN
1	A	192	ASN
1	A	197	ASN
1	A	240	ASN
1	A	303	ASN
1	A	305	ASN
1	A	307	ASN
1	A	315	ASN
1	B	21	HIS
1	B	31	ASN
1	B	71	GLN
1	B	72	ASN
1	B	139	ASN
1	B	156	GLN
1	B	162	ASN
1	B	166	ASN
1	B	168	GLN
1	B	199	GLN
1	B	205	ASN
1	B	222	ASN
1	B	254	ASN
1	B	260	GLN
1	B	275	GLN
1	B	295	GLN
1	B	303	ASN
1	B	320	ASN
1	C	5	ASN
1	C	34	GLN
1	C	46	GLN
1	C	56	GLN
1	C	70	GLN
1	C	71	GLN
1	C	72	ASN
1	C	139	ASN
1	C	156	GLN
1	C	159	ASN
1	C	163	HIS
1	C	166	ASN

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Mol	Chain	Res	Type
1	C	169	ASN
1	C	254	ASN
1	C	262	GLN
1	C	315	ASN
1	C	340	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	$\# Z > 2$
2	DM1	C	401[B]	-	40,42,42	0.80	0	53,66,66	1.57	6 (11%)
2	DM1	C	401[A]	-	40,42,42	0.77	0	53,66,66	1.16	3 (5%)

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	DM1	C	401[B]	-	-	7/12/58/58	0/5/5/5
2	DM1	C	401[A]	-	-	9/12/58/58	0/5/5/5

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	401[B]	DM1	C2'-C3'-C4'	-4.91	102.74	110.08
2	C	401[B]	DM1	O10-C10-C9	4.62	117.91	107.54
2	C	401[A]	DM1	O4-C4-C5	4.27	121.89	115.84
2	C	401[B]	DM1	O4-C4-C5	4.27	121.89	115.84
2	C	401[A]	DM1	O4-C4-C3	-3.49	118.42	124.30
2	C	401[B]	DM1	O4-C4-C3	-3.49	118.42	124.30
2	C	401[B]	DM1	O10-C1'-C2'	-2.93	102.64	108.28
2	C	401[A]	DM1	C21-O4-C4	2.74	121.53	117.51
2	C	401[B]	DM1	C21-O4-C4	2.74	121.53	117.51

There are no chirality outliers.

All (16) torsion outliers are listed below:

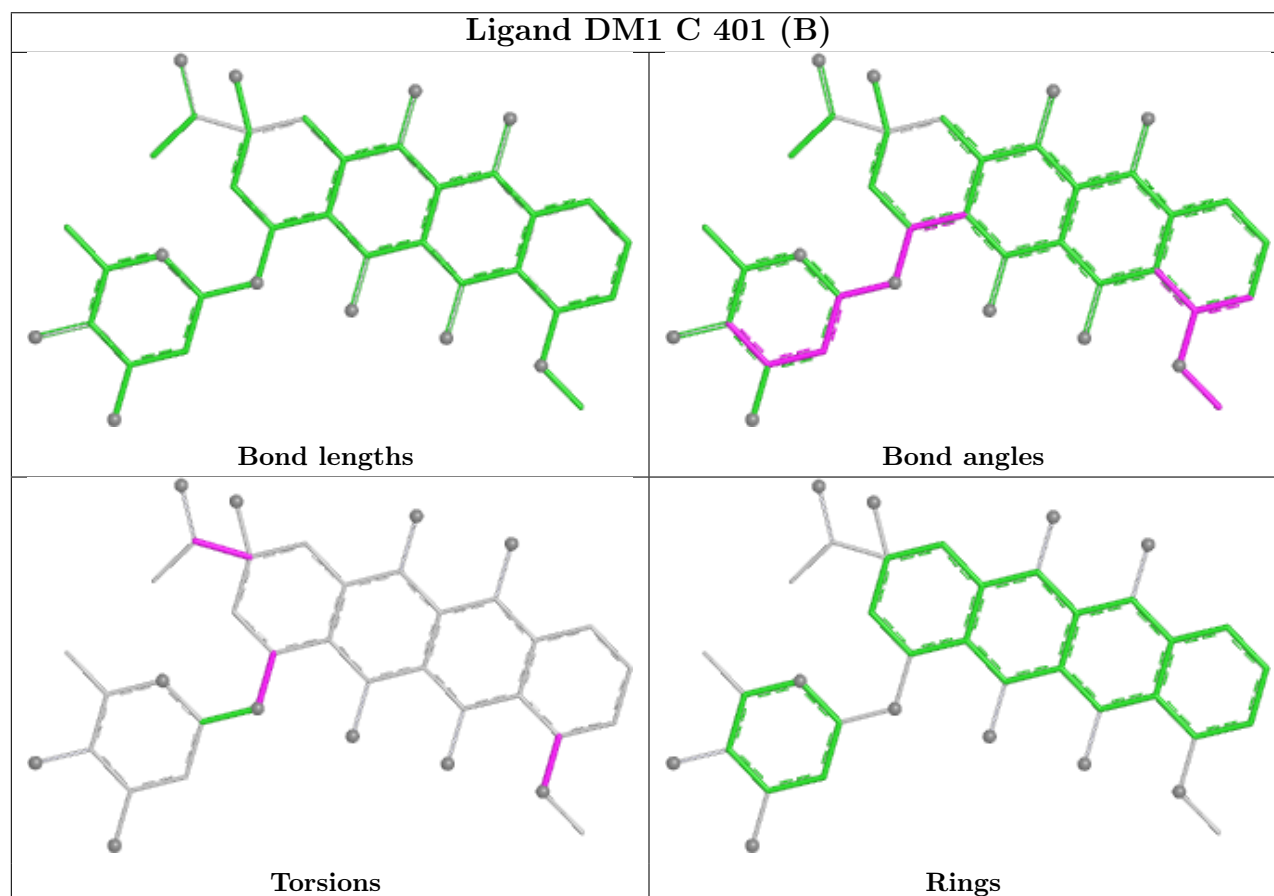
Mol	Chain	Res	Type	Atoms
2	C	401[A]	DM1	C11-C12-C13-O13
2	C	401[A]	DM1	C11-C12-C13-C14
2	C	401[A]	DM1	O12-C12-C13-C14
2	C	401[B]	DM1	C9-C10-O10-C1'
2	C	401[B]	DM1	C11-C12-C13-O13
2	C	401[B]	DM1	C11-C12-C13-C14
2	C	401[B]	DM1	O12-C12-C13-C14
2	C	401[A]	DM1	C2'-C1'-O10-C10
2	C	401[A]	DM1	C3-C4-O4-C21
2	C	401[B]	DM1	C3-C4-O4-C21
2	C	401[A]	DM1	O5'-C1'-O10-C10
2	C	401[A]	DM1	C5-C4-O4-C21
2	C	401[B]	DM1	C5-C4-O4-C21
2	C	401[A]	DM1	C11-C10-O10-C1'
2	C	401[A]	DM1	O12-C12-C13-O13
2	C	401[B]	DM1	O12-C12-C13-O13

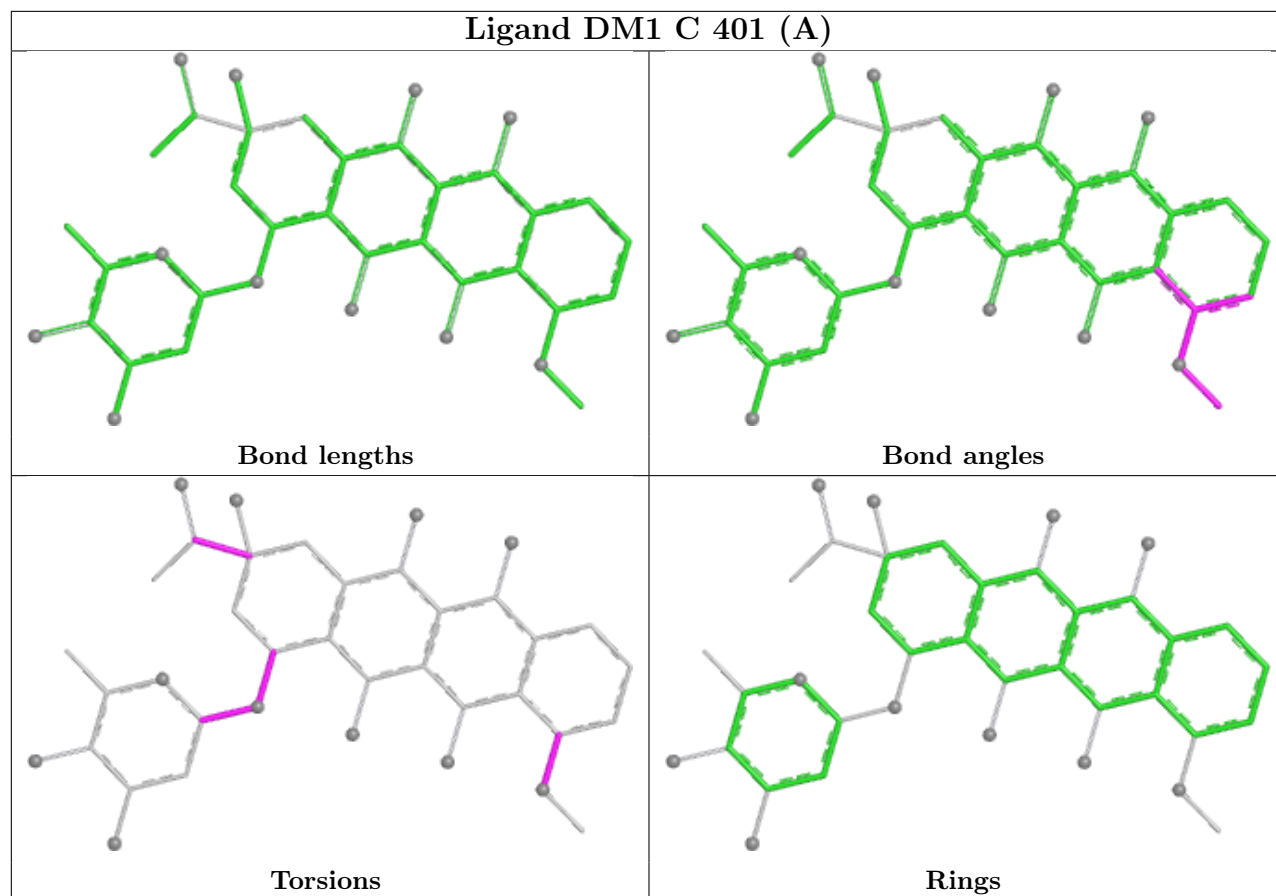
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	401[B]	DM1	2	0
2	C	401[A]	DM1	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

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	340/341 (99%)	0.60	22 (6%) 25 13	56, 88, 104, 112	0
1	B	340/341 (99%)	0.77	34 (10%) 12 6	56, 81, 96, 106	0
1	C	340/341 (99%)	0.77	43 (12%) 8 4	54, 84, 101, 111	0
All	All	1020/1023 (99%)	0.71	99 (9%) 13 7	54, 84, 103, 112	0

All (99) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	132	GLY	5.9
1	C	166	ASN	5.8
1	C	56	GLN	5.8
1	B	129	SER	4.9
1	C	96	ASN	4.6
1	B	23	TRP	4.6
1	B	25	THR	4.4
1	B	97	TYR	4.3
1	A	27	GLY	4.2
1	B	101	TYR	4.2
1	C	80	PHE	4.1
1	A	190	TYR	3.9
1	C	122	TYR	3.9
1	C	7	ASP	3.8
1	A	1	MET	3.8
1	C	162	ASN	3.6
1	B	167	SER	3.5
1	B	28	ASP	3.5
1	C	69	GLU	3.5
1	C	109	MET	3.5
1	B	27	GLY	3.5
1	C	326	TYR	3.4
1	C	202	ARG	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	318	ASP	3.2
1	B	98	GLY	3.1
1	C	92	ASP	3.1
1	B	26	THR	3.1
1	C	102	ASP	3.1
1	C	182	ASP	3.1
1	B	65	ARG	3.0
1	B	29	SER	3.0
1	C	105	SER	3.0
1	B	333	ALA	3.0
1	B	128	THR	3.0
1	A	129	SER	2.9
1	A	125	ASN	2.9
1	B	32	ALA	2.9
1	C	201	ASP	2.9
1	B	164	SER	2.8
1	C	97	TYR	2.8
1	B	198	ASP	2.7
1	A	246	VAL	2.7
1	C	18	VAL	2.7
1	C	322	TYR	2.7
1	B	14	TYR	2.7
1	C	54	PHE	2.6
1	B	165	ILE	2.6
1	A	231	GLU	2.6
1	C	180	GLU	2.6
1	A	118	TRP	2.6
1	B	223	VAL	2.6
1	C	78	LEU	2.6
1	A	128	THR	2.6
1	B	131	ALA	2.6
1	C	94	GLY	2.6
1	C	49	THR	2.6
1	A	28	ASP	2.5
1	A	105	SER	2.5
1	C	325	SER	2.5
1	A	108	ASP	2.5
1	B	31	ASN	2.5
1	B	166	ASN	2.4
1	C	172	GLY	2.4
1	A	10	LYS	2.4
1	C	93	TYR	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	237	ILE	2.4
1	A	171	ASP	2.4
1	A	3	ILE	2.3
1	B	22	VAL	2.3
1	B	186	VAL	2.3
1	C	198	ASP	2.3
1	C	165	ILE	2.3
1	C	194	LYS	2.3
1	B	132	GLY	2.2
1	C	170	GLY	2.2
1	B	24	THR	2.2
1	B	30	LYS	2.2
1	A	69	GLU	2.2
1	C	8	GLY	2.2
1	A	289	ASP	2.2
1	A	71	GLN	2.2
1	B	201	ASP	2.2
1	C	186	VAL	2.1
1	A	66	ALA	2.1
1	C	86	ALA	2.1
1	B	210	GLU	2.1
1	C	120	GLY	2.1
1	C	181	PHE	2.1
1	C	50	ASP	2.1
1	C	161	ASP	2.1
1	A	26	THR	2.1
1	B	123	THR	2.1
1	C	123	THR	2.1
1	C	81	ALA	2.1
1	A	103	VAL	2.1
1	B	312	TYR	2.1
1	C	87	GLU	2.0
1	B	13	LEU	2.0
1	B	334	ALA	2.0

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

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

6.3 Carbohydrates [i](#)

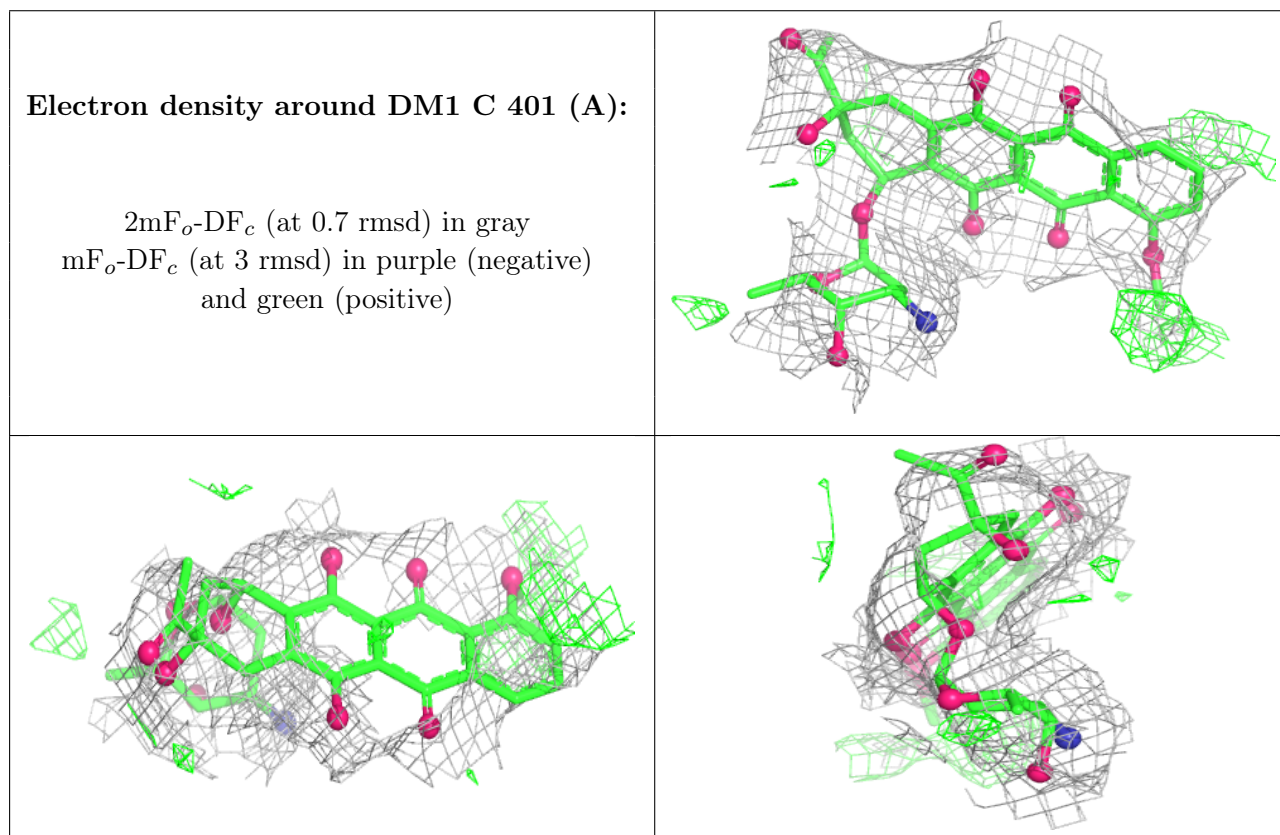
There are no oligosaccharides in this entry.

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.

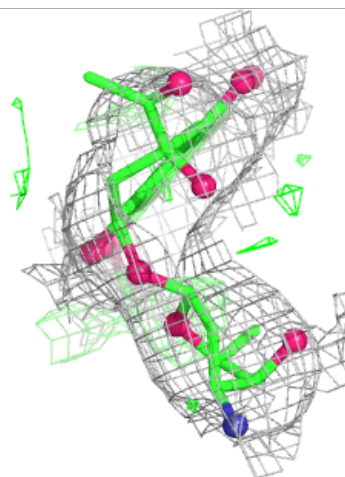
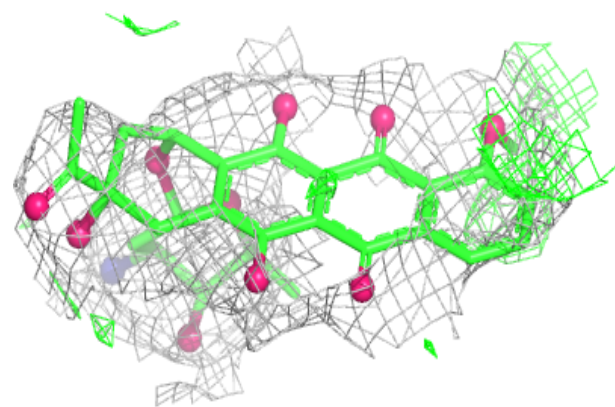
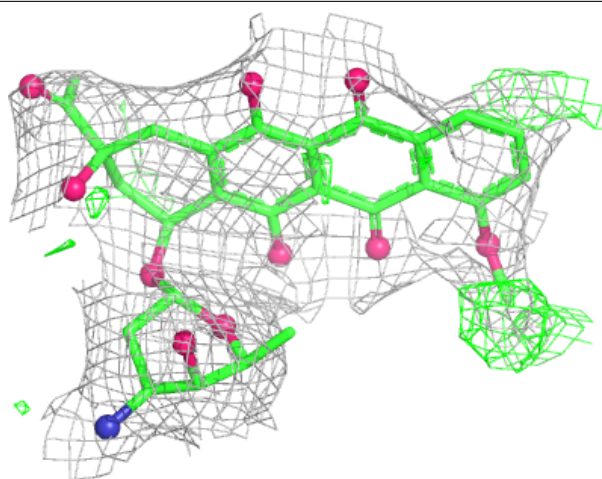
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	DM1	C	401[A]	38/38	0.75	0.22	119,122,124,125	10
2	DM1	C	401[B]	38/38	0.75	0.22	119,122,124,125	10

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.



Electron density around DM1 C 401 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.