Full wwPDB X-ray Structure Validation Report (i)

Aug 21, 2023 – 07:24 PM EDT

PDB ID	:	2QCT
Title	:	Structure of Lyp with inhibitor I-C11
Authors	:	Yu, X.; Sun, J.P.; Zhang, Z.Y.
Deposited on	:	2007-06-19
Resolution	:	2.80 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 (i) 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 (i)) were used in the production of this report:

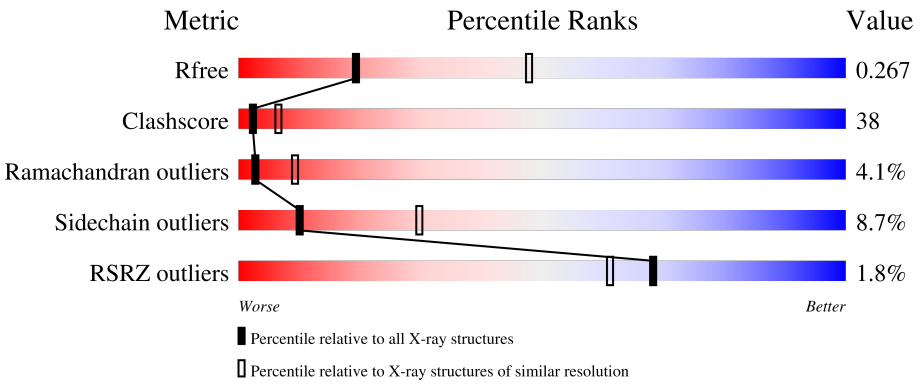
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 2.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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 <=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	313	2% 35% 48% 7% 10%
1	B	313	% 38% 47% 6% • 9%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	561	A	295	-	-	-	X

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4666 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 Tyrosine-protein phosphatase non-receptor type 22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	282	2300	1479	376	429	16	1	0	0
1	B	285	2300	1480	377	427	16	1	0	0

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	HIS	-	expression tag	UNP Q9Y2R2
A	-17	HIS	-	expression tag	UNP Q9Y2R2
A	-16	HIS	-	expression tag	UNP Q9Y2R2
A	-15	HIS	-	expression tag	UNP Q9Y2R2
A	-14	HIS	-	expression tag	UNP Q9Y2R2
A	-13	HIS	-	expression tag	UNP Q9Y2R2
A	-12	SER	-	expression tag	UNP Q9Y2R2
A	-11	SER	-	expression tag	UNP Q9Y2R2
A	-10	GLY	-	expression tag	UNP Q9Y2R2
A	-9	LEU	-	expression tag	UNP Q9Y2R2
A	-8	VAL	-	expression tag	UNP Q9Y2R2
A	-7	PRO	-	expression tag	UNP Q9Y2R2
A	-6	ARG	-	expression tag	UNP Q9Y2R2
A	-5	GLY	-	expression tag	UNP Q9Y2R2
A	-4	SER	-	expression tag	UNP Q9Y2R2
A	-3	HIS	-	expression tag	UNP Q9Y2R2
A	-2	MET	-	expression tag	UNP Q9Y2R2
A	-1	ALA	-	expression tag	UNP Q9Y2R2
A	0	SER	-	expression tag	UNP Q9Y2R2
B	-18	HIS	-	expression tag	UNP Q9Y2R2
B	-17	HIS	-	expression tag	UNP Q9Y2R2
B	-16	HIS	-	expression tag	UNP Q9Y2R2
B	-15	HIS	-	expression tag	UNP Q9Y2R2
B	-14	HIS	-	expression tag	UNP Q9Y2R2
B	-13	HIS	-	expression tag	UNP Q9Y2R2

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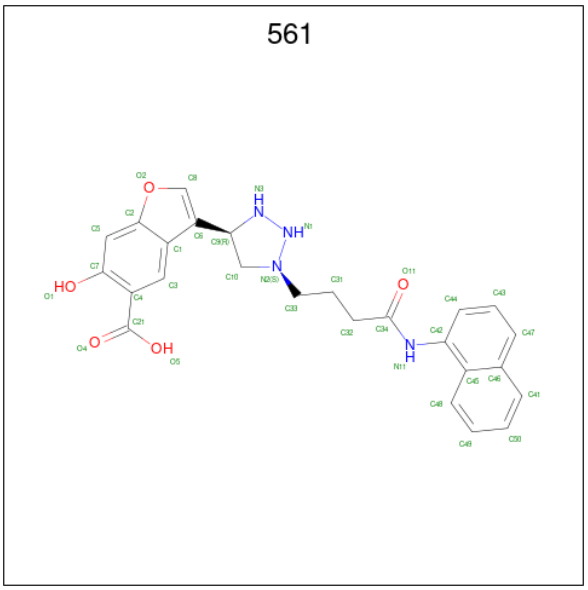
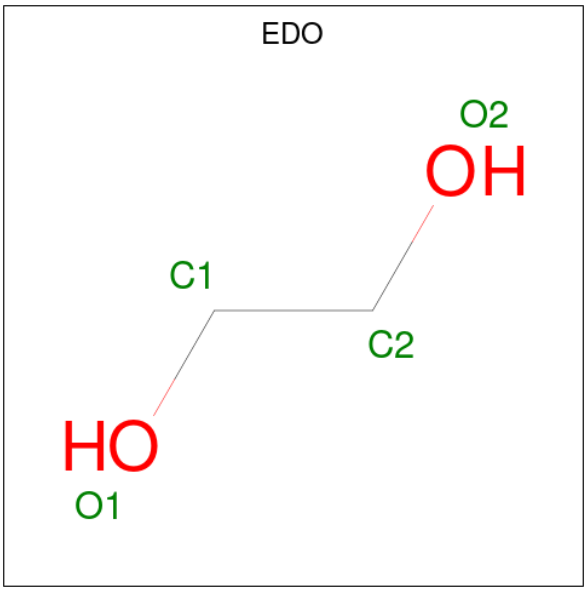
Chain	Residue	Modelled	Actual	Comment	Reference
B	-12	SER	-	expression tag	UNP Q9Y2R2
B	-11	SER	-	expression tag	UNP Q9Y2R2
B	-10	GLY	-	expression tag	UNP Q9Y2R2
B	-9	LEU	-	expression tag	UNP Q9Y2R2
B	-8	VAL	-	expression tag	UNP Q9Y2R2
B	-7	PRO	-	expression tag	UNP Q9Y2R2
B	-6	ARG	-	expression tag	UNP Q9Y2R2
B	-5	GLY	-	expression tag	UNP Q9Y2R2
B	-4	SER	-	expression tag	UNP Q9Y2R2
B	-3	HIS	-	expression tag	UNP Q9Y2R2
B	-2	MET	-	expression tag	UNP Q9Y2R2
B	-1	ALA	-	expression tag	UNP Q9Y2R2
B	0	SER	-	expression tag	UNP Q9Y2R2

- Molecule 2 is 6-HYDROXY-3-{(4R)-1-[4-(1-NAPHTHYLAMINO)-4-OXOBUTYL]-1,2,3-TRIAZOLIDIN-4-YL}-1-BENZOFURAN-5-CARBOXYLIC ACID (three-letter code: 561) (formula: $C_{25}H_{24}N_4O_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	34	25	4	5	0	0

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	4	2	2	0	0
			Total	C	O		
3	B	1	4	2	2	0	0

- Molecule 4 is water.

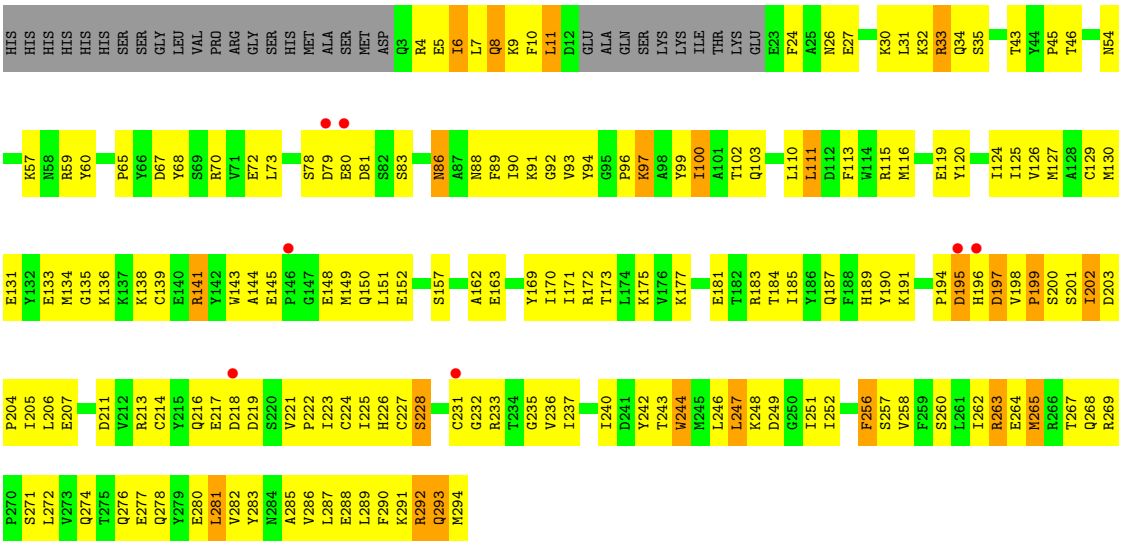
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	11	11	11	0	0
			Total	O		
4	B	13	13	13	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

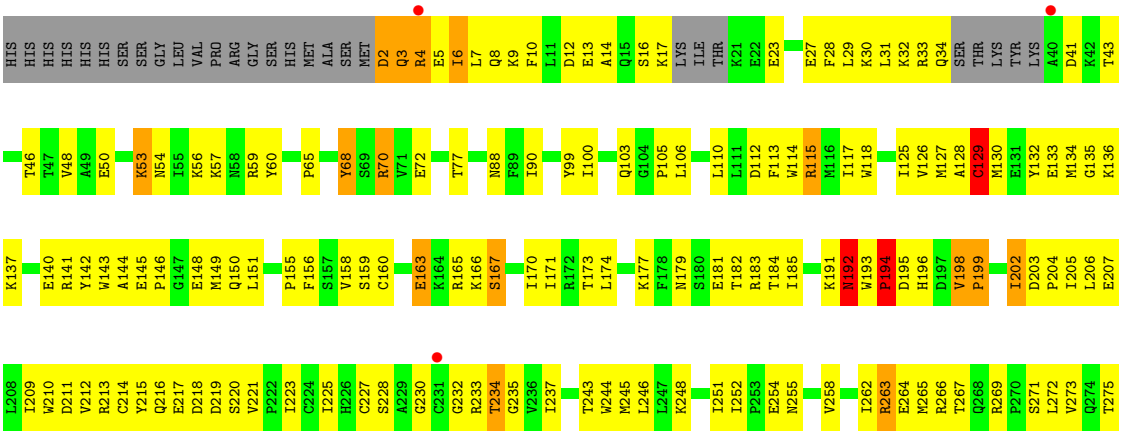
• Molecule 1: Tyrosine-protein phosphatase non-receptor type 22

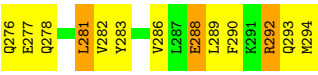
Chain A: 2% 35% 48% 7% 10%



• Molecule 1: Tyrosine-protein phosphatase non-receptor type 22

Chain B: % 38% 47% 6% • 9%




Q276
E277
Q278
L281
V282
Y283
V286
L287
E288
L289
F290
K291
R292
Q293
M294

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	44.90Å 147.94Å 46.16Å 90.00° 98.04° 90.00°	Depositor
Resolution (Å)	50.00 – 2.80 44.46 – 2.69	Depositor EDS
% Data completeness (in resolution range)	94.6 (50.00-2.80) 91.3 (44.46-2.69)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.09	Depositor
$< I/\sigma(I) >$ [1]	3.18 (at 2.69Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.245 , 0.275 0.239 , 0.267	Depositor DCC
R_{free} test set	1112 reflections (7.10%)	wwPDB-VP
Wilson B-factor (Å^2)	53.8	Xtriage
Anisotropy	0.266	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 60.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.049 for l,-k,h	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	4666	wwPDB-VP
Average B, all atoms (Å^2)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.97% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 561, EDO

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	0.44	0/2355	0.71	0/3187
1	B	0.46	0/2354	0.72	1/3186 (0.0%)
All	All	0.45	0/4709	0.71	1/6373 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	3	GLN	N-CA-C	5.34	125.41	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2300	0	2241	177	0
1	B	2300	0	2224	175	0
2	A	34	0	19	0	0
3	A	4	0	6	0	0
3	B	4	0	6	0	0
4	A	11	0	0	1	0
4	B	13	0	0	0	0
All	All	4666	0	4496	349	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 38.

All (349) 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:90:ILE:HB	1:A:99:TYR:HB2	1.33	1.10
1:A:196:HIS:HA	1:A:281:LEU:HD23	1.43	1.01
1:A:5:GLU:CG	1:A:8:GLN:HA	1.91	1.00
1:A:5:GLU:HG2	1:A:8:GLN:HA	1.46	0.97
1:B:4:ARG:C	1:B:6:ILE:H	1.67	0.95
1:B:77:THR:HB	1:B:155:PRO:HG3	1.48	0.92
1:A:202:ILE:HD13	1:A:203:ASP:H	1.35	0.91
1:A:141:ARG:HG3	1:A:141:ARG:HH11	1.35	0.90
1:B:198:VAL:HB	1:B:199:PRO:HD3	1.56	0.87
1:B:202:ILE:HD13	1:B:202:ILE:H	1.37	0.86
1:A:46:THR:HG22	1:A:65:PRO:O	1.76	0.86
1:A:9:LYS:HD3	1:A:11:LEU:HD12	1.57	0.85
1:A:5:GLU:CD	1:A:8:GLN:HA	1.98	0.83
1:A:134:MET:HA	1:B:149:MET:SD	2.19	0.83
1:A:217:GLU:HG3	1:A:218:ASP:H	1.45	0.82
1:B:213:ARG:HH11	1:B:217:GLU:HA	1.47	0.79
1:B:262:ILE:HG22	1:B:266:ARG:HD2	1.63	0.78
1:A:135:GLY:HA2	1:B:151:LEU:HA	1.67	0.77
1:A:206:LEU:HD12	1:A:289:LEU:HD21	1.65	0.77
1:A:278:GLN:O	1:A:282:VAL:HG23	1.86	0.76
1:A:285:ALA:O	1:A:289:LEU:HG	1.87	0.75
1:B:59:ARG:HH12	1:B:106:LEU:HD23	1.52	0.75
1:A:141:ARG:HG3	1:A:141:ARG:NH1	2.01	0.75
1:A:91:LYS:H	1:A:268:GLN:NE2	1.84	0.74
1:A:246:LEU:HB3	1:A:252:ILE:HD13	1.70	0.74
1:A:205:ILE:HG22	1:A:206:LEU:HD22	1.71	0.73
1:B:4:ARG:C	1:B:6:ILE:N	2.41	0.72
1:A:204:PRO:O	1:A:207:GLU:HB2	1.91	0.71
1:B:235:GLY:HA3	1:B:272:LEU:O	1.90	0.71
1:B:117:ILE:HG12	1:B:125:ILE:HD11	1.73	0.70
1:B:227:CYS:SG	1:B:234:THR:HG23	2.31	0.70
1:A:235:GLY:HA3	1:A:272:LEU:O	1.90	0.70
1:B:23:GLU:O	1:B:27:GLU:HB2	1.92	0.70
1:A:5:GLU:HG2	1:A:8:GLN:CA	2.20	0.69
1:A:199:PRO:O	1:A:202:ILE:HD12	1.93	0.69
1:A:244:TRP:HE1	1:A:248:LYS:HZ3	1.39	0.69
1:A:135:GLY:O	1:A:136:LYS:HD2	1.93	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:244:TRP:CZ3	1:B:289:LEU:HD22	2.28	0.69
1:B:243:THR:HG21	1:B:286:VAL:HG13	1.75	0.68
1:B:105:PRO:O	1:B:140:GLU:HB3	1.93	0.68
1:A:197:ASP:C	1:A:199:PRO:HD3	2.14	0.68
1:B:258:VAL:HG21	1:B:283:TYR:HD1	1.58	0.68
1:A:100:ILE:HG12	1:A:222:PRO:HB2	1.75	0.68
1:B:88:ASN:ND2	1:B:269:ARG:HH21	1.91	0.68
1:A:244:TRP:HB2	1:A:289:LEU:HD13	1.75	0.68
1:A:162:ALA:O	1:A:173:THR:HG22	1.94	0.68
1:B:227:CYS:SG	1:B:234:THR:CG2	2.83	0.67
1:B:230:GLY:HA2	1:B:234:THR:HG21	1.77	0.67
1:B:130:MET:HB2	1:B:133:GLU:HG3	1.76	0.66
1:A:89:PHE:CE2	1:A:97:LYS:HG3	2.31	0.66
1:B:293:GLN:O	1:B:294:MET:HG2	1.94	0.66
1:B:59:ARG:NH1	1:B:106:LEU:HD23	2.11	0.66
1:B:3:GLN:HA	1:B:6:ILE:HA	1.78	0.65
1:A:67:ASP:O	1:A:70:ARG:HG2	1.96	0.65
1:A:276:GLN:O	1:A:280:GLU:HG3	1.96	0.65
1:A:91:LYS:H	1:A:268:GLN:HE22	1.45	0.64
1:B:126:VAL:HB	1:B:225:ILE:HG12	1.80	0.64
1:B:251:ILE:HG13	1:B:251:ILE:O	1.98	0.64
1:A:287:LEU:HD11	1:A:291:LYS:HE3	1.79	0.63
1:A:282:VAL:O	1:A:286:VAL:HG23	1.99	0.63
1:A:247:LEU:CD2	1:A:293:GLN:HG3	2.29	0.63
1:A:223:ILE:HG22	1:A:225:ILE:HG13	1.80	0.62
1:B:266:ARG:CZ	1:B:271:SER:HA	2.29	0.62
1:A:127:MET:HG3	1:A:226:HIS:CE1	2.34	0.62
1:B:163:GLU:OE2	1:B:165:ARG:NH1	2.32	0.62
1:A:202:ILE:CD1	1:A:203:ASP:H	2.10	0.62
1:B:5:GLU:HG3	1:B:5:GLU:O	1.99	0.62
1:B:77:THR:HG21	1:B:156:PHE:HE1	1.65	0.61
1:A:258:VAL:O	1:A:262:ILE:HG12	2.01	0.61
1:A:65:PRO:HD3	1:A:86:ASN:OD1	2.01	0.61
1:A:206:LEU:CD1	1:A:289:LEU:HD21	2.29	0.61
1:B:3:GLN:HB2	1:B:254:GLU:OE2	2.01	0.61
1:B:127:MET:HE2	1:B:129:CYS:O	2.00	0.61
1:B:209:ILE:HD11	1:B:237:ILE:HG23	1.82	0.61
1:A:119:GLU:HG2	1:A:119:GLU:O	2.00	0.61
1:A:6:ILE:O	1:A:6:ILE:HG12	2.00	0.60
1:A:197:ASP:O	1:A:199:PRO:HD3	2.02	0.60
1:A:91:LYS:HG3	1:A:268:GLN:NE2	2.17	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:245:MET:HA	1:B:248:LYS:HE3	1.83	0.60
1:B:118:TRP:CH2	1:B:183:ARG:HD3	2.37	0.60
1:A:33:ARG:O	1:A:34:GLN:HB2	2.00	0.60
1:B:65:PRO:HA	1:B:88:ASN:HD21	1.67	0.60
1:B:90:ILE:HB	1:B:99:TYR:HB2	1.85	0.59
1:B:128:ALA:O	1:B:129:CYS:HB3	2.01	0.59
1:A:243:THR:HG21	1:A:286:VAL:HG13	1.85	0.59
1:A:206:LEU:HD22	1:A:206:LEU:H	1.67	0.59
1:A:202:ILE:HD13	1:A:203:ASP:N	2.14	0.58
1:B:193:TRP:CG	1:B:194:PRO:HD2	2.37	0.58
1:B:112:ASP:HA	1:B:115:ARG:HH11	1.68	0.58
1:A:27:GLU:O	1:A:30:LYS:HB2	2.03	0.58
1:A:247:LEU:HD21	1:A:293:GLN:HG3	1.84	0.58
1:B:31:LEU:C	1:B:33:ARG:H	2.07	0.58
1:A:111:LEU:HD12	1:A:111:LEU:O	2.03	0.58
1:B:213:ARG:HG3	1:B:248:LYS:NZ	2.19	0.58
1:B:243:THR:HG21	1:B:286:VAL:CG1	2.33	0.58
1:B:191:LYS:O	1:B:192:ASN:HB2	2.04	0.57
1:B:258:VAL:HG21	1:B:283:TYR:CD1	2.38	0.57
1:B:217:GLU:C	1:B:219:ASP:N	2.57	0.57
1:B:2:ASP:CG	1:B:2:ASP:O	2.41	0.57
1:A:125:ILE:HD12	1:A:185:ILE:HG21	1.87	0.57
1:B:46:THR:O	1:B:50:GLU:HG3	2.04	0.57
1:B:220:SER:O	1:B:221:VAL:HG23	2.04	0.57
1:B:264:GLU:O	1:B:267:THR:HB	2.04	0.57
1:A:102:THR:HG22	1:A:103:GLN:N	2.19	0.57
1:A:130:MET:HB2	1:A:133:GLU:HG3	1.87	0.56
1:B:202:ILE:H	1:B:202:ILE:CD1	2.14	0.56
1:A:151:LEU:N	1:A:151:LEU:HD12	2.20	0.56
1:B:12:ASP:C	1:B:14:ALA:H	2.09	0.56
1:B:210:TRP:CZ3	1:B:214:CYS:SG	2.98	0.56
1:B:144:ALA:O	1:B:160:CYS:HB2	2.05	0.56
1:B:181:GLU:OE2	1:B:183:ARG:HD2	2.06	0.56
1:B:193:TRP:CE2	1:B:233:ARG:HG2	2.41	0.56
1:B:31:LEU:C	1:B:33:ARG:N	2.59	0.56
1:A:5:GLU:OE2	1:A:9:LYS:N	2.38	0.55
1:A:246:LEU:CB	1:A:252:ILE:HD13	2.35	0.55
1:B:246:LEU:HB2	1:B:252:ILE:HD13	1.88	0.55
1:A:288:GLU:O	1:A:292:ARG:HG3	2.07	0.55
1:B:196:HIS:HB2	1:B:199:PRO:CD	2.37	0.55
1:A:244:TRP:O	1:A:248:LYS:HG3	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3:GLN:CB	1:B:254:GLU:OE2	2.55	0.55
1:A:249:ASP:C	1:A:251:ILE:H	2.10	0.55
1:B:88:ASN:HD22	1:B:269:ARG:HE	1.55	0.55
1:A:129:CYS:O	1:A:189:HIS:NE2	2.36	0.55
1:B:100:ILE:HG22	1:B:100:ILE:O	2.06	0.55
1:A:247:LEU:HD23	1:A:247:LEU:O	2.07	0.54
1:A:293:GLN:O	1:A:294:MET:C	2.45	0.54
1:B:225:ILE:HG22	1:B:234:THR:HB	1.88	0.54
1:B:68:TYR:OH	1:B:267:THR:HG22	2.07	0.54
1:B:149:MET:HG2	1:B:150:GLN:H	1.73	0.54
1:B:246:LEU:CB	1:B:252:ILE:HD13	2.38	0.54
1:A:203:ASP:HA	1:A:206:LEU:HD23	1.90	0.54
1:B:255:ASN:OD1	1:B:255:ASN:O	2.26	0.54
1:B:275:THR:HG22	1:B:276:GLN:N	2.23	0.54
1:B:16:SER:O	1:B:17:LYS:HB3	2.08	0.54
1:A:196:HIS:HA	1:A:281:LEU:CD2	2.26	0.53
1:A:59:ARG:HG2	1:A:60:TYR:CE1	2.43	0.53
1:B:88:ASN:HD22	1:B:269:ARG:HH21	1.55	0.53
1:A:110:LEU:O	1:A:113:PHE:HB3	2.08	0.53
1:B:110:LEU:O	1:B:113:PHE:HB3	2.09	0.53
1:A:34:GLN:CD	1:A:263:ARG:HH11	2.12	0.53
1:A:92:GLY:O	1:A:242:TYR:HE1	1.90	0.53
1:B:212:VAL:HG23	1:B:213:ARG:N	2.24	0.53
1:A:243:THR:HG21	1:A:286:VAL:CG1	2.38	0.53
1:A:93:VAL:HG12	1:A:94:TYR:CD2	2.44	0.53
1:A:157:SER:HB2	1:A:177:LYS:HB3	1.89	0.53
1:A:287:LEU:CD1	1:A:291:LYS:HE3	2.39	0.52
1:B:246:LEU:HB2	1:B:252:ILE:CD1	2.39	0.52
1:B:30:LYS:O	1:B:33:ARG:HB2	2.08	0.52
1:B:59:ARG:HG3	1:B:59:ARG:HH11	1.74	0.52
1:A:190:TYR:OH	1:A:194:PRO:HD3	2.09	0.52
1:B:59:ARG:NH1	1:B:106:LEU:CD2	2.72	0.52
1:B:88:ASN:HD22	1:B:269:ARG:NH2	2.07	0.52
1:A:89:PHE:CD2	1:A:97:LYS:HA	2.44	0.52
1:A:169:TYR:HB3	1:A:190:TYR:HD1	1.73	0.52
1:B:59:ARG:NH1	1:B:59:ARG:HG3	2.25	0.52
1:A:91:LYS:HA	1:A:96:PRO:HA	1.92	0.52
1:B:14:ALA:O	1:B:17:LYS:HG2	2.10	0.51
1:A:141:ARG:CD	1:A:143:TRP:CE2	2.94	0.51
1:A:264:GLU:O	1:A:267:THR:HB	2.09	0.51
1:B:217:GLU:C	1:B:219:ASP:H	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:ASN:ND2	1:A:269:ARG:HG3	2.24	0.51
1:B:88:ASN:HD22	1:B:269:ARG:NE	2.08	0.51
1:B:195:ASP:CG	1:B:196:HIS:HD2	2.14	0.51
1:A:172:ARG:HB2	1:A:187:GLN:HB3	1.93	0.51
1:A:231:CYS:HB3	1:A:271:SER:O	2.09	0.51
1:B:70:ARG:CZ	1:B:72:GLU:HG2	2.41	0.51
1:B:262:ILE:O	1:B:266:ARG:HG3	2.11	0.51
1:A:102:THR:O	1:A:226:HIS:HB2	2.10	0.51
1:A:102:THR:HG22	1:A:103:GLN:O	2.11	0.51
1:B:31:LEU:O	1:B:33:ARG:N	2.44	0.51
1:B:130:MET:HB2	1:B:133:GLU:CG	2.40	0.51
1:A:5:GLU:CG	1:A:8:GLN:CA	2.78	0.51
1:A:86:ASN:O	1:A:102:THR:HG23	2.11	0.51
1:B:198:VAL:HB	1:B:199:PRO:CD	2.36	0.51
1:A:102:THR:CG2	1:A:103:GLN:N	2.73	0.51
1:A:194:PRO:CB	1:A:201:SER:O	2.59	0.51
1:A:244:TRP:CD1	1:A:248:LYS:HE2	2.46	0.50
1:B:216:GLN:OE1	1:B:221:VAL:O	2.28	0.50
1:B:263:ARG:NH1	1:B:263:ARG:HG3	2.26	0.50
1:B:181:GLU:OE2	1:B:183:ARG:CD	2.59	0.50
1:B:244:TRP:CE3	1:B:289:LEU:HD13	2.46	0.50
1:A:70:ARG:NH2	1:A:83:SER:O	2.45	0.50
1:A:7:LEU:O	1:A:9:LYS:N	2.44	0.50
1:B:203:ASP:N	1:B:204:PRO:HD2	2.27	0.50
1:B:150:GLN:HG2	1:B:159:SER:HB3	1.93	0.49
1:B:263:ARG:HG3	1:B:263:ARG:HH11	1.77	0.49
1:A:141:ARG:HD2	1:A:143:TRP:CE2	2.48	0.49
1:B:266:ARG:NH2	1:B:271:SER:HA	2.28	0.49
1:B:54:ASN:O	1:B:57:LYS:HB2	2.12	0.49
1:A:129:CYS:SG	1:A:227:CYS:C	2.91	0.49
1:A:196:HIS:O	1:A:198:VAL:N	2.46	0.49
1:A:33:ARG:O	1:A:35:SER:N	2.45	0.49
1:A:202:ILE:CG1	1:A:203:ASP:N	2.75	0.49
1:B:275:THR:HG22	1:B:277:GLU:H	1.78	0.49
1:A:9:LYS:CD	1:A:11:LEU:HD12	2.35	0.49
1:A:269:ARG:HB3	1:A:272:LEU:HG	1.95	0.49
1:B:166:LYS:HE2	1:B:211:ASP:OD2	2.13	0.49
1:B:217:GLU:O	1:B:219:ASP:N	2.46	0.48
1:A:4:ARG:O	1:A:6:ILE:HG22	2.13	0.48
1:B:276:GLN:HA	1:B:276:GLN:HE21	1.78	0.48
1:A:244:TRP:NE1	1:A:248:LYS:NZ	2.62	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:213:ARG:HA	1:B:213:ARG:HD3	1.64	0.48
1:B:275:THR:CG2	1:B:276:GLN:N	2.77	0.48
1:A:24:PHE:HD1	1:A:280:GLU:HG2	1.79	0.48
1:B:112:ASP:O	1:B:115:ARG:HG2	2.13	0.48
1:B:293:GLN:O	1:B:294:MET:CB	2.62	0.48
1:B:193:TRP:CD2	1:B:194:PRO:HD2	2.49	0.48
1:A:6:ILE:O	1:A:6:ILE:CG1	2.62	0.48
1:A:145:GLU:HB2	1:A:148:GLU:OE2	2.13	0.48
1:A:217:GLU:HG3	1:A:218:ASP:N	2.21	0.48
1:A:231:CYS:SG	1:A:269:ARG:NH1	2.87	0.48
1:B:30:LYS:O	1:B:33:ARG:HD3	2.14	0.48
1:A:78:SER:OG	1:A:80:GLU:HG2	2.13	0.47
1:A:111:LEU:HD12	1:A:115:ARG:HG3	1.96	0.47
1:B:265:MET:HB3	1:B:272:LEU:HD12	1.94	0.47
1:A:10:PHE:CD1	1:A:290:PHE:CE1	3.03	0.47
1:A:163:GLU:OE1	1:A:170:ILE:HG21	2.14	0.47
1:B:181:GLU:HG2	1:B:182:THR:N	2.30	0.47
1:A:59:ARG:HG2	1:A:60:TYR:CD1	2.50	0.47
1:B:216:GLN:OE1	1:B:223:ILE:HG13	2.15	0.47
1:B:232:GLY:HA2	1:B:278:GLN:HE22	1.79	0.47
1:B:262:ILE:HD12	1:B:262:ILE:N	2.30	0.47
1:B:145:GLU:O	1:B:148:GLU:HB3	2.15	0.47
1:B:145:GLU:HB3	1:B:146:PRO:HD2	1.97	0.47
1:B:282:VAL:O	1:B:286:VAL:HG23	2.14	0.47
1:B:202:ILE:O	1:B:205:ILE:HG22	2.15	0.47
1:A:4:ARG:O	1:A:4:ARG:CG	2.63	0.47
1:A:100:ILE:HG13	1:A:224:CYS:HA	1.97	0.47
1:B:141:ARG:HG3	1:B:143:TRP:CE2	2.50	0.47
1:A:196:HIS:C	1:A:198:VAL:H	2.18	0.46
1:A:227:CYS:SG	1:A:228:SER:N	2.88	0.46
1:A:265:MET:O	1:A:272:LEU:HD12	2.15	0.46
1:B:29:LEU:C	1:B:29:LEU:HD13	2.35	0.46
1:B:65:PRO:CA	1:B:88:ASN:HD21	2.29	0.46
1:B:141:ARG:NH1	1:B:145:GLU:HG3	2.31	0.46
1:A:249:ASP:C	1:A:251:ILE:N	2.68	0.46
1:A:144:ALA:HB2	1:A:151:LEU:HD13	1.98	0.46
1:B:204:PRO:HA	1:B:207:GLU:CD	2.35	0.46
1:A:202:ILE:HG12	1:A:203:ASP:N	2.30	0.46
1:A:206:LEU:HD22	1:A:206:LEU:N	2.30	0.46
1:A:258:VAL:HG21	1:A:283:TYR:HD1	1.81	0.46
1:B:48:VAL:HG21	1:B:70:ARG:NH1	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:175:LYS:HE3	1:A:184:THR:OG1	2.16	0.46
1:B:204:PRO:HA	1:B:207:GLU:OE2	2.15	0.46
1:B:12:ASP:C	1:B:14:ALA:N	2.70	0.46
1:B:132:TYR:CE1	1:B:137:LYS:HB2	2.51	0.46
1:A:247:LEU:N	1:A:252:ILE:HD11	2.31	0.45
1:B:185:ILE:HD12	1:B:185:ILE:N	2.31	0.45
1:A:130:MET:O	1:A:131:GLU:C	2.53	0.45
1:A:163:GLU:HA	1:A:171:ILE:O	2.17	0.45
1:A:247:LEU:CA	1:A:252:ILE:HD11	2.47	0.45
1:A:281:LEU:HD13	1:A:281:LEU:O	2.17	0.45
1:B:196:HIS:C	1:B:198:VAL:H	2.19	0.45
1:A:126:VAL:HB	1:A:225:ILE:HG12	1.99	0.45
1:B:277:GLU:OE2	1:B:277:GLU:N	2.49	0.45
1:B:293:GLN:O	1:B:294:MET:CG	2.63	0.45
1:A:244:TRP:NE1	1:A:248:LYS:HE2	2.32	0.45
1:B:133:GLU:HB3	1:B:134:MET:CE	2.47	0.45
1:B:262:ILE:CG2	1:B:266:ARG:HD2	2.41	0.45
1:B:88:ASN:ND2	1:B:269:ARG:HE	2.15	0.45
1:B:163:GLU:HA	1:B:171:ILE:O	2.17	0.44
1:A:43:THR:O	1:A:45:PRO:HD3	2.17	0.44
1:B:276:GLN:HA	1:B:276:GLN:NE2	2.33	0.44
1:A:73:LEU:HD21	1:A:116:MET:HB2	2.00	0.44
1:B:28:PHE:O	1:B:31:LEU:HB2	2.17	0.44
1:A:26:ASN:HB3	4:A:305:HOH:O	2.17	0.44
1:A:151:LEU:HA	1:B:135:GLY:HA2	1.98	0.44
1:A:272:LEU:HD23	1:A:272:LEU:HA	1.79	0.44
1:B:110:LEU:CD2	1:B:142:TYR:HB3	2.47	0.44
1:A:141:ARG:HD3	1:A:143:TRP:CE2	2.52	0.44
1:B:181:GLU:HG2	1:B:182:THR:H	1.81	0.44
1:B:272:LEU:HD23	1:B:272:LEU:HA	1.77	0.44
1:B:288:GLU:O	1:B:292:ARG:HB2	2.16	0.44
1:A:32:LYS:C	1:A:33:ARG:O	2.52	0.44
1:A:173:THR:HG23	1:A:173:THR:O	2.18	0.44
1:B:7:LEU:O	1:B:9:LYS:N	2.51	0.44
1:B:174:LEU:O	1:B:184:THR:HA	2.18	0.44
1:B:177:LYS:HG2	1:B:181:GLU:O	2.17	0.44
1:A:202:ILE:CD1	1:A:203:ASP:N	2.76	0.44
1:B:59:ARG:HD3	1:B:228:SER:O	2.17	0.44
1:A:93:VAL:HG12	1:A:94:TYR:CE2	2.53	0.43
1:B:90:ILE:HD12	1:B:272:LEU:HD11	2.00	0.43
1:A:205:ILE:CG2	1:A:206:LEU:N	2.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:202:ILE:HG22	1:B:281:LEU:HD11	1.98	0.43
1:A:292:ARG:O	1:A:294:MET:N	2.51	0.43
1:A:124:ILE:HD12	1:A:216:GLN:HB3	2.01	0.43
1:A:194:PRO:HB3	1:A:201:SER:O	2.18	0.43
1:A:256:PHE:CG	1:A:257:SER:N	2.86	0.43
1:A:260:SER:O	1:A:263:ARG:HB3	2.19	0.43
1:A:100:ILE:HG13	1:A:223:ILE:O	2.18	0.43
1:A:145:GLU:O	1:A:148:GLU:HB2	2.19	0.43
1:A:213:ARG:HD3	1:A:213:ARG:HA	1.81	0.43
1:B:59:ARG:O	1:B:60:TYR:CD2	2.72	0.42
1:B:165:ARG:CZ	1:B:170:ILE:HD13	2.49	0.42
1:A:293:GLN:HB3	1:A:294:MET:H	1.67	0.42
1:B:196:HIS:HB2	1:B:199:PRO:HD3	2.00	0.42
1:B:53:LYS:O	1:B:54:ASN:OD1	2.37	0.42
1:B:114:TRP:CE2	1:B:158:VAL:HG21	2.54	0.42
1:A:54:ASN:OD1	1:A:57:LYS:HD2	2.19	0.42
1:A:26:ASN:HD22	1:A:26:ASN:HA	1.68	0.42
1:A:233:ARG:O	1:A:237:ILE:HD12	2.19	0.42
1:A:236:VAL:HG12	1:A:240:ILE:HD12	2.02	0.42
1:B:10:PHE:HB3	1:B:290:PHE:HD1	1.84	0.42
1:B:216:GLN:HG3	1:B:219:ASP:HB3	2.01	0.42
1:B:230:GLY:HA2	1:B:234:THR:CG2	2.48	0.42
1:A:274:GLN:H	1:A:278:GLN:HE22	1.66	0.42
1:A:247:LEU:HD22	1:A:293:GLN:HG3	1.98	0.42
1:A:81:ASP:OD2	1:A:115:ARG:HD2	2.20	0.42
1:A:202:ILE:HG22	1:A:281:LEU:HD21	2.00	0.42
1:A:177:LYS:HB2	1:A:177:LYS:NZ	2.35	0.42
1:A:219:ASP:CG	1:A:221:VAL:HG22	2.40	0.42
1:A:277:GLU:OE1	1:A:277:GLU:N	2.37	0.42
1:B:4:ARG:O	1:B:6:ILE:N	2.51	0.42
1:B:193:TRP:CZ2	1:B:233:ARG:HG2	2.54	0.42
1:B:213:ARG:HD2	1:B:217:GLU:HA	2.02	0.42
1:B:166:LYS:HB3	1:B:167:SER:H	1.65	0.41
1:B:213:ARG:HG3	1:B:248:LYS:HZ2	1.85	0.41
1:A:249:ASP:O	1:A:251:ILE:N	2.53	0.41
1:B:41:ASP:O	1:B:43:THR:N	2.45	0.41
1:B:88:ASN:HD22	1:B:269:ARG:CZ	2.33	0.41
1:A:9:LYS:HD3	1:A:11:LEU:CD1	2.41	0.41
1:A:11:LEU:H	1:A:11:LEU:HG	1.43	0.41
1:B:182:THR:O	1:B:183:ARG:HG3	2.21	0.41
1:B:33:ARG:O	1:B:34:GLN:C	2.58	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:141:ARG:HD3	1:B:143:TRP:O	2.21	0.41
1:A:59:ARG:NH1	1:A:138:LYS:O	2.53	0.41
1:A:91:LYS:HG3	1:A:268:GLN:HE21	1.83	0.41
1:A:92:GLY:C	1:A:242:TYR:HE1	2.23	0.41
1:B:196:HIS:HB2	1:B:199:PRO:HD2	2.01	0.41
1:A:149:MET:HG2	1:A:150:GLN:N	2.35	0.41
1:B:65:PRO:CB	1:B:88:ASN:HD21	2.33	0.41
1:B:125:ILE:HD12	1:B:185:ILE:HG21	2.02	0.41
1:B:213:ARG:HH11	1:B:217:GLU:CA	2.23	0.41
1:A:31:LEU:O	1:A:33:ARG:O	2.38	0.41
1:A:72:GLU:H	1:A:72:GLU:HG2	1.69	0.41
1:A:198:VAL:O	1:A:200:SER:N	2.53	0.41
1:B:133:GLU:HB3	1:B:134:MET:HE3	2.02	0.41
1:B:209:ILE:CD1	1:B:237:ILE:HG23	2.49	0.41
1:B:232:GLY:CA	1:B:278:GLN:HE22	2.34	0.41
1:A:34:GLN:CD	1:A:263:ARG:NH1	2.75	0.40
1:A:162:ALA:H	1:A:173:THR:CG2	2.34	0.40
1:B:135:GLY:O	1:B:136:LYS:HD2	2.21	0.40
1:A:89:PHE:HZ	1:A:120:TYR:CE2	2.39	0.40
1:A:94:TYR:CD2	1:A:94:TYR:N	2.88	0.40
1:B:53:LYS:HA	1:B:56:LYS:HZ1	1.86	0.40
1:A:10:PHE:HD1	1:A:290:PHE:CD1	2.39	0.40
1:A:204:PRO:HA	1:A:207:GLU:HB2	2.03	0.40
1:B:141:ARG:HA	1:B:143:TRP:CZ3	2.56	0.40
1:B:251:ILE:O	1:B:251:ILE:CG1	2.69	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	278/313 (89%)	238 (86%)	31 (11%)	9 (3%)	4 13

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	B	279/313 (89%)	228 (82%)	37 (13%)	14 (5%)	2 6
All	All	557/626 (89%)	466 (84%)	68 (12%)	23 (4%)	3 9

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	8	GLN
1	A	197	ASP
1	B	6	ILE
1	B	8	GLN
1	B	192	ASN
1	A	195	ASP
1	B	4	ARG
1	B	129	CYS
1	B	199	PRO
1	A	191	LYS
1	A	199	PRO
1	A	292	ARG
1	B	53	LYS
1	B	167	SER
1	B	273	VAL
1	A	33	ARG
1	B	32	LYS
1	B	194	PRO
1	B	198	VAL
1	A	256	PHE
1	B	179	ASN
1	B	218	ASP
1	A	232	GLY

5.3.2 Protein sidechains (i)

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	250/287 (87%)	226 (90%)	24 (10%)	8 24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	246/287 (86%)	227 (92%)	19 (8%)	13	35
All	All	496/574 (86%)	453 (91%)	43 (9%)	10	30

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	ILE
1	A	11	LEU
1	A	68	TYR
1	A	79	ASP
1	A	86	ASN
1	A	97	LYS
1	A	100	ILE
1	A	111	LEU
1	A	139	CYS
1	A	141	ARG
1	A	152	GLU
1	A	181	GLU
1	A	183	ARG
1	A	195	ASP
1	A	202	ILE
1	A	211	ASP
1	A	214	CYS
1	A	228	SER
1	A	244	TRP
1	A	247	LEU
1	A	263	ARG
1	A	265	MET
1	A	281	LEU
1	A	293	GLN
1	B	2	ASP
1	B	13	GLU
1	B	68	TYR
1	B	70	ARG
1	B	103	GLN
1	B	115	ARG
1	B	129	CYS
1	B	163	GLU
1	B	173	THR
1	B	192	ASN
1	B	194	PRO
1	B	202	ILE

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Mol	Chain	Res	Type
1	B	206	LEU
1	B	215	TYR
1	B	234	THR
1	B	263	ARG
1	B	281	LEU
1	B	288	GLU
1	B	292	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	26	ASN
1	A	88	ASN
1	A	150	GLN
1	A	268	GLN
1	A	278	GLN
1	B	88	ASN
1	B	192	ASN
1	B	196	HIS
1	B	255	ASN
1	B	276	GLN
1	B	278	GLN
1	B	284	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

3 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	EDO	A	301	-	3,3,3	0.52	0	2,2,2	0.18	0
3	EDO	B	302	-	3,3,3	0.64	0	2,2,2	0.18	0
2	561	A	295	-	29,38,38	6.77	17 (58%)	35,54,54	5.63	21 (60%)

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	EDO	A	301	-	-	0/1/1/1	-
3	EDO	B	302	-	-	0/1/1/1	-
2	561	A	295	-	-	7/14/27/27	0/5/5/5

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	295	561	C4-C7	20.28	1.72	1.40
2	A	295	561	C4-C21	-16.59	1.14	1.49
2	A	295	561	C6-C9	-13.61	1.28	1.52
2	A	295	561	O4-C21	9.89	1.51	1.22
2	A	295	561	C5-C2	9.69	1.56	1.37
2	A	295	561	C5-C7	7.32	1.44	1.37
2	A	295	561	C42-N11	7.13	1.59	1.41
2	A	295	561	C32-C34	-6.06	1.39	1.51
2	A	295	561	O1-C7	4.88	1.46	1.36
2	A	295	561	C3-C1	4.28	1.50	1.42
2	A	295	561	O5-C21	-4.28	1.17	1.30
2	A	295	561	C43-C44	3.80	1.46	1.38
2	A	295	561	C42-C45	2.84	1.49	1.43
2	A	295	561	C47-C46	2.83	1.48	1.41
2	A	295	561	C1-C2	2.55	1.49	1.43
2	A	295	561	C50-C49	2.45	1.44	1.38
2	A	295	561	C43-C47	2.25	1.41	1.36

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	295	561	C42-N11-C34	19.53	158.49	128.28
2	A	295	561	O5-C21-O4	-11.37	98.11	123.35
2	A	295	561	C3-C4-C7	10.55	127.07	118.58
2	A	295	561	C7-C4-C21	-9.11	110.33	120.03
2	A	295	561	C5-C7-C4	-8.65	113.75	120.13
2	A	295	561	C45-C42-N11	8.63	132.94	118.36
2	A	295	561	O1-C7-C4	6.03	132.80	121.70
2	A	295	561	C41-C46-C45	4.88	125.55	119.12
2	A	295	561	C44-C42-N11	-4.64	110.46	123.29
2	A	295	561	O4-C21-C4	4.63	133.18	121.94
2	A	295	561	O11-C34-N11	-4.58	115.28	123.63
2	A	295	561	O5-C21-C4	4.46	128.15	115.31
2	A	295	561	C42-C45-C46	4.11	124.02	118.34
2	A	295	561	O11-C34-C32	4.02	129.37	122.02
2	A	295	561	C48-C45-C46	-3.97	112.75	117.89
2	A	295	561	C4-C3-C1	-3.88	113.67	120.86
2	A	295	561	C33-C31-C32	-2.81	104.62	112.10
2	A	295	561	O1-C7-C5	-2.73	113.45	120.85
2	A	295	561	C47-C46-C41	-2.19	118.06	123.19
2	A	295	561	C47-C46-C45	-2.09	116.37	119.12
2	A	295	561	C49-C48-C45	2.04	123.72	120.89

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	295	561	C31-C33-N2-C10
2	A	295	561	C32-C34-N11-C42
2	A	295	561	C44-C42-N11-C34
2	A	295	561	C45-C42-N11-C34
2	A	295	561	O11-C34-N11-C42
2	A	295	561	C32-C31-C33-N2
2	A	295	561	O4-C21-C4-C7

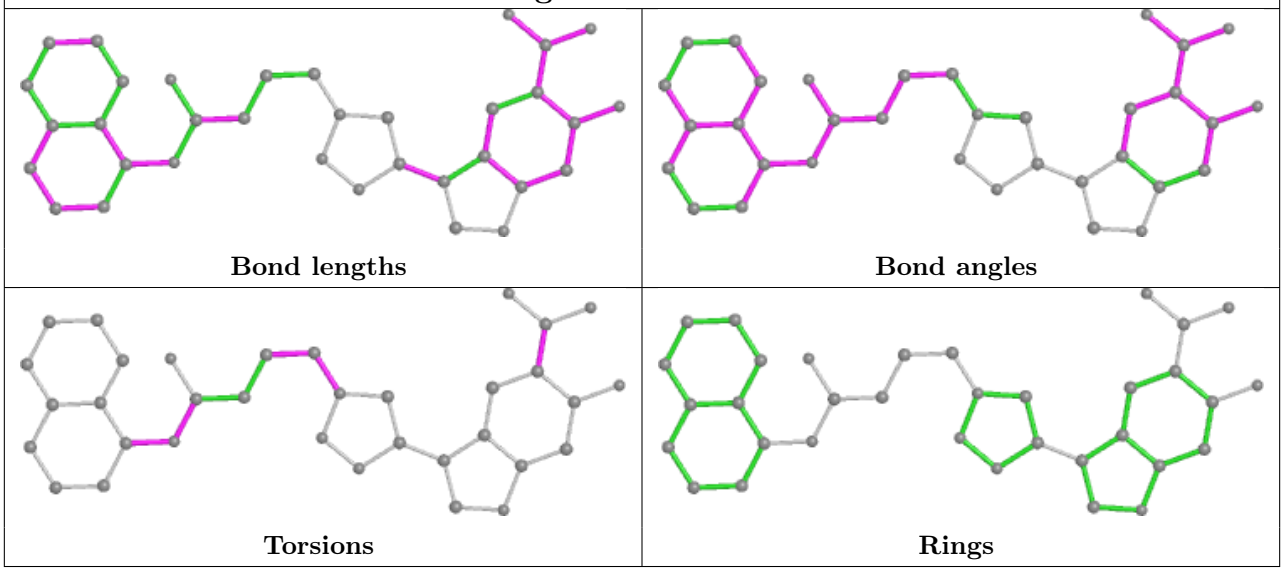
There are no ring outliers.

No monomer is involved in short contacts.

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 then 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.

Ligand 561 A 295



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 (i)

6.1 Protein, DNA and RNA chains (i)

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	282/313 (90%)	-0.06	7 (2%)	57	47	27, 51, 72, 98	1 (0%)
1	B	285/313 (91%)	-0.12	3 (1%)	80	75	26, 47, 75, 84	1 (0%)
All	All	567/626 (90%)	-0.09	10 (1%)	68	61	26, 50, 74, 98	2 (0%)

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	195	ASP	6.7
1	A	196	HIS	5.2
1	B	40	ALA	3.0
1	A	79	ASP	2.9
1	B	231	CYS	2.5
1	A	146	PRO	2.4
1	B	4	ARG	2.3
1	A	218	ASP	2.2
1	A	80	GLU	2.2
1	A	231	CYS	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 monosaccharides in this entry.

6.4 Ligands (i)

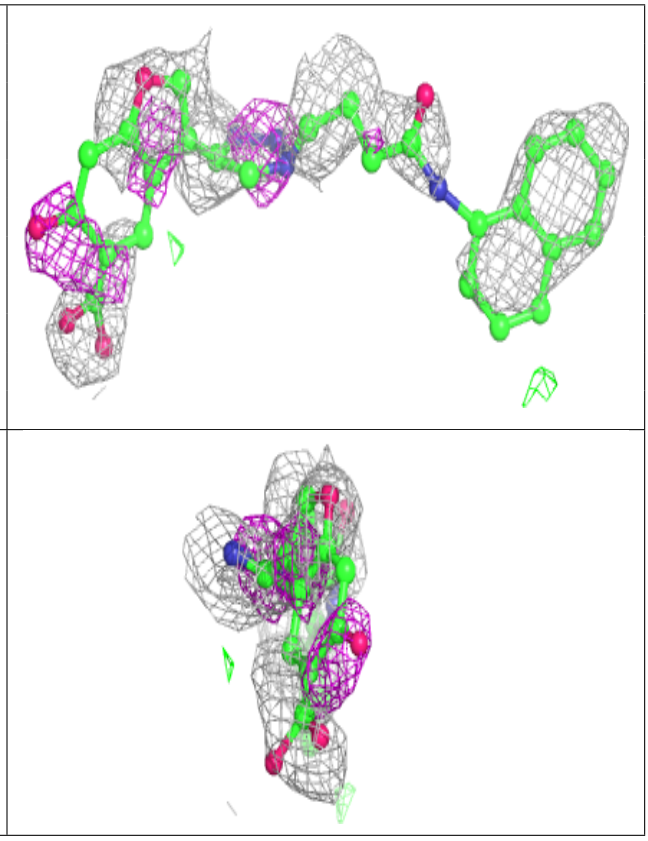
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	561	A	295	34/34	0.54	0.42	40,66,76,76	0
3	EDO	B	302	4/4	0.81	0.18	46,48,48,51	0
3	EDO	A	301	4/4	0.90	0.20	46,46,47,48	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.

Electron density around 561 A 295:

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.