



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 26, 2023 – 04:07 AM EDT

PDB ID : 3E6E  
Title : Crystal structure of Alanine racemase from *E.faecalis* complex with cycloserine  
Authors : Hwang, K.Y.; Priyadarshi, A.; Lee, E.H.; Sung, M.W.  
Deposited on : 2008-08-15  
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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) 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 : 2.36  
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) : 2.36

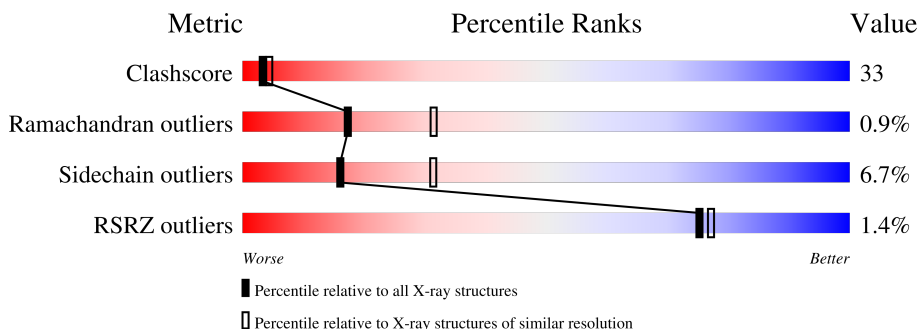
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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))
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (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  $\geq 3$ , 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	371	
1	B	371	
1	C	371	

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	DCS	A	372	X	-	-	-
2	DCS	B	372	X	-	-	-
2	DCS	C	372	X	-	X	-

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 8833 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.

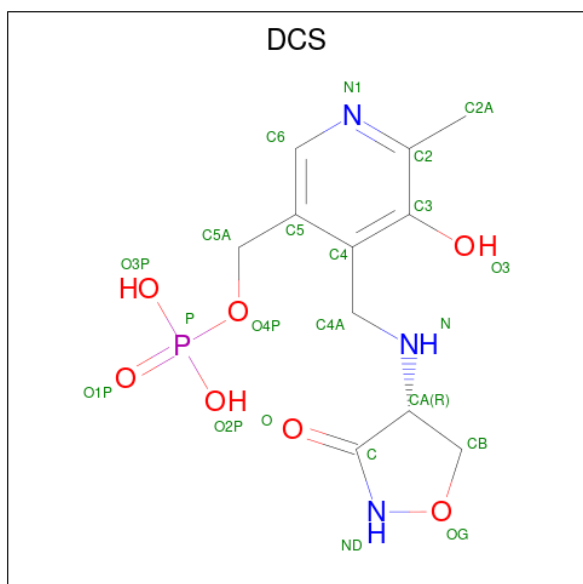
- Molecule 1 is a protein called Alanine racemase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	370	Total 2879	C 1835	N 494	O 538	S 12	0	0	0
1	B	370	Total 2879	C 1835	N 494	O 538	S 12	0	0	0
1	C	370	Total 2879	C 1835	N 494	O 538	S 12	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	329	PRO	SER	engineered mutation	UNP Q837J0
B	329	PRO	SER	engineered mutation	UNP Q837J0
C	329	PRO	SER	engineered mutation	UNP Q837J0

- Molecule 2 is D-[3-HYDROXY-2-METHYL-5-PHOSPHONOXYMETHYL-PYRIDIN-4-YLMETHYL]-N,O-CYCLOSERYLAMIDE (three-letter code: DCS) (formula: C<sub>11</sub>H<sub>16</sub>N<sub>3</sub>O<sub>7</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			22	11	3	7	1		
2	B	1	Total	C	N	O	P	0	0
			22	11	3	7	1		
2	C	1	Total	C	N	O	P	0	0
			22	11	3	7	1		

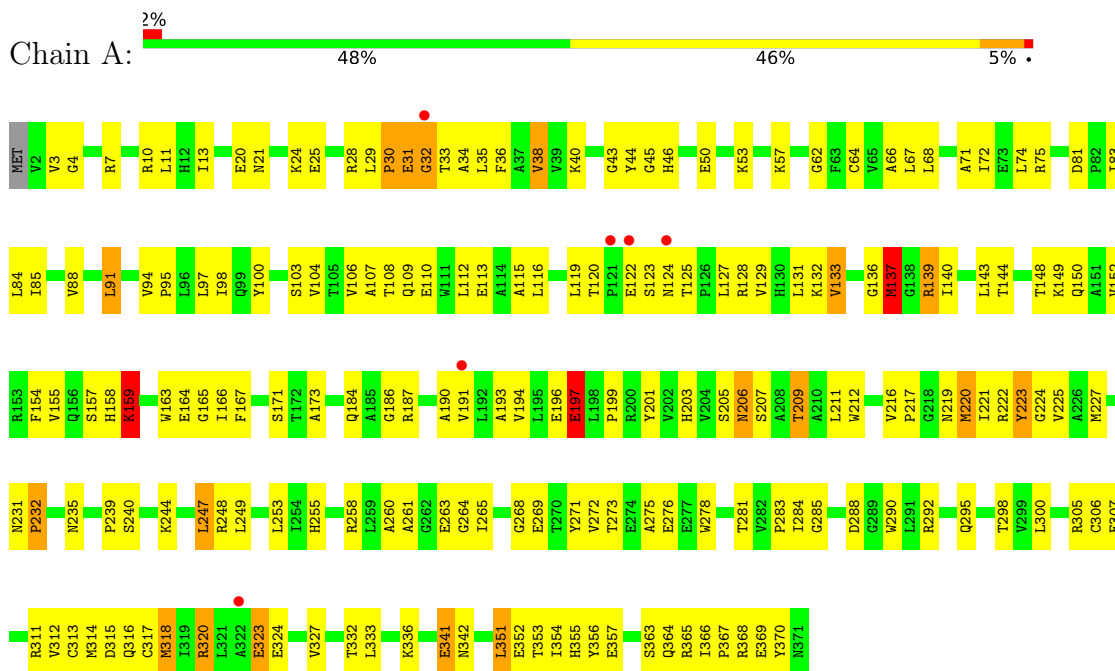
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	51	Total	O	0	0
			51	51		
3	B	40	Total	O	0	0
			40	40		
3	C	39	Total	O	0	0
			39	39		

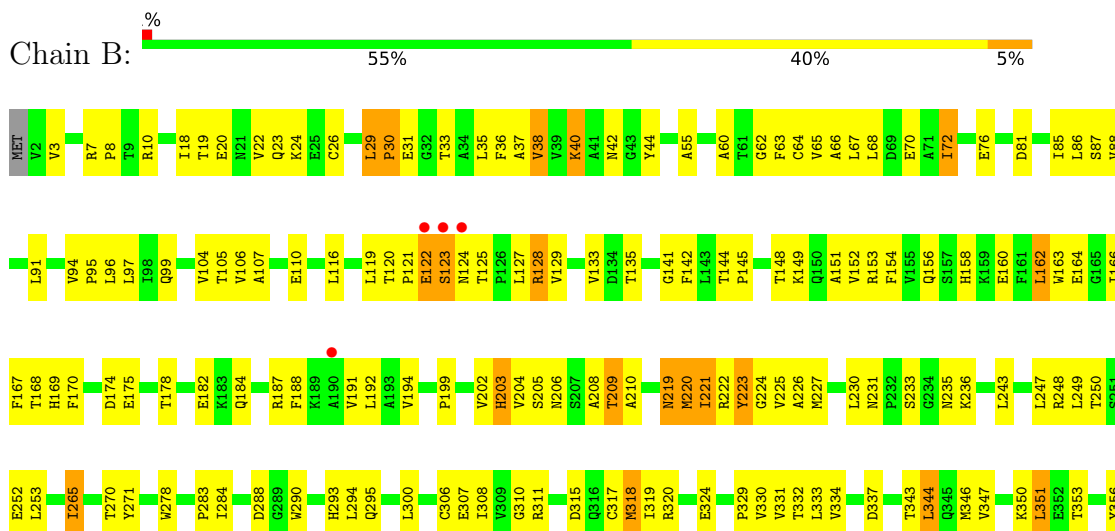
### 3 Residue-property plots

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: Alanine racemase

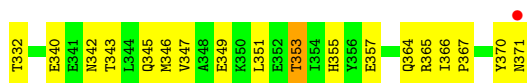
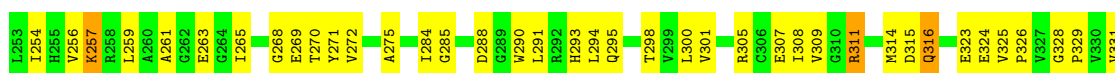
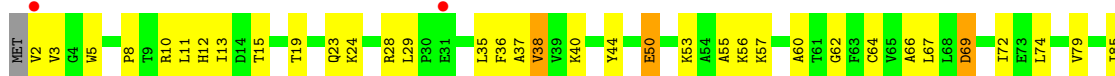


- Molecule 1: Alanine racemase





- Molecule 1: Alanine racemase



## 4 Data and refinement statistics i

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	94.60Å 156.19Å 146.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.50 41.90 – 2.52	Depositor EDS
% Data completeness (in resolution range)	92.8 (50.00-2.50) 94.8 (41.90-2.52)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.82 (at 2.51Å)	Xtrriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.210 , 0.260 0.208 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	28.7	Xtrriage
Anisotropy	0.192	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 42.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.42$ , $\langle L^2 \rangle = 0.24$	Xtrriage
Estimated twinning fraction	0.046 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.062 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtrriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	8833	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.95% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

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

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	0.41	0/2942	0.68	2/4001 (0.0%)
1	B	0.40	0/2942	0.66	0/4001
1	C	0.38	0/2942	0.65	0/4001
All	All	0.40	0/8826	0.66	2/12003 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	2
All	All	0	3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	31	GLU	CB-CA-C	-7.30	95.81	110.40
1	A	32	GLY	N-CA-C	-6.98	95.64	113.10

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	159	LYS	Peptide
1	B	123	SER	Peptide
1	B	29	LEU	Peptide

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2879	0	2870	214	0
1	B	2879	0	2870	180	0
1	C	2879	0	2870	189	0
2	A	22	0	12	3	0
2	B	22	0	12	2	0
2	C	22	0	12	8	0
3	A	51	0	0	4	0
3	B	40	0	0	3	0
3	C	39	0	0	2	0
All	All	8833	0	8646	569	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 33.

All (569) 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:35:LEU:HD11	1:B:223:TYR:HB2	1.25	1.15
1:A:206:ASN:ND2	1:A:209:THR:HG23	1.66	1.10
1:B:64:CYS:HB3	1:B:86:LEU:HD21	1.31	1.07
1:A:136:GLY:O	1:A:137:MET:HB3	1.58	1.03
1:C:120:THR:HG23	1:C:123:SER:HB2	1.43	1.01
1:A:10:ARG:HG2	1:A:10:ARG:HH11	1.25	1.00
1:A:159:LYS:O	1:A:159:LYS:HG2	1.59	0.99
1:A:165:GLY:HA2	1:A:199:PRO:HG2	1.45	0.98
2:A:372:DCS:HND	1:C:314:MET:H	1.12	0.97
1:B:153:ARG:HH21	1:B:156:GLN:NE2	1.63	0.96
1:B:97:LEU:HD13	1:B:104:VAL:HG21	1.48	0.95
1:A:206:ASN:ND2	1:A:209:THR:H	1.64	0.95
1:C:145:PRO:HG3	1:C:191:VAL:HG22	1.48	0.94
1:A:295:GLN:NE2	1:A:311:ARG:HD3	1.85	0.91
1:B:206:ASN:H	1:B:209:THR:CG2	1.83	0.91
1:A:295:GLN:HE22	1:A:311:ARG:HH11	1.20	0.89
1:B:206:ASN:OD1	1:B:209:THR:HG22	1.72	0.88
1:B:145:PRO:HG3	1:B:191:VAL:HG22	1.55	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:336:LYS:HG2	1:A:341:GLU:HG2	1.57	0.86
1:C:206:ASN:ND2	1:C:209:THR:H	1.73	0.86
1:A:137:MET:HB2	1:A:171:SER:HB3	1.56	0.85
1:A:149:LYS:HE3	1:A:194:VAL:HG12	1.58	0.84
1:B:202:VAL:H	1:B:219:ASN:HD21	1.21	0.84
1:A:206:ASN:HD21	1:A:209:THR:H	1.24	0.83
1:B:120:THR:HG23	1:B:122:GLU:OE1	1.77	0.83
1:A:13:ILE:HD13	1:A:46:HIS:O	1.79	0.82
1:C:252:GLU:HA	1:C:331:VAL:HG23	1.61	0.82
1:B:252:GLU:HA	1:B:331:VAL:HG23	1.60	0.82
1:A:288:ASP:HB3	1:A:366:ILE:HD11	1.60	0.82
1:B:33:THR:HG22	1:B:219:ASN:HA	1.62	0.81
1:A:97:LEU:HD13	1:A:104:VAL:HG11	1.62	0.80
1:B:206:ASN:H	1:B:209:THR:HG23	1.45	0.80
1:B:91:LEU:HD12	1:B:91:LEU:H	1.46	0.79
1:A:11:LEU:HD13	1:A:249:LEU:HD13	1.64	0.79
1:A:196:GLU:O	1:A:197:GLU:HB2	1.84	0.78
1:C:353:THR:HG21	1:C:357:GLU:OE1	1.84	0.78
1:C:242:ALA:HA	3:C:410:HOH:O	1.83	0.78
1:A:35:LEU:HD21	1:A:223:TYR:HB2	1.66	0.78
1:A:295:GLN:HE22	1:A:311:ARG:NH1	1.81	0.77
1:C:145:PRO:HA	1:C:191:VAL:HG13	1.66	0.77
1:B:168:THR:HG22	1:B:204:VAL:HG12	1.67	0.76
1:C:130:HIS:NE2	1:C:164:GLU:HG3	2.01	0.75
1:B:233:SER:HB2	1:B:236:LYS:HB2	1.68	0.75
1:A:225:VAL:HG11	1:A:356:TYR:CZ	2.21	0.75
1:C:145:PRO:HG3	1:C:191:VAL:CG2	2.17	0.74
1:C:325:VAL:HG13	1:C:329:PRO:HG2	1.69	0.74
1:C:144:THR:HG22	1:C:147:GLU:H	1.53	0.74
1:A:91:LEU:O	1:A:94:VAL:HG23	1.88	0.74
1:C:145:PRO:CG	1:C:191:VAL:HG22	2.17	0.74
1:A:10:ARG:HG2	1:A:10:ARG:NH1	1.94	0.73
1:B:288:ASP:HB3	1:B:366:ILE:HD11	1.68	0.73
1:B:144:THR:O	1:B:148:THR:HG23	1.89	0.73
1:B:202:VAL:H	1:B:219:ASN:ND2	1.87	0.73
1:A:314:MET:H	2:C:372:DCS:HND	1.36	0.73
1:B:29:LEU:HB3	1:B:30:PRO:HA	1.70	0.73
1:A:167:PHE:HB2	1:A:203:HIS:O	1.89	0.72
1:B:135:THR:CG2	1:B:184:GLN:HE21	2.03	0.72
1:A:159:LYS:HB3	1:A:159:LYS:NZ	2.03	0.72
1:A:163:TRP:CE2	1:A:199:PRO:HG3	2.24	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:136:GLY:O	1:A:137:MET:CB	2.36	0.72
1:B:135:THR:HG23	1:B:184:GLN:HB3	1.70	0.72
1:B:167:PHE:HB3	1:B:203:HIS:CD2	2.25	0.71
1:B:191:VAL:O	1:B:194:VAL:HG12	1.91	0.71
1:A:133:VAL:HG21	1:A:191:VAL:HG21	1.73	0.71
1:A:320:ARG:HH11	1:A:320:ARG:HB2	1.56	0.71
1:A:94:VAL:HA	1:A:97:LEU:HD12	1.72	0.71
1:B:121:PRO:C	1:B:122:GLU:HG2	2.11	0.71
1:B:65:VAL:HG21	1:B:70:GLU:HB3	1.73	0.71
1:C:325:VAL:CG1	1:C:329:PRO:HG2	2.21	0.70
1:A:247:LEU:HD13	1:A:248:ARG:N	2.06	0.70
1:B:135:THR:HG23	1:B:184:GLN:HE21	1.54	0.70
2:A:372:DCS:HND	1:C:314:MET:N	1.88	0.70
1:A:247:LEU:HD13	1:A:248:ARG:H	1.56	0.69
1:A:106:VAL:HG21	1:A:112:LEU:HG	1.73	0.69
1:C:163:TRP:CZ2	1:C:199:PRO:HD3	2.27	0.69
1:B:295:GLN:HE22	1:B:311:ARG:HH11	1.39	0.69
1:A:320:ARG:HH11	1:A:320:ARG:CB	2.06	0.69
1:C:163:TRP:CZ3	1:C:166:ILE:HB	2.29	0.68
1:C:3:VAL:HG12	1:C:367:PRO:HG3	1.76	0.68
1:A:261:ALA:HB2	1:A:275:ALA:HA	1.76	0.67
1:B:96:LEU:HD23	1:B:99:GLN:NE2	2.09	0.67
1:B:220:MET:HE1	1:B:222:ARG:HG2	1.76	0.67
1:B:265:ILE:C	1:B:265:ILE:HD13	2.14	0.67
1:B:153:ARG:HH21	1:B:156:GLN:HE22	1.40	0.67
1:C:345:GLN:HE21	1:C:355:HIS:CD2	2.13	0.67
1:C:265:ILE:HD11	1:C:309:VAL:HG23	1.77	0.67
1:B:224:GLY:O	1:B:227:MET:HG2	1.95	0.66
1:C:120:THR:CG2	1:C:123:SER:HB2	2.23	0.66
1:B:8:PRO:HB2	1:B:252:GLU:HG2	1.77	0.66
1:A:40:LYS:HD2	1:C:315:ASP:OD2	1.95	0.66
1:A:88:VAL:HG22	1:C:254:ILE:HD12	1.77	0.66
1:B:153:ARG:HH21	1:B:156:GLN:HE21	1.43	0.66
1:B:120:THR:HG23	1:B:122:GLU:CD	2.14	0.66
1:C:231:ASN:HD22	1:C:231:ASN:C	1.99	0.66
1:A:50:GLU:HG3	1:A:370:TYR:CZ	2.30	0.65
1:A:163:TRP:CZ2	1:A:199:PRO:HG3	2.30	0.65
1:A:295:GLN:HE22	1:A:311:ARG:HD3	1.61	0.65
1:C:133:VAL:HG13	1:C:168:THR:HB	1.79	0.65
1:A:123:SER:C	1:A:125:THR:H	2.00	0.65
1:A:314:MET:HB2	2:C:372:DCS:ND	2.12	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:372:DCS:O3P	3:C:374:HOH:O	2.15	0.64
1:A:224:GLY:O	1:A:227:MET:HG2	1.97	0.64
1:B:120:THR:O	1:B:122:GLU:HG2	1.96	0.64
1:A:225:VAL:HG11	1:A:356:TYR:CE2	2.31	0.64
1:B:97:LEU:HD22	1:B:104:VAL:HG22	1.79	0.64
1:B:163:TRP:CZ2	1:B:199:PRO:HD3	2.32	0.64
1:C:50:GLU:HG3	1:C:370:TYR:CZ	2.33	0.64
1:B:29:LEU:HD21	1:B:221:ILE:HG21	1.79	0.64
1:A:139:ARG:HG3	1:A:140:ILE:H	1.63	0.63
1:C:265:ILE:HG12	1:C:271:TYR:HD2	1.63	0.63
1:A:171:SER:H	1:A:184:GLN:HE22	1.46	0.63
1:A:336:LYS:HG2	1:A:341:GLU:CG	2.28	0.63
1:A:106:VAL:CG1	1:A:131:LEU:HD12	2.28	0.63
1:A:305:ARG:NH2	1:A:342:ASN:OD1	2.30	0.63
1:A:363:SER:OG	1:A:365:ARG:HG2	1.99	0.63
1:A:94:VAL:N	1:A:95:PRO:HD2	2.13	0.62
1:C:93:TYR:HB3	1:C:96:LEU:HD13	1.81	0.62
1:A:132:LYS:HD3	1:A:140:ILE:HG13	1.80	0.62
1:A:292:ARG:HH11	1:C:353:THR:HG22	1.63	0.62
1:A:155:VAL:HG11	1:A:163:TRP:HB2	1.81	0.62
1:A:298:THR:HG22	1:A:307:GLU:HA	1.81	0.62
1:B:210:ALA:CB	1:B:221:ILE:HD12	2.29	0.62
1:A:7:ARG:HH12	1:A:365:ARG:HH21	1.48	0.62
1:C:345:GLN:O	1:C:349:GLU:HG3	1.98	0.62
1:B:153:ARG:NH2	1:B:156:GLN:NE2	2.43	0.62
1:B:363:SER:OG	1:B:365:ARG:HG2	1.99	0.62
1:B:168:THR:HG22	1:B:204:VAL:CG1	2.29	0.62
1:A:173:ALA:CB	1:A:209:THR:HG22	2.29	0.62
1:B:65:VAL:CG2	1:B:70:GLU:HB3	2.29	0.62
1:C:130:HIS:HE2	1:C:164:GLU:HG3	1.63	0.62
1:A:33:THR:HG23	1:A:219:ASN:C	2.20	0.61
1:A:46:HIS:NE2	1:A:247:LEU:HB2	2.15	0.61
1:A:364:GLN:OE1	1:C:364:GLN:HG2	2.01	0.61
1:B:315:ASP:OD1	1:B:365:ARG:NH2	2.32	0.61
1:C:12:HIS:HE1	1:C:250:THR:OG1	1.82	0.61
1:C:109:GLN:HG3	1:C:110:GLU:OE1	2.00	0.61
1:C:247:LEU:HD13	1:C:248:ARG:N	2.15	0.61
1:C:19:THR:O	1:C:23:GLN:HG3	1.99	0.61
1:C:97:LEU:CD1	1:C:104:VAL:HG11	2.31	0.61
1:A:255:HIS:CE1	1:C:140:ILE:HA	2.36	0.61
1:A:315:ASP:OD2	1:C:40:LYS:HD2	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:231:ASN:HD22	1:C:232:PRO:N	1.98	0.61
1:C:56:LYS:HA	1:C:60:ALA:HB3	1.83	0.61
1:A:35:LEU:HD13	1:A:35:LEU:C	2.21	0.60
1:A:97:LEU:HD22	1:A:104:VAL:CG1	2.32	0.60
1:B:142:PHE:HB2	1:B:148:THR:HG22	1.82	0.60
1:B:167:PHE:HB2	1:B:203:HIS:O	2.00	0.60
1:C:109:GLN:O	1:C:113:GLU:HG3	2.01	0.60
1:C:236:LYS:C	1:C:237:LEU:HD12	2.22	0.60
1:A:206:ASN:C	1:A:206:ASN:HD22	2.04	0.60
1:C:50:GLU:HG3	1:C:370:TYR:CE1	2.36	0.60
1:C:24:LYS:O	1:C:28:ARG:HG3	2.00	0.60
1:C:135:THR:O	1:C:184:GLN:HG2	2.01	0.60
1:C:270:THR:HG21	1:C:311:ARG:CZ	2.31	0.60
1:B:284:ILE:HD13	1:B:333:LEU:HD22	1.83	0.60
1:B:225:VAL:HG13	1:B:226:ALA:N	2.17	0.60
1:C:236:LYS:HB3	1:C:237:LEU:HD12	1.84	0.60
1:A:28:ARG:HH21	1:A:240:SER:HB3	1.66	0.59
1:B:247:LEU:C	1:B:247:LEU:HD23	2.22	0.59
1:C:163:TRP:CH2	1:C:199:PRO:HD3	2.36	0.59
1:C:229:GLY:HA2	1:C:243:LEU:HB3	1.84	0.59
1:A:165:GLY:HA2	1:A:199:PRO:CG	2.26	0.59
1:C:85:ILE:O	1:C:105:THR:HG22	2.03	0.59
1:C:163:TRP:HZ3	1:C:166:ILE:HB	1.67	0.59
1:B:220:MET:HE3	1:B:221:ILE:O	2.02	0.59
1:A:154:PHE:O	1:A:157:SER:HB2	2.02	0.59
1:C:343:THR:OG1	1:C:346:MET:HG3	2.02	0.59
1:A:159:LYS:HB3	1:A:159:LYS:HZ3	1.67	0.59
1:B:116:LEU:HD11	1:B:158:HIS:CE1	2.38	0.58
1:B:162:LEU:HD13	1:B:162:LEU:O	2.03	0.58
1:B:135:THR:CG2	1:B:184:GLN:HB3	2.33	0.58
1:B:145:PRO:HG3	1:B:191:VAL:CG2	2.28	0.58
1:A:225:VAL:CG1	1:A:356:TYR:CE2	2.87	0.58
1:A:300:LEU:HB2	1:A:332:THR:HB	1.86	0.58
1:A:353:THR:HG22	1:C:293:HIS:CE1	2.38	0.58
1:B:38:VAL:HG13	1:B:224:GLY:CA	2.34	0.58
1:A:158:HIS:O	1:A:159:LYS:HD2	2.03	0.58
1:C:146:GLU:O	1:C:150:GLN:HG3	2.02	0.58
1:C:148:THR:HG21	1:C:191:VAL:HG12	1.86	0.58
1:B:210:ALA:HB2	1:B:221:ILE:HD12	1.86	0.58
1:B:65:VAL:HG22	1:B:70:GLU:OE2	2.04	0.58
1:B:91:LEU:HD12	1:B:91:LEU:N	2.17	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:211:LEU:HD12	1:A:232:PRO:HG3	1.86	0.57
1:B:187:ARG:O	1:B:191:VAL:HG23	2.04	0.57
1:A:45:GLY:O	1:A:368:ARG:NH1	2.37	0.57
1:B:306:CYS:HB3	1:B:320:ARG:O	2.04	0.57
1:C:148:THR:HG21	1:C:191:VAL:CG1	2.33	0.57
1:C:183:LYS:HE2	1:C:187:ARG:NH2	2.19	0.57
1:C:15:THR:H	1:C:371:ASN:ND2	2.02	0.57
1:C:140:ILE:HG22	1:C:141:GLY:N	2.18	0.57
1:C:205:SER:HB2	1:C:209:THR:HB	1.87	0.57
1:A:290:TRP:CZ2	1:A:333:LEU:HD23	2.39	0.57
1:C:206:ASN:HD22	1:C:209:THR:H	1.49	0.57
1:B:38:VAL:HG13	1:B:224:GLY:HA2	1.86	0.57
1:B:163:TRP:CH2	1:B:199:PRO:HD3	2.40	0.56
1:C:91:LEU:HA	1:C:94:VAL:HG23	1.88	0.56
1:A:167:PHE:CB	1:A:203:HIS:O	2.53	0.56
1:A:323:GLU:HB3	3:A:413:HOH:O	2.04	0.56
1:A:139:ARG:HG3	1:A:140:ILE:N	2.21	0.55
1:C:5:TRP:HA	1:C:10:ARG:HH12	1.70	0.55
1:B:19:THR:O	1:B:23:GLN:HB2	2.06	0.55
1:B:125:THR:HG22	1:B:125:THR:O	2.05	0.55
1:C:66:ALA:O	1:C:67:LEU:HD23	2.06	0.55
1:A:44:TYR:HE2	1:A:225:VAL:CG1	2.19	0.55
1:B:72:ILE:HD11	1:B:76:GLU:OE1	2.05	0.55
1:C:291:LEU:O	1:C:294:LEU:HB2	2.06	0.55
1:B:120:THR:CG2	1:B:122:GLU:OE1	2.52	0.55
1:B:121:PRO:C	1:B:122:GLU:CG	2.75	0.55
1:B:203:HIS:CD2	1:B:203:HIS:N	2.75	0.55
1:C:15:THR:H	1:C:371:ASN:HD21	1.55	0.55
1:C:155:VAL:HG11	1:C:163:TRP:HB3	1.89	0.55
1:A:97:LEU:CD1	1:A:104:VAL:HG11	2.35	0.55
1:A:132:LYS:NZ	1:A:139:ARG:HD2	2.22	0.54
1:B:145:PRO:CG	1:B:191:VAL:HG22	2.32	0.54
1:B:148:THR:O	1:B:151:ALA:HB3	2.08	0.54
1:B:278:TRP:CZ2	1:B:324:GLU:HB2	2.42	0.54
1:B:64:CYS:HB3	1:B:86:LEU:CD2	2.22	0.54
1:C:133:VAL:CG1	1:C:168:THR:HB	2.37	0.54
1:A:148:THR:O	1:A:152:VAL:HG23	2.07	0.54
1:A:206:ASN:HD21	1:A:209:THR:HG23	1.67	0.54
1:B:194:VAL:HG22	1:B:194:VAL:O	2.08	0.54
1:A:317:CYS:HA	1:A:318:MET:CE	2.37	0.54
1:A:363:SER:O	1:A:368:ARG:NH2	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:278:TRP:CD1	1:A:323:GLU:O	2.61	0.53
1:C:86:LEU:C	1:C:105:THR:HG21	2.28	0.53
1:B:110:GLU:N	1:B:110:GLU:OE1	2.42	0.53
1:C:3:VAL:CG1	1:C:367:PRO:HG3	2.38	0.53
1:A:123:SER:O	1:A:125:THR:N	2.42	0.53
1:A:247:LEU:CD1	1:A:248:ARG:N	2.71	0.53
1:B:353:THR:HG21	1:B:357:GLU:OE1	2.09	0.53
1:B:8:PRO:HB2	1:B:252:GLU:CG	2.38	0.53
1:B:188:PHE:CE2	1:B:192:LEU:HD11	2.44	0.53
1:A:108:THR:HB	1:A:110:GLU:HG2	1.91	0.53
1:B:253:LEU:HD12	1:B:329:PRO:HG2	1.91	0.53
1:C:86:LEU:HD13	2:C:372:DCS:C2	2.39	0.53
1:B:3:VAL:HG12	1:B:367:PRO:HG3	1.90	0.52
1:C:233:SER:HB2	1:C:236:LYS:HB2	1.91	0.52
1:A:115:ALA:O	1:A:119:LEU:HG	2.10	0.52
1:B:247:LEU:HD23	1:B:248:ARG:N	2.24	0.52
1:B:295:GLN:HE22	1:B:311:ARG:HD3	1.74	0.52
1:C:74:LEU:O	1:C:79:VAL:HG22	2.09	0.52
1:C:174:ASP:O	1:C:236:LYS:HE2	2.09	0.52
1:A:207:SER:HB2	2:A:372:DCS:O1P	2.08	0.52
1:B:158:HIS:HB3	1:B:160:GLU:OE1	2.09	0.52
1:C:261:ALA:HB2	1:C:275:ALA:HA	1.90	0.52
1:B:219:ASN:C	1:B:219:ASN:HD22	2.11	0.52
1:B:230:LEU:HD21	1:B:344:LEU:HD13	1.91	0.52
1:C:324:GLU:O	1:C:325:VAL:HG23	2.09	0.52
1:A:53:LYS:O	1:A:57:LYS:HG2	2.10	0.52
1:B:119:LEU:HD11	1:B:127:LEU:HB2	1.92	0.52
1:B:178:THR:O	1:B:182:GLU:HG3	2.10	0.52
1:A:4:GLY:HA2	1:C:69:ASP:OD2	2.10	0.52
1:A:50:GLU:HG3	1:A:370:TYR:CE1	2.45	0.52
1:A:320:ARG:HH11	1:A:320:ARG:CG	2.21	0.52
1:C:290:TRP:CD2	1:C:294:LEU:HD13	2.45	0.52
1:B:18:ILE:O	1:B:22:VAL:HG23	2.09	0.52
1:A:3:VAL:HG12	1:A:367:PRO:HG3	1.93	0.51
1:C:298:THR:HG22	1:C:307:GLU:HA	1.91	0.51
1:A:123:SER:C	1:A:125:THR:N	2.64	0.51
1:B:10:ARG:HD2	3:B:405:HOH:O	2.11	0.51
1:B:94:VAL:N	1:B:95:PRO:HD2	2.25	0.51
1:C:187:ARG:O	1:C:191:VAL:HG23	2.10	0.51
1:C:206:ASN:HD22	1:C:206:ASN:C	2.14	0.51
1:C:285:GLY:HA3	1:C:314:MET:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:236:LYS:HB3	1:C:237:LEU:CD1	2.41	0.51
1:B:265:ILE:CG2	1:B:271:TYR:HD2	2.24	0.51
1:B:300:LEU:HD13	1:B:337:ASP:HB3	1.91	0.51
1:B:265:ILE:HD13	1:B:265:ILE:O	2.10	0.51
1:C:263:GLU:OE2	1:C:263:GLU:HA	2.10	0.51
1:A:84:LEU:HD12	1:A:85:ILE:N	2.26	0.51
1:B:22:VAL:HG21	1:B:55:ALA:HA	1.91	0.51
1:A:258:ARG:HD3	1:A:276:GLU:OE2	2.11	0.51
1:C:231:ASN:ND2	1:C:233:SER:H	2.09	0.51
1:C:265:ILE:HD11	1:C:309:VAL:CG2	2.39	0.50
1:A:261:ALA:CB	1:A:275:ALA:HA	2.41	0.50
1:B:249:LEU:H	1:B:334:VAL:HB	1.76	0.50
1:B:270:THR:HG21	1:B:311:ARG:CZ	2.42	0.50
1:A:7:ARG:HD2	1:A:283:PRO:O	2.12	0.50
1:A:25:GLU:OE1	1:A:29:LEU:HD13	2.11	0.50
1:A:50:GLU:CD	1:A:50:GLU:H	2.14	0.50
1:A:290:TRP:CH2	1:A:333:LEU:HD23	2.46	0.50
1:B:121:PRO:O	1:B:122:GLU:CG	2.60	0.50
1:C:241:TYR:CE1	1:C:243:LEU:HD23	2.47	0.50
1:A:28:ARG:HG3	1:A:28:ARG:HH11	1.76	0.50
1:A:106:VAL:HG13	1:A:131:LEU:HD12	1.93	0.50
1:B:29:LEU:HB3	1:B:30:PRO:CA	2.39	0.50
1:B:290:TRP:CE2	1:B:294:LEU:HD13	2.47	0.50
1:C:13:ILE:HB	1:C:370:TYR:CD1	2.46	0.50
1:C:144:THR:HG22	1:C:146:GLU:N	2.26	0.50
1:A:88:VAL:CG2	1:C:254:ILE:HD12	2.41	0.50
1:A:353:THR:HG22	1:C:293:HIS:HE1	1.77	0.50
1:B:203:HIS:CD2	1:B:203:HIS:H	2.30	0.50
1:A:206:ASN:ND2	1:A:206:ASN:C	2.65	0.49
1:A:231:ASN:ND2	1:A:239:PRO:HD3	2.27	0.49
1:B:225:VAL:HB	1:B:356:TYR:CE2	2.47	0.49
1:B:265:ILE:CD1	1:B:310:GLY:HA3	2.42	0.49
1:C:115:ALA:O	1:C:117:GLN:O	2.30	0.49
1:C:290:TRP:HE1	1:C:308:ILE:CD1	2.24	0.49
1:A:278:TRP:CH2	1:A:324:GLU:OE2	2.66	0.49
1:A:298:THR:HG22	1:A:307:GLU:CA	2.43	0.49
1:C:37:ALA:HB1	1:C:227:MET:SD	2.53	0.49
1:C:176:ILE:HG13	1:C:177:ASP:N	2.27	0.49
1:A:187:ARG:O	1:A:191:VAL:HG23	2.13	0.49
1:A:190:ALA:O	1:A:193:ALA:HB3	2.12	0.49
1:B:88:VAL:HG13	3:B:386:HOH:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:38:VAL:HG13	1:A:224:GLY:HA2	1.95	0.49
1:A:75:ARG:HG3	1:A:100:TYR:HB3	1.93	0.49
1:A:313:CYS:HB2	1:A:316:GLN:O	2.11	0.49
1:C:97:LEU:HD11	1:C:104:VAL:HG11	1.94	0.49
1:A:154:PHE:CE1	1:A:158:HIS:CD2	3.01	0.49
1:A:354:ILE:HG13	1:A:356:TYR:HB2	1.94	0.49
1:C:35:LEU:HD23	1:C:221:ILE:HD11	1.93	0.49
1:A:220:MET:CE	1:A:222:ARG:HG3	2.43	0.49
1:C:72:ILE:HG23	1:C:100:TYR:CE2	2.47	0.49
1:C:97:LEU:HD13	1:C:104:VAL:HG11	1.95	0.49
1:A:7:ARG:NH1	1:A:365:ARG:HH21	2.11	0.49
1:B:63:PHE:CE1	1:B:81:ASP:HB2	2.48	0.49
1:C:192:LEU:HA	1:C:195:LEU:HD12	1.95	0.49
1:A:205:SER:HB2	1:A:221:ILE:HG22	1.95	0.49
1:C:370:TYR:O	1:C:371:ASN:C	2.51	0.49
1:C:167:PHE:HB3	1:C:203:HIS:CE1	2.48	0.49
1:B:97:LEU:HD22	1:B:104:VAL:CG2	2.41	0.48
1:B:142:PHE:CB	1:B:148:THR:HG22	2.43	0.48
1:B:167:PHE:HB3	1:B:203:HIS:NE2	2.27	0.48
1:B:230:LEU:O	1:B:243:LEU:HD13	2.13	0.48
1:A:31:GLU:OE1	1:A:31:GLU:HA	2.14	0.48
1:C:222:ARG:NE	2:C:372:DCS:N1	2.49	0.48
1:A:155:VAL:CG1	1:A:163:TRP:HB2	2.43	0.48
1:B:220:MET:CE	1:B:222:ARG:HG2	2.43	0.48
1:C:35:LEU:HD13	1:C:35:LEU:C	2.34	0.48
1:A:38:VAL:HB	1:A:64:CYS:HB2	1.95	0.48
1:A:212:TRP:CH2	1:A:232:PRO:HG2	2.49	0.48
1:A:268:GLY:O	1:A:269:GLU:HB3	2.13	0.48
1:B:104:VAL:HG12	1:B:105:THR:O	2.13	0.48
1:B:265:ILE:HD13	1:B:310:GLY:HA3	1.95	0.48
1:C:91:LEU:O	1:C:94:VAL:HG23	2.13	0.48
1:C:220:MET:HE1	1:C:222:ARG:HG2	1.94	0.48
1:A:44:TYR:HE2	1:A:225:VAL:HG13	1.77	0.48
1:A:144:THR:O	1:A:148:THR:HG23	2.12	0.48
1:A:220:MET:HE3	1:A:222:ARG:HG3	1.96	0.48
1:B:30:PRO:CD	1:B:31:GLU:N	2.77	0.48
1:B:170:PHE:HE2	1:B:204:VAL:HG23	1.79	0.48
1:B:293:HIS:O	1:B:350:LYS:HE3	2.14	0.48
1:B:219:ASN:ND2	1:B:219:ASN:C	2.68	0.47
1:B:295:GLN:NE2	1:B:311:ARG:HH11	2.09	0.47
1:C:38:VAL:HB	1:C:64:CYS:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:43:GLY:O	1:A:44:TYR:HB2	2.14	0.47
1:A:278:TRP:CZ2	1:A:324:GLU:OE2	2.68	0.47
1:A:318:MET:SD	1:C:139:ARG:HB3	2.54	0.47
1:B:106:VAL:HG23	1:B:106:VAL:O	2.15	0.47
1:B:206:ASN:N	1:B:209:THR:HG23	2.22	0.47
1:C:53:LYS:O	1:C:57:LYS:HG3	2.14	0.47
1:A:273:THR:HB	1:A:275:ALA:O	2.14	0.47
1:B:294:LEU:HG	1:B:351:LEU:HD11	1.95	0.47
1:C:131:LEU:HD12	1:C:163:TRP:CE3	2.50	0.47
1:B:116:LEU:HD23	1:B:116:LEU:O	2.14	0.47
1:C:300:LEU:HB2	1:C:332:THR:HB	1.97	0.47
1:C:10:ARG:HH11	1:C:367:PRO:HB2	1.79	0.47
1:B:223:TYR:HB3	1:B:227:MET:HE2	1.97	0.47
1:A:154:PHE:CZ	1:A:158:HIS:CD2	3.03	0.46
1:B:167:PHE:CB	1:B:203:HIS:O	2.64	0.46
1:C:133:VAL:HG11	1:C:188:PHE:CD1	2.50	0.46
1:C:206:ASN:HD22	1:C:206:ASN:H	1.62	0.46
1:C:294:LEU:HD21	1:C:347:VAL:HG13	1.96	0.46
1:B:38:VAL:HA	1:B:64:CYS:HB2	1.97	0.46
1:C:364:GLN:OE1	1:C:364:GLN:HA	2.14	0.46
1:B:37:ALA:HA	1:B:227:MET:HE3	1.96	0.46
1:A:20:GLU:O	1:A:24:LYS:HG2	2.15	0.46
1:B:91:LEU:H	1:B:91:LEU:CD1	2.22	0.46
1:C:265:ILE:CD1	1:C:309:VAL:HG23	2.45	0.46
1:B:278:TRP:CH2	1:B:324:GLU:HB2	2.50	0.46
1:A:336:LYS:HE3	1:A:341:GLU:HG3	1.98	0.46
1:C:13:ILE:N	1:C:13:ILE:HD12	2.31	0.46
1:C:131:LEU:HD12	1:C:163:TRP:CZ3	2.51	0.46
1:A:143:LEU:N	1:A:143:LEU:HD12	2.31	0.46
1:A:201:TYR:HB3	1:A:203:HIS:HD2	1.81	0.46
1:A:75:ARG:NH1	1:A:81:ASP:O	2.44	0.46
1:C:106:VAL:HG11	1:C:112:LEU:HG	1.98	0.46
1:A:173:ALA:HB2	1:A:209:THR:HG22	1.98	0.46
1:A:253:LEU:O	1:A:327:VAL:HG13	2.16	0.46
1:B:36:PHE:HB2	1:B:220:MET:CE	2.45	0.46
1:B:107:ALA:HB1	1:B:141:GLY:H	1.80	0.46
1:C:222:ARG:HE	2:C:372:DCS:C6	2.26	0.46
1:A:10:ARG:HH11	1:A:10:ARG:CG	2.07	0.46
1:A:94:VAL:O	1:A:97:LEU:HB2	2.15	0.46
1:A:98:ILE:HG23	1:A:125:THR:OG1	2.16	0.46
1:A:186:GLY:HA3	3:A:408:HOH:O	2.14	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:317:CYS:HA	1:A:318:MET:HE1	1.97	0.45
1:B:96:LEU:HD23	1:B:99:GLN:HE21	1.78	0.45
1:B:145:PRO:HA	1:B:191:VAL:HG13	1.98	0.45
1:C:117:GLN:O	1:C:118:GLN:C	2.55	0.45
1:C:269:GLU:HG3	1:C:269:GLU:O	2.15	0.45
1:A:167:PHE:HB3	1:A:203:HIS:CE1	2.52	0.45
1:B:347:VAL:HG12	1:B:351:LEU:HD23	1.98	0.45
1:C:291:LEU:N	1:C:294:LEU:HD12	2.30	0.45
1:A:205:SER:HA	1:A:209:THR:OG1	2.17	0.45
1:C:74:LEU:HB3	1:C:79:VAL:HG21	1.99	0.45
1:C:133:VAL:HG11	1:C:188:PHE:HD1	1.82	0.45
1:C:29:LEU:HD21	1:C:221:ILE:HD13	1.98	0.45
1:B:116:LEU:HD12	1:B:154:PHE:CZ	2.52	0.45
1:B:300:LEU:HB2	1:B:332:THR:HB	1.98	0.45
1:C:149:LYS:HD2	1:C:194:VAL:HG22	1.97	0.45
1:C:284:ILE:O	1:C:284:ILE:HG23	2.16	0.45
1:A:216:VAL:HG22	1:A:217:PRO:HD2	1.98	0.45
1:A:255:HIS:HB3	1:A:281:THR:HB	1.99	0.45
1:A:357:GLU:OE2	1:C:291:LEU:HD22	2.16	0.45
1:A:107:ALA:O	1:A:108:THR:HG23	2.17	0.45
1:B:20:GLU:O	1:B:24:LYS:HG3	2.17	0.45
1:C:11:LEU:HG	1:C:366:ILE:HG21	1.99	0.45
1:C:257:LYS:HD2	1:C:259:LEU:HG	1.99	0.45
1:A:94:VAL:N	1:A:95:PRO:CD	2.80	0.44
1:B:87:SER:HA	3:B:404:HOH:O	2.16	0.44
1:C:117:GLN:O	1:C:119:LEU:N	2.50	0.44
1:A:365:ARG:O	1:A:367:PRO:HD3	2.17	0.44
1:C:55:ALA:HB2	1:C:227:MET:HE1	1.99	0.44
1:C:133:VAL:HG12	1:C:167:PHE:O	2.17	0.44
1:C:167:PHE:HB2	1:C:203:HIS:O	2.18	0.44
1:C:305:ARG:NH1	1:C:340:GLU:HB3	2.32	0.44
1:A:66:ALA:C	1:A:67:LEU:HD23	2.38	0.44
1:A:263:GLU:O	1:A:272:VAL:HA	2.18	0.44
1:B:347:VAL:HG12	1:B:351:LEU:CD2	2.47	0.44
1:C:12:HIS:C	1:C:13:ILE:HD12	2.37	0.44
1:A:3:VAL:CG1	1:A:367:PRO:HG3	2.47	0.44
1:A:351:LEU:O	1:A:352:GLU:HB2	2.17	0.44
1:C:97:LEU:HD13	1:C:104:VAL:CG1	2.48	0.44
1:C:130:HIS:HE2	1:C:164:GLU:CG	2.30	0.44
1:A:295:GLN:NE2	1:A:311:ARG:HH11	2.01	0.44
1:A:103:SER:HA	1:A:128:ARG:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:295:GLN:HG3	3:A:388:HOH:O	2.17	0.44
1:C:144:THR:CG2	1:C:146:GLU:H	2.30	0.44
1:C:295:GLN:OE1	1:C:311:ARG:HD2	2.18	0.44
1:B:65:VAL:HG21	1:B:70:GLU:CB	2.46	0.44
1:C:166:ILE:HD13	1:C:192:LEU:CD1	2.48	0.44
1:C:167:PHE:CG	1:C:203:HIS:CE1	3.06	0.44
1:B:44:TYR:OH	2:B:372:DCS:O2P	2.25	0.43
1:A:314:MET:HB2	2:C:372:DCS:HND	1.82	0.43
1:B:210:ALA:HB1	1:B:221:ILE:HD12	1.98	0.43
1:C:237:LEU:HD12	1:C:237:LEU:N	2.33	0.43
1:C:265:ILE:HG12	1:C:271:TYR:CD2	2.48	0.43
1:A:29:LEU:O	1:A:31:GLU:N	2.51	0.43
1:A:314:MET:CB	2:C:372:DCS:ND	2.81	0.43
1:C:288:ASP:CG	1:C:365:ARG:HH21	2.20	0.43
1:A:298:THR:HA	1:A:306:CYS:O	2.19	0.43
1:B:40:LYS:HZ2	1:B:66:ALA:HB2	1.82	0.43
1:B:91:LEU:HA	1:B:94:VAL:HG23	2.00	0.43
1:C:35:LEU:CD2	1:C:221:ILE:HD11	2.48	0.43
1:C:305:ARG:NH2	1:C:342:ASN:OD1	2.52	0.43
1:A:268:GLY:O	1:A:269:GLU:CB	2.66	0.43
1:B:225:VAL:CG1	1:B:226:ALA:N	2.80	0.43
1:C:145:PRO:HB3	1:C:191:VAL:HA	1.99	0.43
1:A:194:VAL:HG12	1:A:194:VAL:O	2.18	0.43
1:B:128:ARG:HG2	1:B:164:GLU:OE2	2.19	0.43
1:A:10:ARG:NH1	1:A:10:ARG:CG	2.68	0.43
1:A:29:LEU:C	1:A:31:GLU:H	2.20	0.43
1:B:166:ILE:HD13	1:B:192:LEU:CD2	2.48	0.43
1:B:205:SER:HA	1:B:209:THR:HG21	2.01	0.43
1:C:206:ASN:HD21	1:C:209:THR:H	1.56	0.43
1:A:158:HIS:O	1:A:159:LYS:HB3	2.19	0.43
1:B:36:PHE:CE1	1:B:62:GLY:HA3	2.54	0.43
1:B:149:LYS:HD2	1:B:194:VAL:HG22	1.99	0.43
1:C:36:PHE:HA	1:C:62:GLY:O	2.18	0.43
1:C:140:ILE:CG2	1:C:141:GLY:N	2.82	0.43
1:A:317:CYS:HA	1:A:318:MET:HE2	2.00	0.43
1:B:294:LEU:HD21	1:B:347:VAL:HG13	2.01	0.43
1:C:117:GLN:H	1:C:117:GLN:HG2	1.65	0.43
1:C:127:LEU:C	1:C:127:LEU:CD2	2.87	0.43
1:A:35:LEU:CD2	1:A:223:TYR:HB2	2.41	0.42
1:A:110:GLU:O	1:A:113:GLU:HG2	2.19	0.42
1:B:7:ARG:HD2	1:B:283:PRO:HB2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:107:ALA:HB1	1:B:141:GLY:N	2.34	0.42
1:B:122:GLU:HB2	1:B:123:SER:H	1.47	0.42
1:C:145:PRO:CA	1:C:191:VAL:HG22	2.48	0.42
1:C:174:ASP:HB2	1:C:233:SER:HA	2.00	0.42
1:A:29:LEU:HG	1:A:30:PRO:HD2	2.01	0.42
1:A:292:ARG:HA	1:A:312:VAL:HB	2.01	0.42
1:A:318:MET:HE2	1:A:318:MET:H	1.83	0.42
1:C:231:ASN:C	1:C:231:ASN:ND2	2.70	0.42
1:C:247:LEU:HD13	1:C:247:LEU:C	2.38	0.42
1:A:35:LEU:HD21	1:A:223:TYR:CB	2.42	0.42
1:A:265:ILE:CG2	1:A:318:MET:HG3	2.49	0.42
1:A:284:ILE:HA	1:A:288:ASP:OD1	2.19	0.42
1:B:248:ARG:HA	1:B:334:VAL:O	2.19	0.42
1:C:15:THR:N	1:C:371:ASN:ND2	2.66	0.42
1:A:38:VAL:HA	1:A:64:CYS:O	2.18	0.42
1:B:343:THR:O	1:B:346:MET:HB2	2.20	0.42
1:C:206:ASN:ND2	1:C:209:THR:OG1	2.52	0.42
1:A:128:ARG:HB3	1:A:164:GLU:OE2	2.20	0.42
1:A:116:LEU:HD13	1:A:116:LEU:C	2.40	0.42
1:A:290:TRP:CE2	1:A:333:LEU:HD23	2.55	0.42
1:B:174:ASP:HB3	1:B:208:ALA:HB2	2.02	0.42
1:B:343:THR:O	1:B:346:MET:N	2.53	0.42
1:B:365:ARG:O	1:B:367:PRO:HD3	2.19	0.42
1:C:268:GLY:O	1:C:269:GLU:C	2.58	0.42
1:C:44:TYR:CD1	1:C:44:TYR:N	2.88	0.42
1:A:72:ILE:HG23	1:A:100:TYR:CE2	2.55	0.42
1:A:74:LEU:HB2	1:A:83:ILE:HD13	2.02	0.42
1:A:120:THR:HB	1:A:123:SER:HB2	2.01	0.42
1:B:66:ALA:C	1:B:67:LEU:HD12	2.39	0.42
1:B:231:ASN:C	1:B:231:ASN:OD1	2.58	0.42
1:C:149:LYS:HD2	1:C:194:VAL:HG13	2.02	0.42
1:A:10:ARG:HD3	1:A:369:GLU:OE1	2.20	0.42
1:B:129:VAL:HG23	1:B:129:VAL:O	2.20	0.42
1:B:307:GLU:O	1:B:319:ILE:HA	2.20	0.42
1:B:330:VAL:CG1	1:B:331:VAL:N	2.83	0.42
1:C:206:ASN:ND2	1:C:206:ASN:C	2.73	0.42
1:A:109:GLN:OE1	1:A:150:GLN:HG2	2.20	0.41
1:A:206:ASN:ND2	1:A:209:THR:N	2.48	0.41
1:A:264:GLY:HA2	1:A:271:TYR:O	2.19	0.41
1:C:174:ASP:OD2	1:C:236:LYS:NZ	2.52	0.41
1:C:256:VAL:HG11	1:C:325:VAL:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:THR:HG22	1:A:34:ALA:N	2.35	0.41
1:A:136:GLY:HA3	1:A:184:GLN:HG2	2.03	0.41
1:B:35:LEU:O	1:B:60:ALA:HA	2.20	0.41
1:C:174:ASP:O	1:C:236:LYS:CE	2.68	0.41
1:B:65:VAL:CG2	1:B:70:GLU:CB	2.97	0.41
1:B:169:HIS:CE1	2:B:372:DCS:C3	3.02	0.41
1:A:36:PHE:CZ	1:A:62:GLY:HA3	2.56	0.41
1:C:323:GLU:O	1:C:324:GLU:C	2.58	0.41
1:A:295:GLN:NE2	3:A:388:HOH:O	2.50	0.41
1:B:120:THR:O	1:B:122:GLU:CG	2.65	0.41
1:B:223:TYR:HB3	1:B:227:MET:CE	2.51	0.41
1:C:325:VAL:HG12	1:C:326:PRO:O	2.20	0.41
1:A:21:ASN:HD21	1:A:244:LYS:H	1.68	0.41
1:A:127:LEU:O	1:A:129:VAL:HG13	2.20	0.41
1:A:143:LEU:HD21	1:C:257:LYS:HD3	2.01	0.41
1:C:36:PHE:HB2	1:C:220:MET:CE	2.50	0.41
1:C:328:GLY:N	1:C:329:PRO:CD	2.84	0.41
1:B:36:PHE:CD1	1:B:62:GLY:HA3	2.56	0.41
1:A:353:THR:CG2	1:C:293:HIS:CE1	3.03	0.41
1:C:56:LYS:HD2	1:C:60:ALA:O	2.21	0.41
1:A:68:LEU:O	1:A:71:ALA:HB3	2.21	0.41
1:A:129:VAL:HG22	1:A:163:TRP:HA	2.03	0.41
1:B:72:ILE:O	1:B:72:ILE:HG13	2.18	0.41
1:B:152:VAL:HG23	1:B:153:ARG:N	2.34	0.41
1:B:153:ARG:NH2	1:B:156:GLN:HE21	2.10	0.41
1:B:324:GLU:O	1:B:324:GLU:HG3	2.21	0.41
1:C:74:LEU:C	1:C:79:VAL:HG22	2.41	0.41
1:A:44:TYR:HE2	1:A:225:VAL:HG12	1.86	0.41
1:A:258:ARG:HB2	1:A:278:TRP:CZ3	2.56	0.41
1:A:268:GLY:HA2	1:C:172:THR:HG22	2.02	0.41
1:B:68:LEU:HA	1:B:85:ILE:HD13	2.03	0.41
1:B:127:LEU:HD12	1:B:129:VAL:CG1	2.50	0.41
1:B:278:TRP:CZ3	1:B:324:GLU:CD	2.95	0.41
1:B:317:CYS:C	1:B:318:MET:HE3	2.41	0.41
1:C:216:VAL:O	1:C:216:VAL:HG13	2.20	0.41
1:C:365:ARG:O	1:C:367:PRO:HD3	2.20	0.41
1:A:260:ALA:O	1:A:261:ALA:C	2.59	0.40
1:B:26:CYS:O	1:B:30:PRO:HB3	2.21	0.40
1:C:148:THR:CB	1:C:191:VAL:CG1	2.99	0.40
1:C:206:ASN:ND2	1:C:206:ASN:H	2.19	0.40
1:C:251:SER:OG	1:C:252:GLU:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:203:HIS:HB3	1:A:220:MET:O	2.21	0.40
1:A:285:GLY:HA3	1:A:314:MET:O	2.21	0.40
1:B:294:LEU:HD21	1:B:351:LEU:CD2	2.51	0.40
1:A:137:MET:O	1:A:137:MET:HG3	2.21	0.40
1:C:35:LEU:C	1:C:35:LEU:CD1	2.90	0.40
1:C:107:ALA:HB2	1:C:140:ILE:HG22	2.03	0.40
1:A:30:PRO:C	1:A:32:GLY:H	2.24	0.40
1:A:225:VAL:CG1	1:A:356:TYR:CZ	3.00	0.40
1:A:278:TRP:CZ3	1:A:324:GLU:OE2	2.75	0.40
1:A:278:TRP:CE2	1:A:324:GLU:OE2	2.75	0.40
1:B:38:VAL:HB	1:B:64:CYS:HB2	2.03	0.40
1:B:166:ILE:O	1:B:166:ILE:HG23	2.21	0.40
1:C:29:LEU:HD11	1:C:221:ILE:HD11	2.03	0.40
1:C:206:ASN:H	1:C:209:THR:HB	1.86	0.40
1:A:35:LEU:C	1:A:35:LEU:CD1	2.87	0.40
1:B:308:ILE:HG12	1:B:319:ILE:HG22	2.03	0.40
1:C:8:PRO:CG	1:C:252:GLU:HG2	2.52	0.40
1:C:315:ASP:HB2	1:C:316:GLN:OE1	2.22	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	368/371 (99%)	331 (90%)	30 (8%)	7 (2%)	<b>8</b> <b>13</b>
1	B	368/371 (99%)	332 (90%)	35 (10%)	1 (0%)	41 61
1	C	368/371 (99%)	340 (92%)	26 (7%)	2 (0%)	29 48
All	All	1104/1113 (99%)	1003 (91%)	91 (8%)	10 (1%)	<b>17</b> <b>31</b>

All (10) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	A	124	ASN
1	A	137	MET
1	A	197	GLU
1	B	30	PRO
1	C	118	GLN
1	A	30	PRO
1	A	91	LEU
1	A	323	GLU
1	A	232	PRO
1	C	217	PRO

### 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	305/306 (100%)	286 (94%)	19 (6%)	18	35
1	B	305/306 (100%)	282 (92%)	23 (8%)	13	26
1	C	305/306 (100%)	286 (94%)	19 (6%)	18	35
All	All	915/918 (100%)	854 (93%)	61 (7%)	16	31

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	VAL
1	A	122	GLU
1	A	133	VAL
1	A	137	MET
1	A	139	ARG
1	A	159	LYS
1	A	166	ILE
1	A	197	GLU
1	A	206	ASN
1	A	209	THR
1	A	220	MET
1	A	223	TYR
1	A	235	ASN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	247	LEU
1	A	318	MET
1	A	320	ARG
1	A	341	GLU
1	A	351	LEU
1	A	355	HIS
1	B	38	VAL
1	B	40	LYS
1	B	42	ASN
1	B	72	ILE
1	B	122	GLU
1	B	124	ASN
1	B	128	ARG
1	B	133	VAL
1	B	162	LEU
1	B	175	GLU
1	B	203	HIS
1	B	209	THR
1	B	219	ASN
1	B	220	MET
1	B	221	ILE
1	B	223	TYR
1	B	235	ASN
1	B	250	THR
1	B	265	ILE
1	B	318	MET
1	B	344	LEU
1	B	351	LEU
1	B	365	ARG
1	C	2	VAL
1	C	38	VAL
1	C	50	GLU
1	C	69	ASP
1	C	105	THR
1	C	109	GLN
1	C	120	THR
1	C	127	LEU
1	C	206	ASN
1	C	220	MET
1	C	223	TYR
1	C	231	ASN
1	C	257	LYS

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Mol	Chain	Res	Type
1	C	272	VAL
1	C	301	VAL
1	C	311	ARG
1	C	316	GLN
1	C	351	LEU
1	C	353	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	21	ASN
1	A	158	HIS
1	A	184	GLN
1	A	206	ASN
1	A	235	ASN
1	A	295	GLN
1	A	345	GLN
1	A	371	ASN
1	B	12	HIS
1	B	99	GLN
1	B	118	GLN
1	B	156	GLN
1	B	158	HIS
1	B	184	GLN
1	B	219	ASN
1	B	235	ASN
1	B	295	GLN
1	B	345	GLN
1	C	12	HIS
1	C	99	GLN
1	C	118	GLN
1	C	206	ASN
1	C	231	ASN
1	C	355	HIS
1	C	371	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
2	DCS	A	372	-	22,23,23	4.18	11 (50%)	25,33,33	1.62	5 (20%)
2	DCS	C	372	-	22,23,23	4.31	11 (50%)	25,33,33	1.53	5 (20%)
2	DCS	B	372	-	22,23,23	4.22	11 (50%)	25,33,33	1.55	7 (28%)

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	DCS	A	372	-	1/1/3/5	1/10/21/21	0/2/2/2
2	DCS	C	372	-	1/1/3/5	0/10/21/21	0/2/2/2
2	DCS	B	372	-	1/1/3/5	2/10/21/21	0/2/2/2

All (33) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	372	DCS	CA-C	-13.11	1.42	1.52
2	A	372	DCS	CA-C	-12.83	1.43	1.52
2	B	372	DCS	CA-C	-12.80	1.43	1.52
2	B	372	DCS	CB-CA	-7.71	1.37	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	372	DCS	CB-CA	-7.64	1.37	1.54
2	C	372	DCS	CB-CA	-7.57	1.37	1.54
2	A	372	DCS	O-C	6.80	1.36	1.23
2	B	372	DCS	O-C	6.59	1.36	1.23
2	C	372	DCS	O-C	6.48	1.36	1.23
2	B	372	DCS	C5-C4	5.50	1.48	1.40
2	A	372	DCS	C2-N1	5.29	1.43	1.33
2	C	372	DCS	C5-C4	5.25	1.47	1.40
2	C	372	DCS	C2-N1	5.02	1.43	1.33
2	B	372	DCS	C2-N1	4.96	1.43	1.33
2	A	372	DCS	C5-C4	4.58	1.46	1.40
2	C	372	DCS	C3-C4	4.49	1.46	1.40
2	C	372	DCS	OG-CB	-4.43	1.35	1.44
2	A	372	DCS	OG-CB	-4.38	1.35	1.44
2	B	372	DCS	OG-CB	-4.18	1.35	1.44
2	A	372	DCS	C3-C4	3.81	1.45	1.40
2	B	372	DCS	C3-C4	3.63	1.45	1.40
2	C	372	DCS	CA-N	-3.11	1.39	1.46
2	B	372	DCS	CA-N	-2.89	1.40	1.46
2	B	372	DCS	C-ND	-2.87	1.31	1.34
2	C	372	DCS	C-ND	-2.79	1.31	1.34
2	A	372	DCS	CA-N	-2.58	1.40	1.46
2	A	372	DCS	C-ND	-2.45	1.31	1.34
2	C	372	DCS	P-O3P	-2.42	1.45	1.54
2	B	372	DCS	P-O3P	-2.41	1.45	1.54
2	A	372	DCS	P-O3P	-2.20	1.46	1.54
2	A	372	DCS	P-O2P	-2.19	1.46	1.54
2	B	372	DCS	P-O2P	-2.16	1.46	1.54
2	C	372	DCS	P-O2P	-2.01	1.47	1.54

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	372	DCS	C4A-N-CA	3.69	120.92	113.92
2	C	372	DCS	C6-N1-C2	3.40	125.47	119.17
2	B	372	DCS	C6-N1-C2	3.31	125.30	119.17
2	A	372	DCS	C6-C5-C4	3.20	120.38	118.12
2	C	372	DCS	C3-C2-N1	-3.10	116.76	120.77
2	A	372	DCS	C6-N1-C2	3.01	124.74	119.17
2	C	372	DCS	C4A-N-CA	2.73	119.09	113.92
2	B	372	DCS	C3-C2-N1	-2.72	117.25	120.77
2	A	372	DCS	C5-C6-N1	-2.69	119.34	123.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	372	DCS	C5-C6-N1	-2.61	119.48	123.82
2	A	372	DCS	C3-C2-N1	-2.56	117.46	120.77
2	C	372	DCS	C5-C6-N1	-2.34	119.92	123.82
2	B	372	DCS	O4P-C5A-C5	2.18	113.51	109.35
2	B	372	DCS	C6-C5-C4	2.17	119.65	118.12
2	C	372	DCS	CB-OG-ND	2.10	108.92	105.72
2	B	372	DCS	CB-OG-ND	2.04	108.83	105.72
2	B	372	DCS	C5A-C5-C6	-2.00	116.08	119.37

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	372	DCS	CA
2	B	372	DCS	CA
2	C	372	DCS	CA

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	372	DCS	C4-C5-C5A-O4P
2	B	372	DCS	C6-C5-C5A-O4P
2	A	372	DCS	C5-C4-C4A-N

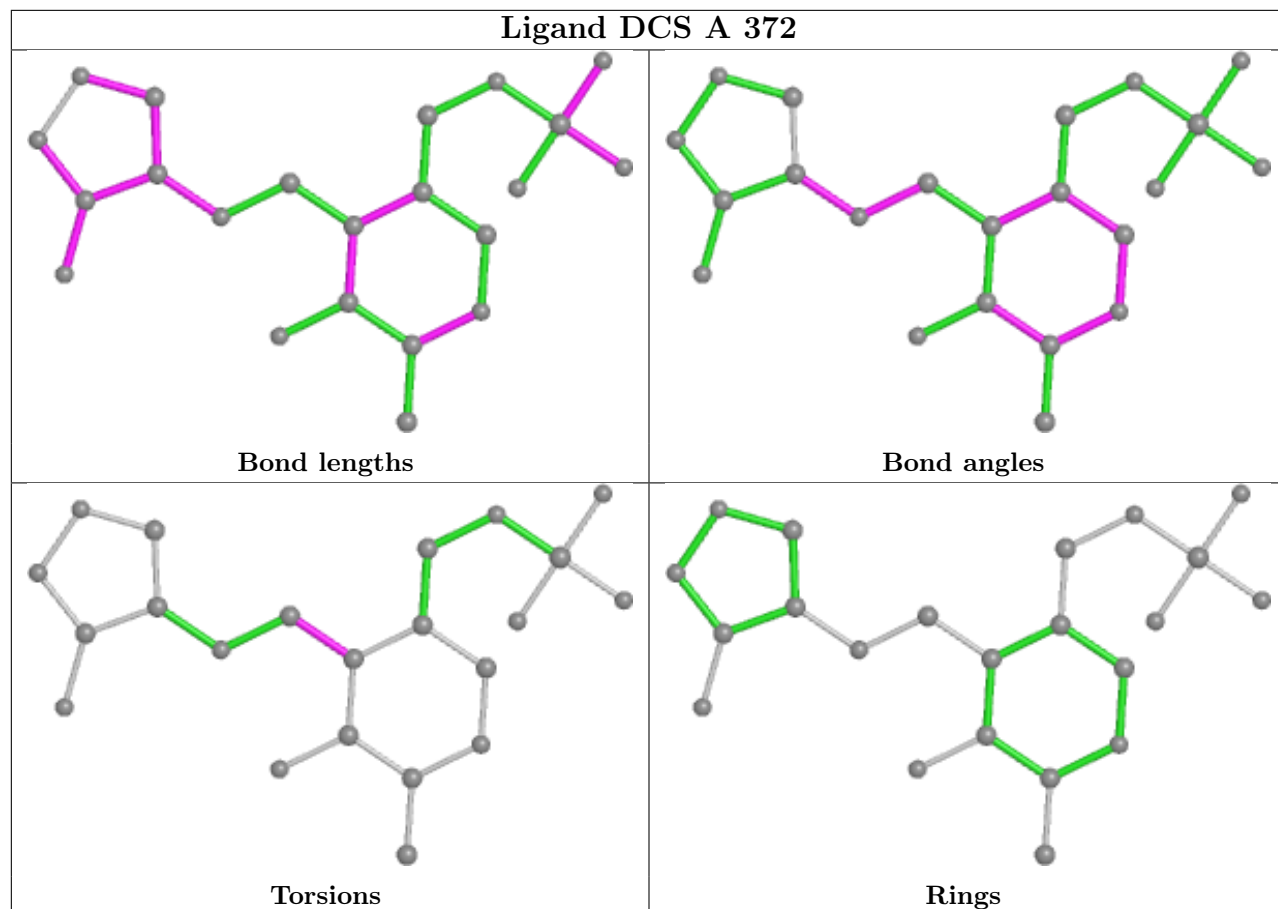
There are no ring outliers.

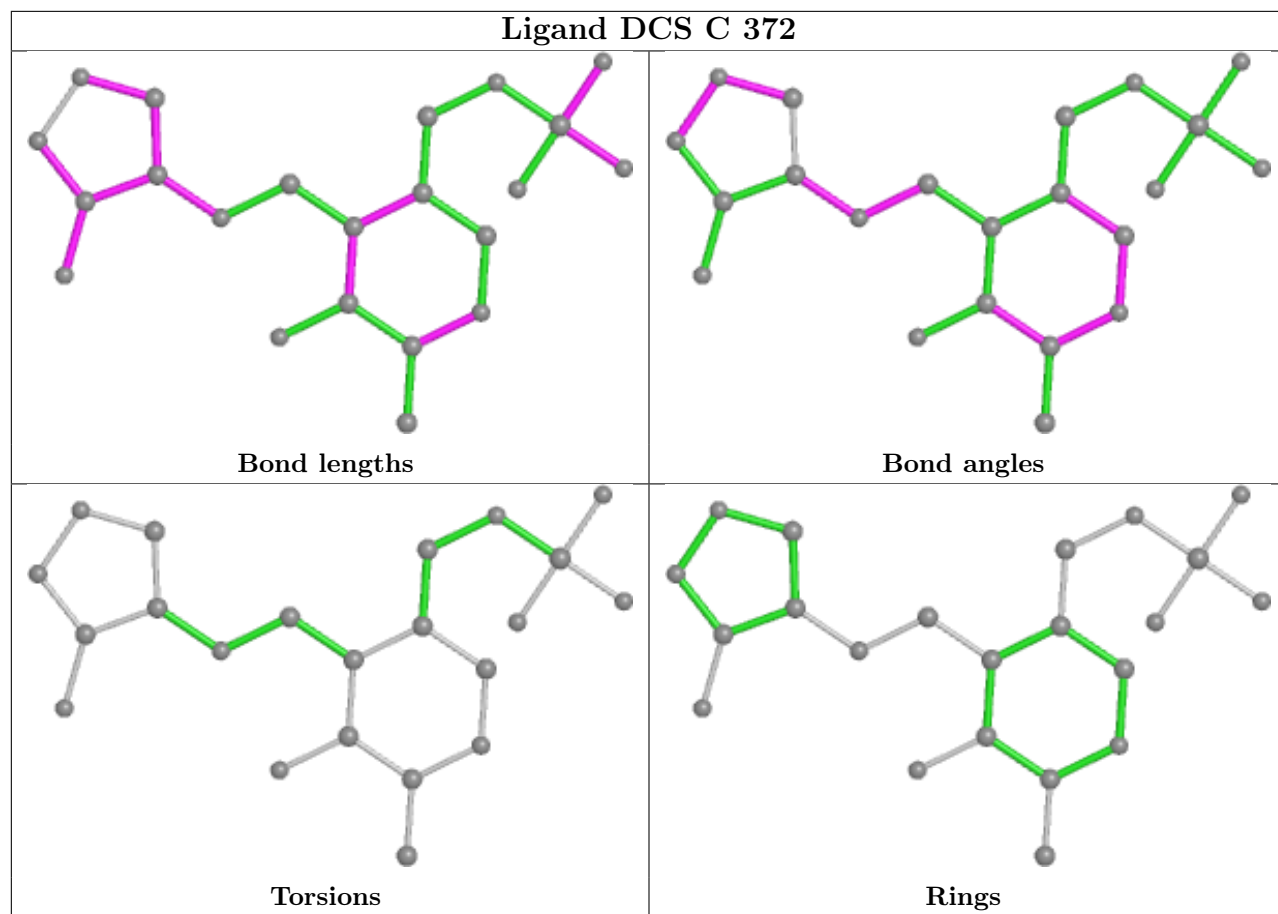
3 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	372	DCS	3	0
2	C	372	DCS	8	0
2	B	372	DCS	2	0

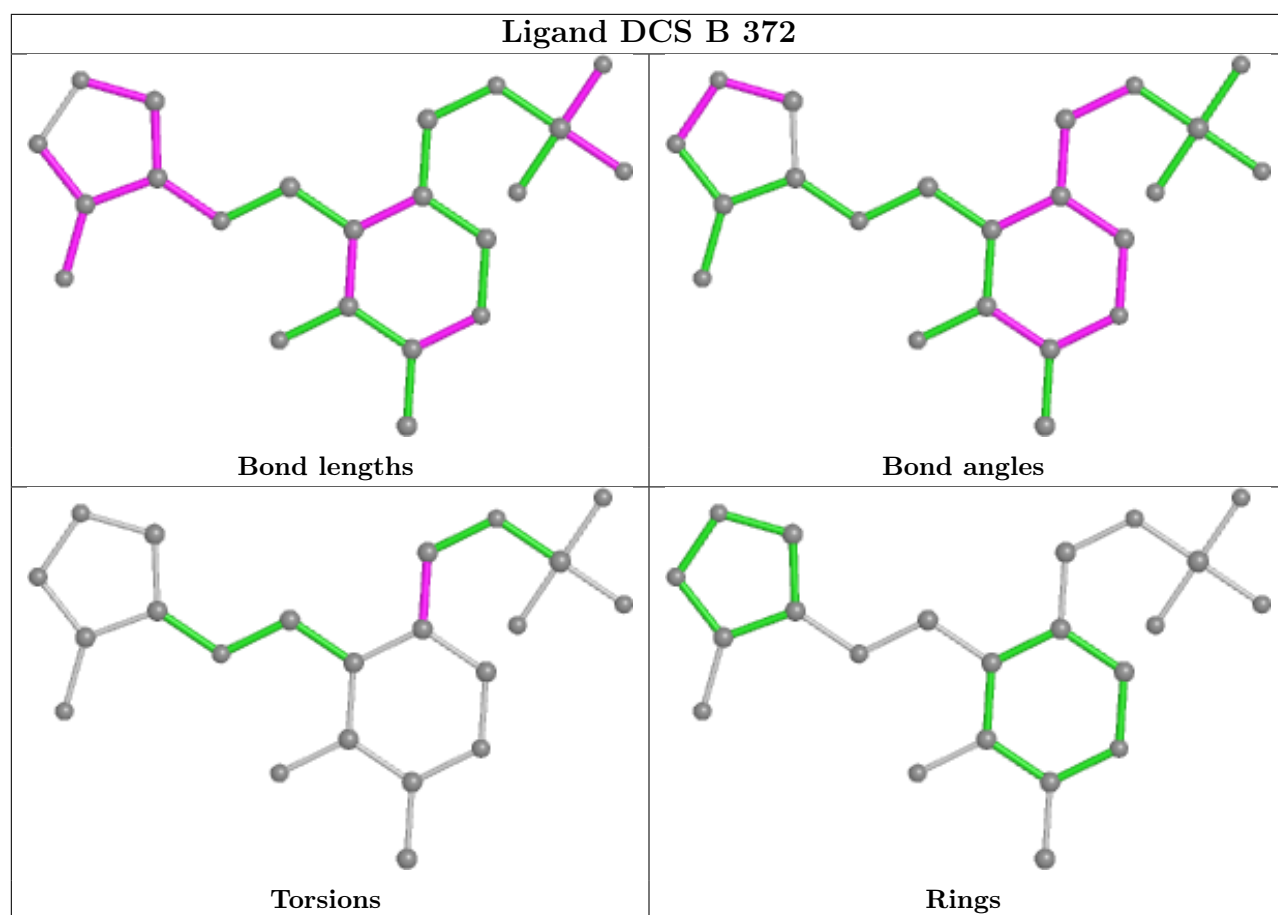
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	370/371 (99%)	-0.11	6 (1%) 72 74	12, 24, 43, 71	0
1	B	370/371 (99%)	-0.17	4 (1%) 80 82	6, 24, 42, 75	0
1	C	370/371 (99%)	-0.13	5 (1%) 75 77	13, 26, 40, 53	0
All	All	1110/1113 (99%)	-0.13	15 (1%) 75 77	6, 25, 41, 75	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	123	SER	6.0
1	A	122	GLU	4.1
1	B	124	ASN	4.0
1	A	121	PRO	3.7
1	A	32	GLY	2.8
1	C	121	PRO	2.4
1	C	94	VAL	2.4
1	A	322	ALA	2.4
1	B	190	ALA	2.4
1	C	371	ASN	2.3
1	A	191	VAL	2.2
1	A	124	ASN	2.2
1	B	122	GLU	2.1
1	C	31	GLU	2.1
1	C	2	VAL	2.1

### 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](#)

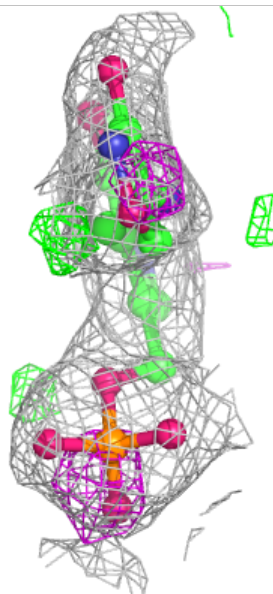
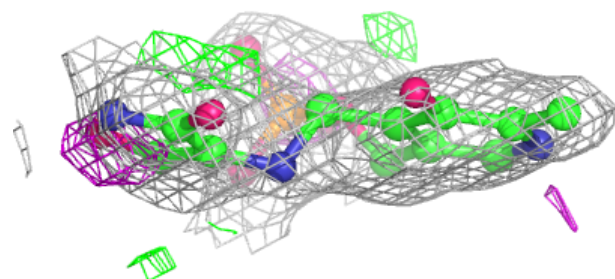
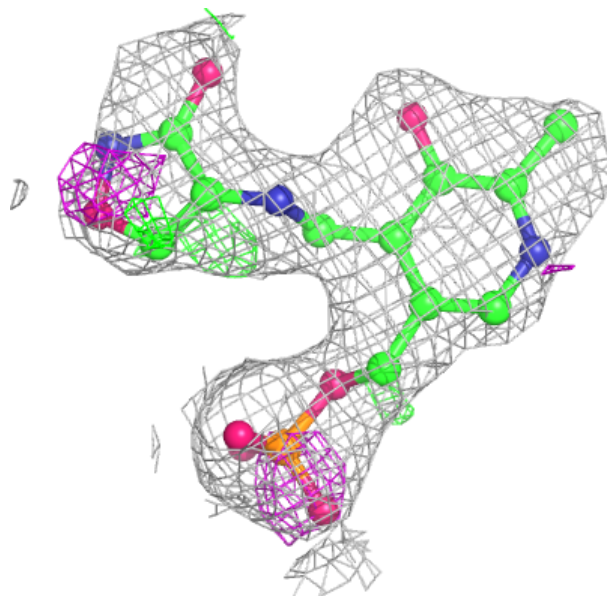
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	DCS	B	372	22/22	0.92	0.17	24,32,43,45	0
2	DCS	A	372	22/22	0.94	0.14	24,29,38,39	0
2	DCS	C	372	22/22	0.94	0.15	15,20,41,43	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.

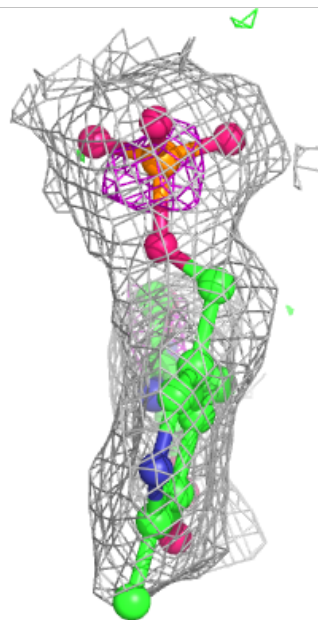
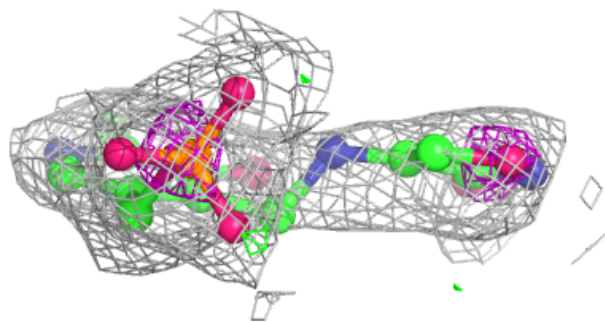
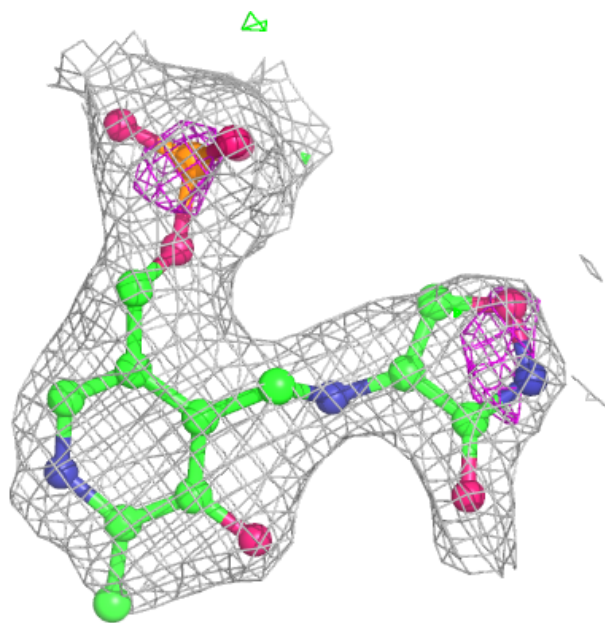
**Electron density around DCS B 372:**

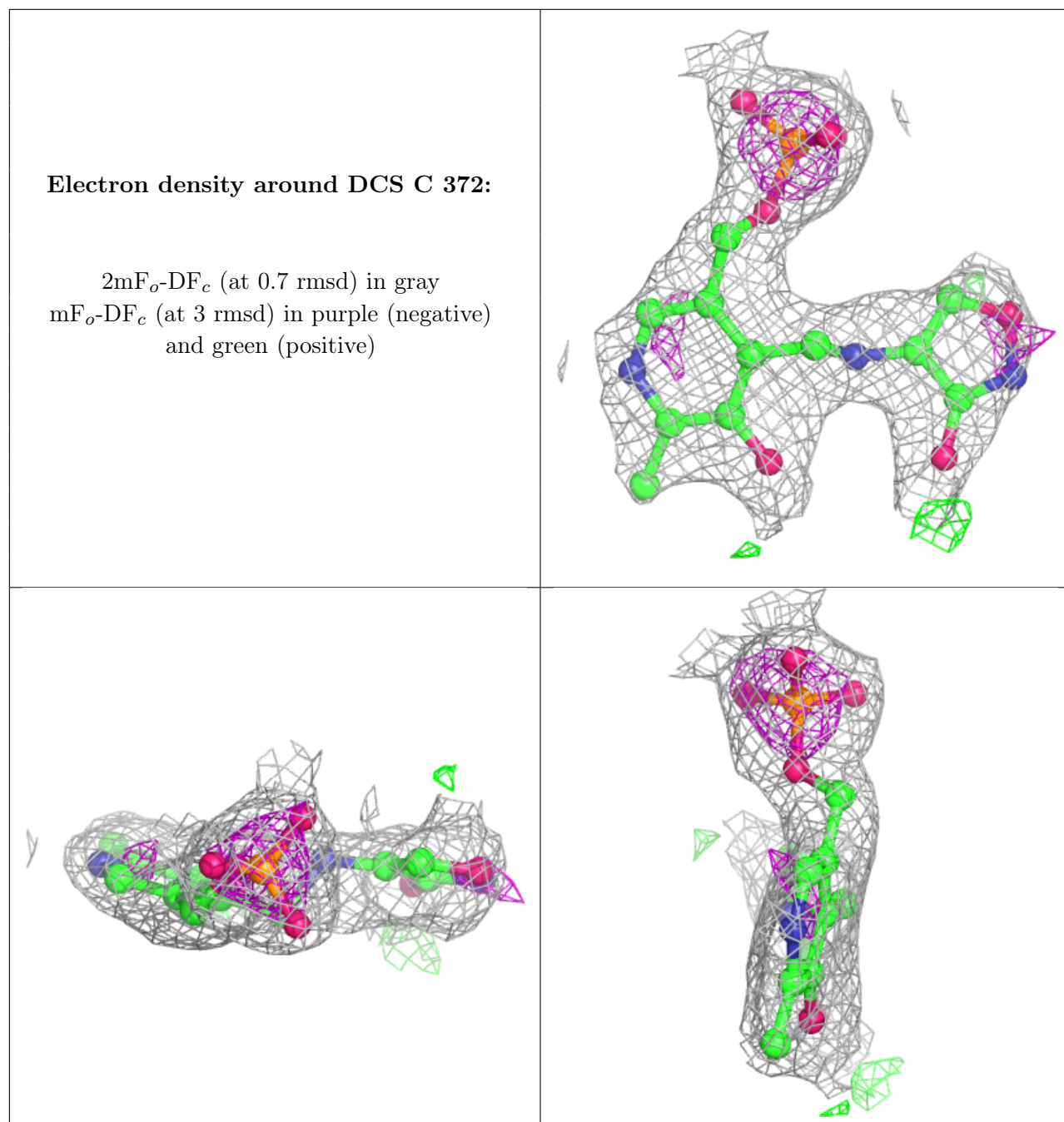
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around DCS A 372:**

$2mF_o-DF_c$  (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.