



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:57 AM UTC

PDB ID : 3RBM / pdb_00003rbm
Title : Crystal structure of Plasmodium vivax geranylgeranylpyrophosphate synthase complexed with BPH -703
Authors : Liu, Y.L.; No, J.H.; Oldfield, E.
Deposited on : 2011-03-29
Resolution : 2.61 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

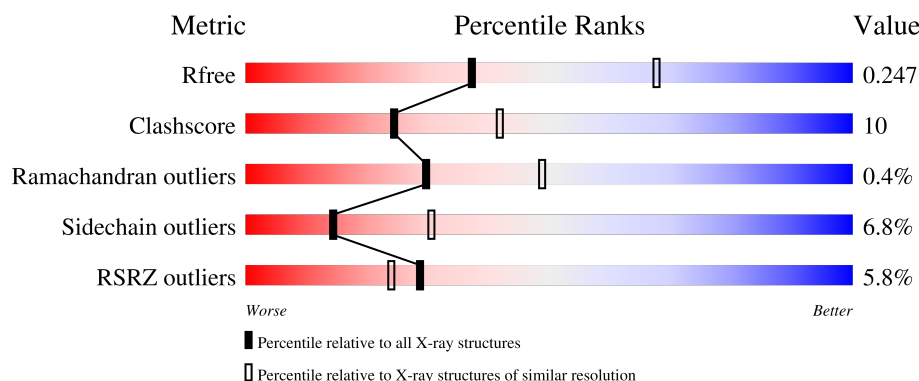
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.61 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	4951 (2.64-2.60)
Clashscore	190562	5303 (2.64-2.60)
Ramachandran outliers	187476	5217 (2.64-2.60)
Sidechain outliers	187428	5217 (2.64-2.60)
RSRZ outliers	180081	4950 (2.64-2.60)

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	396	4% 73% 16% 10%
1	B	396	6% 74% 15% 9%
1	C	396	6% 73% 15% 10%
1	D	396	6% 72% 16% 10%

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
3	B73	B	2001	-	-	X	-
3	B73	C	2001	-	X	X	-
3	B73	D	2001	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12025 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 Farnesyl pyrophosphate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	355	Total	C	N	O	S	13	0	0
			2888	1882	456	535	15			
1	B	362	Total	C	N	O	S	10	0	0
			2938	1909	467	547	15			
1	C	356	Total	C	N	O	S	13	0	0
			2894	1885	457	537	15			
1	D	357	Total	C	N	O	S	13	1	0
			2899	1888	458	538	15			

There are 92 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP A5K4U6
A	2	GLY	-	expression tag	UNP A5K4U6
A	3	SER	-	expression tag	UNP A5K4U6
A	4	SER	-	expression tag	UNP A5K4U6
A	5	HIS	-	expression tag	UNP A5K4U6
A	6	HIS	-	expression tag	UNP A5K4U6
A	7	HIS	-	expression tag	UNP A5K4U6
A	8	HIS	-	expression tag	UNP A5K4U6
A	9	HIS	-	expression tag	UNP A5K4U6
A	10	HIS	-	expression tag	UNP A5K4U6
A	11	SER	-	expression tag	UNP A5K4U6
A	12	SER	-	expression tag	UNP A5K4U6
A	13	GLY	-	expression tag	UNP A5K4U6
A	14	ARG	-	expression tag	UNP A5K4U6
A	15	GLU	-	expression tag	UNP A5K4U6
A	16	ASN	-	expression tag	UNP A5K4U6
A	17	LEU	-	expression tag	UNP A5K4U6
A	18	TYR	-	expression tag	UNP A5K4U6
A	19	PHE	-	expression tag	UNP A5K4U6
A	20	GLN	-	expression tag	UNP A5K4U6
A	21	GLY	-	expression tag	UNP A5K4U6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	134	MET	THR	SEE REMARK 999	UNP A5K4U6
A	227	ASP	ASN	SEE REMARK 999	UNP A5K4U6
B	1	MET	-	expression tag	UNP A5K4U6
B	2	GLY	-	expression tag	UNP A5K4U6
B	3	SER	-	expression tag	UNP A5K4U6
B	4	SER	-	expression tag	UNP A5K4U6
B	5	HIS	-	expression tag	UNP A5K4U6
B	6	HIS	-	expression tag	UNP A5K4U6
B	7	HIS	-	expression tag	UNP A5K4U6
B	8	HIS	-	expression tag	UNP A5K4U6
B	9	HIS	-	expression tag	UNP A5K4U6
B	10	HIS	-	expression tag	UNP A5K4U6
B	11	SER	-	expression tag	UNP A5K4U6
B	12	SER	-	expression tag	UNP A5K4U6
B	13	GLY	-	expression tag	UNP A5K4U6
B	14	ARG	-	expression tag	UNP A5K4U6
B	15	GLU	-	expression tag	UNP A5K4U6
B	16	ASN	-	expression tag	UNP A5K4U6
B	17	LEU	-	expression tag	UNP A5K4U6
B	18	TYR	-	expression tag	UNP A5K4U6
B	19	PHE	-	expression tag	UNP A5K4U6
B	20	GLN	-	expression tag	UNP A5K4U6
B	21	GLY	-	expression tag	UNP A5K4U6
B	134	MET	THR	SEE REMARK 999	UNP A5K4U6
B	227	ASP	ASN	SEE REMARK 999	UNP A5K4U6
C	1	MET	-	expression tag	UNP A5K4U6
C	2	GLY	-	expression tag	UNP A5K4U6
C	3	SER	-	expression tag	UNP A5K4U6
C	4	SER	-	expression tag	UNP A5K4U6
C	5	HIS	-	expression tag	UNP A5K4U6
C	6	HIS	-	expression tag	UNP A5K4U6
C	7	HIS	-	expression tag	UNP A5K4U6
C	8	HIS	-	expression tag	UNP A5K4U6
C	9	HIS	-	expression tag	UNP A5K4U6
C	10	HIS	-	expression tag	UNP A5K4U6
C	11	SER	-	expression tag	UNP A5K4U6
C	12	SER	-	expression tag	UNP A5K4U6
C	13	GLY	-	expression tag	UNP A5K4U6
C	14	ARG	-	expression tag	UNP A5K4U6
C	15	GLU	-	expression tag	UNP A5K4U6
C	16	ASN	-	expression tag	UNP A5K4U6
C	17	LEU	-	expression tag	UNP A5K4U6

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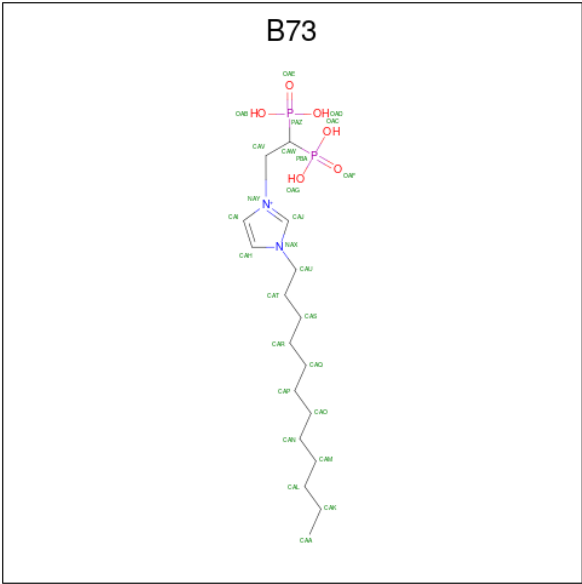
Chain	Residue	Modelled	Actual	Comment	Reference
C	18	TYR	-	expression tag	UNP A5K4U6
C	19	PHE	-	expression tag	UNP A5K4U6
C	20	GLN	-	expression tag	UNP A5K4U6
C	21	GLY	-	expression tag	UNP A5K4U6
C	134	MET	THR	SEE REMARK 999	UNP A5K4U6
C	227	ASP	ASN	SEE REMARK 999	UNP A5K4U6
D	1	MET	-	expression tag	UNP A5K4U6
D	2	GLY	-	expression tag	UNP A5K4U6
D	3	SER	-	expression tag	UNP A5K4U6
D	4	SER	-	expression tag	UNP A5K4U6
D	5	HIS	-	expression tag	UNP A5K4U6
D	6	HIS	-	expression tag	UNP A5K4U6
D	7	HIS	-	expression tag	UNP A5K4U6
D	8	HIS	-	expression tag	UNP A5K4U6
D	9	HIS	-	expression tag	UNP A5K4U6
D	10	HIS	-	expression tag	UNP A5K4U6
D	11	SER	-	expression tag	UNP A5K4U6
D	12	SER	-	expression tag	UNP A5K4U6
D	13	GLY	-	expression tag	UNP A5K4U6
D	14	ARG	-	expression tag	UNP A5K4U6
D	15	GLU	-	expression tag	UNP A5K4U6
D	16	ASN	-	expression tag	UNP A5K4U6
D	17	LEU	-	expression tag	UNP A5K4U6
D	18	TYR	-	expression tag	UNP A5K4U6
D	19	PHE	-	expression tag	UNP A5K4U6
D	20	GLN	-	expression tag	UNP A5K4U6
D	21	GLY	-	expression tag	UNP A5K4U6
D	134	MET	THR	SEE REMARK 999	UNP A5K4U6
D	227	ASP	ASN	SEE REMARK 999	UNP A5K4U6

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	3	Total Mg 3 3	0	0
2	B	3	Total Mg 3 3	0	0
2	C	3	Total Mg 3 3	0	0
2	D	3	Total Mg 3 3	0	0

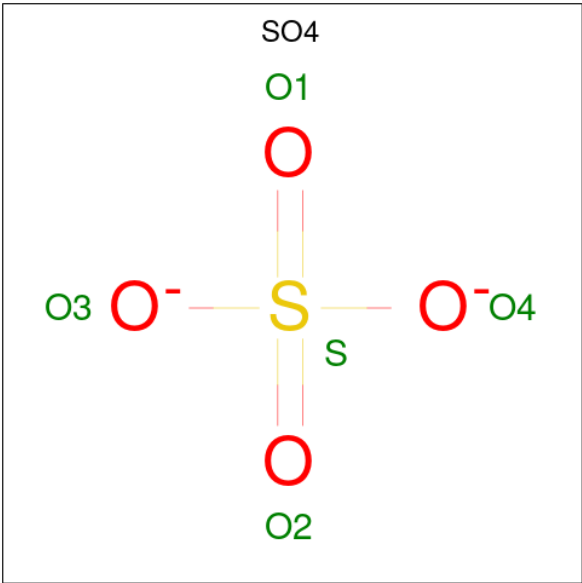
- Molecule 3 is 3-(2,2-diphosphonoethyl)-1-dodecyl-1H-imidazol-3-ium (CCD ID: B73)

(formula: C₁₇H₃₅N₂O₆P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			27	17	2	6	2		
3	B	1	Total	C	N	O	P	0	0
			27	17	2	6	2		
3	C	1	Total	C	N	O	P	0	0
			27	17	2	6	2		
3	D	1	Total	C	N	O	P	0	0
			27	17	2	6	2		

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O S 5 4 1	0	0
4	B	1	Total O S 5 4 1	0	0
4	C	1	Total O S 5 4 1	0	0
4	D	1	Total O S 5 4 1	0	0

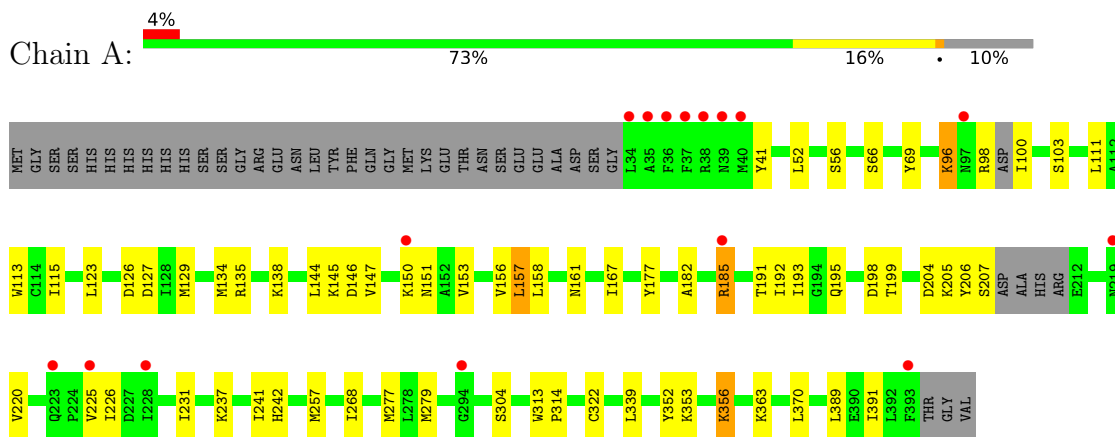
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	72	Total O 72 72	0	0
5	B	81	Total O 81 81	0	0
5	C	56	Total O 56 56	0	0
5	D	57	Total O 57 57	0	0

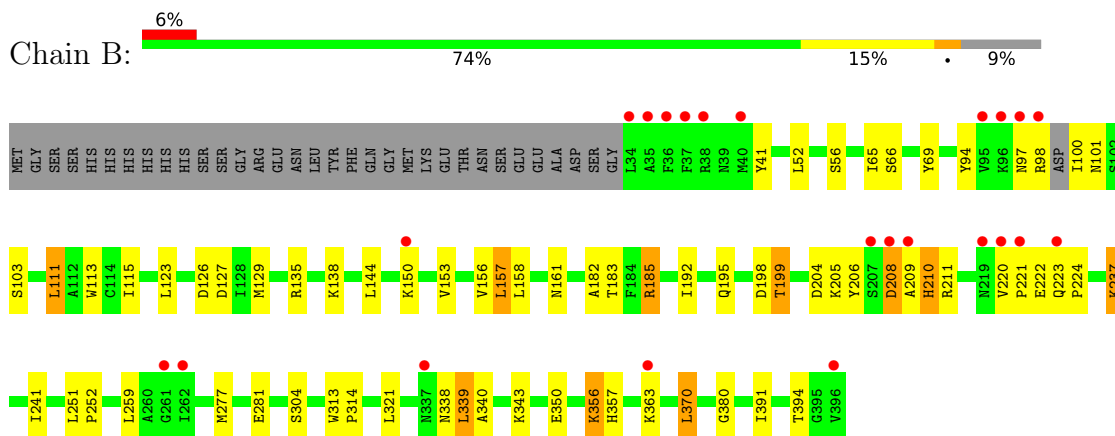
3 Residue-property plots [i](#)

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.

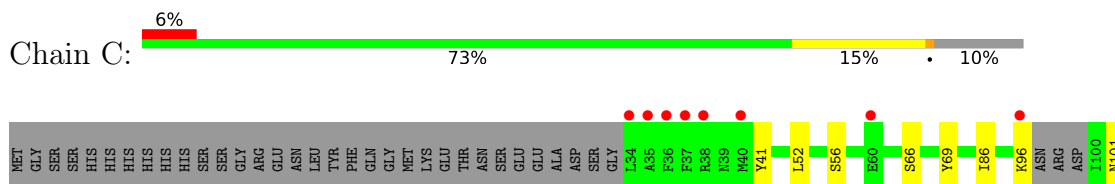
- Molecule 1: Farnesyl pyrophosphate synthase

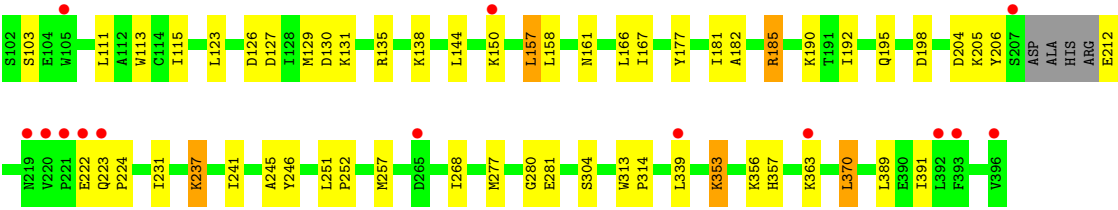


- Molecule 1: Farnesyl pyrophosphate synthase

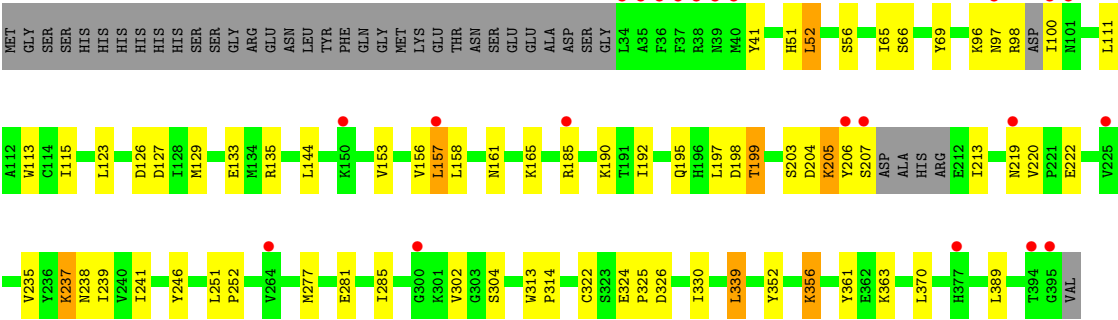


- Molecule 1: Farnesyl pyrophosphate synthase





● Molecule 1: Farnesyl pyrophosphate synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	107.68Å 107.95Å 140.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.58 – 2.61 45.58 – 2.61	Depositor EDS
% Data completeness (in resolution range)	99.2 (45.58-2.61) 99.3 (45.58-2.61)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.08 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.208 , 0.253 0.205 , 0.247	Depositor DCC
R_{free} test set	2554 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	31.6	Xtriage
Anisotropy	0.085	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 43.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.016 for k,h,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	12025	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.10% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: B73, SO4, MG

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	0.64	0/2948	0.79	3/3985 (0.1%)
1	B	0.63	1/3000 (0.0%)	0.79	1/4058 (0.0%)
1	C	0.58	0/2954	0.76	2/3993 (0.1%)
1	D	0.63	0/2959	0.77	1/4000 (0.0%)
All	All	0.62	1/11861 (0.0%)	0.78	7/16036 (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	B	0	2
1	D	0	1
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	356	LYS	C-O	-5.31	1.18	1.24

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	210	HIS	N-CA-C	-7.05	104.33	114.12
1	C	356	LYS	CB-CG-CD	-6.60	96.13	111.30
1	C	356	LYS	CG-CD-CE	-6.47	96.42	111.30
1	A	356	LYS	CB-CG-CD	-6.13	97.20	111.30
1	D	356	LYS	CG-CD-CE	-5.87	97.79	111.30
1	A	356	LYS	CG-CD-CE	-5.35	99.00	111.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	231	ILE	N-CA-C	5.19	111.77	106.21

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	97	ASN	Mainchain,Peptide
1	D	97	ASN	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	2888	0	2840	60	0
1	B	2938	0	2875	60	0
1	C	2894	0	2848	44	0
1	D	2899	0	2850	75	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
2	C	3	0	0	0	0
2	D	3	0	0	0	0
3	A	27	0	31	18	0
3	B	27	0	31	23	0
3	C	27	0	31	28	0
3	D	27	0	31	21	0
4	A	5	0	0	1	0
4	B	5	0	0	0	0
4	C	5	0	0	0	0
4	D	5	0	0	0	0
5	A	72	0	0	3	0
5	B	81	0	0	0	0
5	C	56	0	0	3	0
5	D	57	0	0	1	0
All	All	12025	0	11537	229	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 10.

All (229) 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)
3:C:2001:B73:HAAA	1:D:157:LEU:CB	1.72	1.19
1:A:98:ARG:O	1:A:100:ILE:N	1.77	1.17
1:A:157:LEU:HB2	3:B:2001:B73:HALA	1.16	1.14
3:C:2001:B73:CAL	1:D:157:LEU:HB2	1.77	1.14
1:C:192:ILE:HD11	1:D:157:LEU:HD13	1.27	1.12
3:C:2001:B73:CAA	1:D:157:LEU:HG	1.86	1.05
3:C:2001:B73:HAL	1:D:157:LEU:CB	1.87	1.05
3:C:2001:B73:HAL	1:D:157:LEU:HB2	1.38	1.05
1:A:157:LEU:HD13	1:B:192:ILE:HD11	1.39	1.03
3:A:2001:B73:HAAB	1:B:157:LEU:HG	1.40	1.02
3:C:2001:B73:HAA	3:D:2001:B73:CAA	1.89	1.00
3:C:2001:B73:CAK	1:D:157:LEU:HB2	1.90	1.00
3:C:2001:B73:HAAA	1:D:157:LEU:CG	1.90	1.00
1:A:192:ILE:HD11	1:B:157:LEU:HD13	1.44	1.00
3:A:2001:B73:HALA	1:B:153:VAL:CG1	1.95	0.97
1:D:156:VAL:HG12	3:D:2001:B73:CAA	1.94	0.96
3:C:2001:B73:HAA	3:D:2001:B73:HAAA	1.47	0.94
3:A:2001:B73:HALA	1:B:153:VAL:HG12	1.50	0.94
1:A:182:ALA:HA	1:A:185:ARG:HH22	1.32	0.93
3:C:2001:B73:HAAB	1:D:157:LEU:HG	1.53	0.91
1:B:98:ARG:CB	1:B:100:ILE:N	2.35	0.90
1:A:182:ALA:HA	1:A:185:ARG:NH2	1.87	0.89
3:C:2001:B73:CAA	1:D:157:LEU:CB	2.50	0.89
1:D:156:VAL:HG12	3:D:2001:B73:HAAB	1.54	0.88
1:A:129:MET:HE1	1:A:195:GLN:HG3	1.54	0.87
1:B:156:VAL:HG11	3:B:2001:B73:HAM	1.57	0.87
3:C:2001:B73:CAA	1:D:157:LEU:CG	2.49	0.86
1:D:156:VAL:CG1	3:D:2001:B73:CAA	2.53	0.86
3:C:2001:B73:HAAA	1:D:157:LEU:CA	2.06	0.85
1:A:157:LEU:HB2	3:B:2001:B73:CAL	2.04	0.85
3:C:2001:B73:HAL	1:D:157:LEU:CG	2.08	0.82
1:D:156:VAL:CG1	3:D:2001:B73:HAAB	2.10	0.81
3:C:2001:B73:HAA	3:D:2001:B73:HAA	1.63	0.81
3:C:2001:B73:CAA	1:D:157:LEU:HB2	2.09	0.79
1:C:185:ARG:CZ	5:C:443:HOH:O	2.30	0.78
1:D:129:MET:HE1	1:D:195:GLN:HG3	1.66	0.77
1:B:208:ASP:O	1:B:210:HIS:N	2.16	0.77
1:B:204:ASP:OD2	1:B:222:GLU:HG3	1.83	0.77
1:C:129:MET:HE1	1:C:195:GLN:HG3	1.64	0.77
1:A:199:THR:HG23	1:B:150:LYS:HE2	1.67	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:157:LEU:CB	3:B:2001:B73:HALA	2.08	0.75
1:A:69:TYR:CE1	1:A:158:LEU:HD22	2.22	0.74
1:C:182:ALA:HA	1:C:185:ARG:HH22	1.52	0.74
1:A:241:ILE:HG23	1:A:277:MET:SD	2.27	0.74
1:A:153:VAL:HG13	3:B:2001:B73:HAA	1.70	0.73
1:D:156:VAL:HG12	3:D:2001:B73:HAA	1.71	0.71
3:A:2001:B73:HALA	1:B:153:VAL:HG13	1.72	0.69
1:C:182:ALA:HA	1:C:185:ARG:NH2	2.06	0.69
1:A:153:VAL:HG12	3:B:2001:B73:HAKA	1.75	0.68
3:A:2001:B73:HAK	3:B:2001:B73:HAAA	1.76	0.68
3:C:2001:B73:HAOA	1:D:157:LEU:HD12	1.74	0.68
1:A:127:ASP:OD2	1:A:135:ARG:HD2	1.95	0.67
1:A:153:VAL:HG13	3:B:2001:B73:CAK	2.24	0.67
1:A:153:VAL:CG1	3:B:2001:B73:HAKA	2.25	0.66
1:C:241:ILE:HG23	1:C:277:MET:SD	2.36	0.65
1:A:41:TYR:HB2	1:A:113:TRP:CZ2	2.31	0.65
1:C:129:MET:HE1	1:C:195:GLN:CG	2.25	0.65
1:A:157:LEU:HD12	3:B:2001:B73:HAOA	1.79	0.64
1:C:157:LEU:HD22	1:C:161:ASN:ND2	2.12	0.64
1:A:156:VAL:HG11	3:A:2001:B73:HAKA	1.78	0.64
1:B:135:ARG:NH2	3:B:2001:B73:OAD	2.29	0.64
1:B:204:ASP:N	1:B:222:GLU:OE2	2.22	0.64
1:C:205:LYS:HB3	1:C:206:TYR:HD2	1.63	0.64
1:C:185:ARG:NH2	5:C:443:HOH:O	2.29	0.63
1:B:127:ASP:OD2	1:B:135:ARG:HD2	1.99	0.63
4:A:3001:SO4:O3	5:A:427:HOH:O	2.16	0.62
1:B:208:ASP:C	1:B:210:HIS:H	2.08	0.62
1:A:153:VAL:HG13	3:B:2001:B73:CAA	2.30	0.61
3:C:2001:B73:HAAA	1:D:157:LEU:HA	1.82	0.61
1:C:313:TRP:HB3	1:C:314:PRO:HD3	1.83	0.61
1:D:69:TYR:CE1	1:D:158:LEU:HD22	2.36	0.61
1:A:313:TRP:HB3	1:A:314:PRO:HD3	1.83	0.61
1:B:338:ASN:HD21	1:D:133:GLU:CD	2.08	0.60
3:C:2001:B73:HAL	1:D:157:LEU:HG	1.82	0.60
1:C:245:ALA:HB2	1:C:280:GLY:HA3	1.82	0.60
1:B:69:TYR:CE1	1:B:158:LEU:HD22	2.35	0.60
1:B:129:MET:HE1	1:B:195:GLN:HG3	1.82	0.60
1:A:153:VAL:CG1	3:B:2001:B73:CAK	2.80	0.59
1:C:353:LYS:O	1:C:357:HIS:HD2	1.86	0.59
1:A:157:LEU:HG	3:B:2001:B73:HAMA	1.84	0.58
1:D:129:MET:HE1	1:D:195:GLN:CG	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:192:ILE:CD1	1:D:157:LEU:HD13	2.19	0.58
1:C:212:GLU:N	5:C:408:HOH:O	2.37	0.57
1:C:167:ILE:HG22	1:C:177:TYR:HE1	1.70	0.57
1:A:156:VAL:CG1	3:A:2001:B73:HAKA	2.35	0.56
3:A:2001:B73:HAAB	1:B:157:LEU:CG	2.26	0.56
3:A:2001:B73:CAK	3:B:2001:B73:HAAA	2.35	0.56
1:C:204:ASP:N	1:C:222:GLU:OE2	2.34	0.56
1:D:156:VAL:HG11	3:D:2001:B73:HAKA	1.87	0.56
1:A:145:LYS:HE3	1:B:221:PRO:HG3	1.88	0.56
1:A:98:ARG:HA	1:A:100:ILE:HG13	1.89	0.55
1:D:126:ASP:OD2	3:D:2001:B73:HAW	2.07	0.55
1:B:340:ALA:HB2	1:D:302:VAL:CG1	2.37	0.55
1:D:313:TRP:HB3	1:D:314:PRO:HD3	1.88	0.55
3:A:2001:B73:HAK	3:B:2001:B73:CAA	2.37	0.55
1:B:251:LEU:N	1:B:252:PRO:HD2	2.21	0.54
1:C:41:TYR:HB2	1:C:113:TRP:CZ2	2.43	0.54
3:A:2001:B73:HAN	1:B:157:LEU:HD12	1.88	0.54
3:A:2001:B73:HAA	3:B:2001:B73:HAL	1.89	0.54
1:B:157:LEU:HD22	1:B:161:ASN:ND2	2.23	0.54
3:C:2001:B73:CAA	3:D:2001:B73:HAA	2.35	0.53
3:A:2001:B73:CAA	3:B:2001:B73:HAL	2.38	0.53
1:D:156:VAL:CG1	3:D:2001:B73:HAKA	2.39	0.53
1:D:156:VAL:HG11	3:D:2001:B73:CAK	2.38	0.53
1:B:237:LYS:HD3	1:B:281:GLU:OE2	2.09	0.53
1:A:182:ALA:CA	1:A:185:ARG:HH22	2.14	0.53
1:C:69:TYR:CE1	1:C:158:LEU:HD22	2.43	0.53
1:C:257:MET:HE1	1:C:268:ILE:HG23	1.90	0.53
1:B:111:LEU:HD22	1:B:259:LEU:HD22	1.90	0.52
1:D:157:LEU:HD22	1:D:161:ASN:ND2	2.25	0.52
1:C:192:ILE:HD11	1:D:157:LEU:CD1	2.20	0.52
1:B:340:ALA:HB2	1:D:302:VAL:HG11	1.91	0.52
1:C:157:LEU:HD13	1:D:192:ILE:HD11	1.91	0.52
1:D:98:ARG:O	1:D:100:ILE:N	2.42	0.51
1:A:158:LEU:HB2	1:B:192:ILE:HG21	1.92	0.51
1:C:127:ASP:OD2	1:C:135:ARG:HD2	2.11	0.51
1:D:190:LYS:HD3	1:D:246:TYR:CE1	2.44	0.51
1:B:313:TRP:HB3	1:B:314:PRO:HD3	1.92	0.51
1:A:241:ILE:CG2	1:A:277:MET:SD	2.97	0.50
1:D:156:VAL:CG1	3:D:2001:B73:CAK	2.89	0.50
1:A:157:LEU:HG	3:B:2001:B73:CAL	2.41	0.50
1:A:257:MET:HE1	1:A:268:ILE:HG23	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:204:ASP:O	1:C:205:LYS:C	2.54	0.50
1:D:127:ASP:OD2	1:D:135:ARG:HD2	2.12	0.50
1:D:197:LEU:HB3	1:D:239:ILE:HG12	1.93	0.50
3:C:2001:B73:HAK	1:D:153:VAL:O	2.10	0.50
1:B:41:TYR:HB2	1:B:113:TRP:CZ2	2.47	0.49
1:D:324:GLU:N	1:D:325:PRO:CD	2.75	0.49
3:C:2001:B73:HAAA	1:D:157:LEU:CD2	2.41	0.49
1:A:153:VAL:O	3:B:2001:B73:HAK	2.13	0.49
1:A:157:LEU:HD22	1:A:161:ASN:ND2	2.26	0.49
1:A:225:VAL:HG13	5:A:411:HOH:O	2.11	0.49
1:D:135:ARG:NH2	3:D:2001:B73:OAD	2.39	0.49
1:A:69:TYR:CD1	1:A:158:LEU:HD22	2.47	0.49
1:C:126:ASP:OD2	3:C:2001:B73:HAW	2.12	0.49
1:C:231:ILE:HG22	1:C:231:ILE:O	2.12	0.49
1:A:145:LYS:HE3	1:B:221:PRO:CG	2.42	0.49
1:D:241:ILE:HG23	1:D:277:MET:SD	2.53	0.49
1:A:279:MET:HE2	1:A:389:LEU:HD13	1.95	0.48
1:B:183:THR:HG22	1:B:251:LEU:CD1	2.43	0.48
1:C:157:LEU:HD12	3:D:2001:B73:HAO	1.94	0.48
1:C:205:LYS:HB3	1:C:206:TYR:CD2	2.47	0.48
1:C:223:GLN:HA	1:C:224:PRO:HD3	1.74	0.48
3:C:2001:B73:CAL	1:D:157:LEU:HG	2.43	0.48
1:A:129:MET:HE1	1:A:195:GLN:CG	2.35	0.48
1:A:146:ASP:O	1:B:205:LYS:NZ	2.37	0.48
1:C:237:LYS:HD3	1:C:281:GLU:OE2	2.12	0.48
1:D:41:TYR:HB2	1:D:113:TRP:CZ2	2.48	0.48
1:D:156:VAL:HG11	3:D:2001:B73:HAAB	1.93	0.48
1:A:205:LYS:HB3	1:A:206:TYR:HD2	1.79	0.48
1:D:322:CYS:HA	1:D:352:TYR:CE2	2.49	0.48
3:C:2001:B73:HANA	1:D:157:LEU:CD1	2.44	0.47
1:D:205:LYS:HB3	1:D:206:TYR:HD2	1.79	0.47
1:A:158:LEU:O	1:A:158:LEU:HG	2.13	0.47
1:B:223:GLN:HA	1:B:224:PRO:HD3	1.71	0.47
1:D:251:LEU:N	1:D:252:PRO:HD2	2.30	0.47
3:C:2001:B73:CAO	1:D:157:LEU:HD12	2.41	0.47
1:D:51:HIS:CE1	1:D:165:LYS:HE3	2.49	0.47
1:D:156:VAL:HG11	3:D:2001:B73:CAA	2.39	0.47
1:B:204:ASP:OD2	1:B:222:GLU:CG	2.60	0.47
3:C:2001:B73:OAG	3:C:2001:B73:NAY	2.48	0.47
1:B:321:LEU:HD11	1:B:357:HIS:CE1	2.49	0.46
1:C:391:ILE:HD12	1:C:391:ILE:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96:LYS:HE2	1:A:96:LYS:HA	1.97	0.46
1:B:183:THR:HG22	1:B:251:LEU:HD12	1.98	0.46
1:A:204:ASP:O	1:A:205:LYS:C	2.58	0.46
1:B:182:ALA:HA	1:B:185:ARG:NH2	2.31	0.46
1:B:277:MET:HE2	1:B:277:MET:N	2.31	0.46
1:C:135:ARG:NH2	3:C:2001:B73:OAD	2.45	0.45
1:A:41:TYR:HB2	1:A:113:TRP:CE2	2.52	0.45
1:B:101:ASN:OD1	1:B:101:ASN:C	2.58	0.45
1:C:158:LEU:O	1:C:158:LEU:HG	2.16	0.45
1:B:340:ALA:CB	1:D:302:VAL:HG11	2.47	0.45
1:B:391:ILE:HA	1:B:394:THR:HG22	1.99	0.45
1:A:157:LEU:HG	3:B:2001:B73:CAM	2.47	0.44
1:C:69:TYR:CD1	1:C:158:LEU:HD22	2.52	0.44
1:A:322:CYS:HA	1:A:352:TYR:CE2	2.52	0.44
1:D:156:VAL:HB	3:D:2001:B73:HAKA	1.99	0.44
1:B:339:LEU:HD21	1:D:339:LEU:HA	1.99	0.44
3:D:2001:B73:HAAB	3:D:2001:B73:HAMA	1.65	0.44
3:A:2001:B73:HAOA	1:B:157:LEU:HD12	1.98	0.44
1:C:157:LEU:HD22	1:C:161:ASN:HD22	1.81	0.44
1:C:251:LEU:HB3	1:C:252:PRO:CD	2.47	0.44
1:D:203:SER:OG	1:D:205:LYS:HB2	2.18	0.43
1:D:204:ASP:O	1:D:205:LYS:C	2.60	0.43
1:A:147:VAL:O	1:A:151:ASN:HB2	2.18	0.43
1:C:101:ASN:C	1:C:101:ASN:OD1	2.61	0.43
1:D:326:ASP:O	1:D:330:ILE:HG13	2.18	0.43
1:D:389:LEU:HD12	1:D:389:LEU:HA	1.85	0.43
1:A:167:ILE:HG22	1:A:177:TYR:HE1	1.83	0.43
1:B:251:LEU:HB3	1:B:252:PRO:CD	2.48	0.43
1:C:370:LEU:HD13	1:C:389:LEU:HD23	2.01	0.43
1:A:220:VAL:HG22	1:D:220:VAL:HG22	2.00	0.42
1:D:219:ASN:HB2	5:D:402:HOH:O	2.19	0.42
3:A:2001:B73:CAN	1:B:157:LEU:HD12	2.48	0.42
1:D:313:TRP:N	1:D:314:PRO:CD	2.82	0.42
1:A:191:THR:HA	1:A:242:HIS:O	2.18	0.42
1:B:205:LYS:HB3	1:B:206:TYR:HD2	1.85	0.42
1:D:156:VAL:CB	3:D:2001:B73:HAKA	2.49	0.42
1:A:126:ASP:OD2	3:A:2001:B73:HAW	2.19	0.42
1:A:145:LYS:CE	1:B:221:PRO:HG3	2.49	0.42
3:A:2001:B73:HAAB	1:B:157:LEU:HB2	2.00	0.42
1:D:237:LYS:HD3	1:D:281:GLU:OE2	2.19	0.42
1:B:370:LEU:HD12	1:B:370:LEU:HA	1.94	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:98:ARG:C	1:A:100:ILE:N	2.67	0.42
1:B:126:ASP:OD2	3:B:2001:B73:HAW	2.20	0.42
1:C:167:ILE:HG22	1:C:177:TYR:CE1	2.54	0.41
1:D:204:ASP:N	1:D:222:GLU:OE2	2.37	0.41
1:B:208:ASP:C	1:B:210:HIS:N	2.73	0.41
1:C:130:ASP:O	1:C:131:LYS:C	2.64	0.41
1:A:352:TYR:O	1:A:353:LYS:HB2	2.20	0.41
1:D:235:VAL:O	1:D:238:ASN:HB2	2.21	0.41
1:C:182:ALA:CA	1:C:185:ARG:HH22	2.29	0.41
1:D:52:LEU:HD12	1:D:52:LEU:HA	1.90	0.41
3:A:2001:B73:HAAB	1:B:157:LEU:CB	2.50	0.41
1:D:285:ILE:HD12	1:D:361:TYR:CZ	2.56	0.41
1:A:145:LYS:HG3	1:B:220:VAL:O	2.21	0.41
1:A:391:ILE:O	1:A:391:ILE:HD12	2.21	0.41
1:B:204:ASP:O	1:B:205:LYS:C	2.64	0.41
1:B:343:LYS:HG2	1:D:339:LEU:HD21	2.03	0.41
1:C:150:LYS:HE3	1:D:199:THR:HG23	2.02	0.41
1:A:150:LYS:HE3	1:B:199:THR:HG23	2.04	0.40
1:B:94:TYR:O	1:B:380:GLY:HA3	2.22	0.40
1:B:156:VAL:CG1	3:B:2001:B73:HAM	2.40	0.40
1:C:166:LEU:HD23	1:C:166:LEU:HA	1.95	0.40
1:A:207:SER:O	5:A:399:HOH:O	2.22	0.40
1:A:225:VAL:HG12	1:A:226:ILE:N	2.37	0.40
1:B:158:LEU:O	1:B:158:LEU:HG	2.17	0.40
1:C:190:LYS:HD3	1:C:246:TYR:CE1	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	349/396 (88%)	337 (97%)	11 (3%)	1 (0%)	36 56

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	358/396 (90%)	341 (95%)	15 (4%)	2 (1%)	21	39
1	C	350/396 (88%)	334 (95%)	15 (4%)	1 (0%)	36	56
1	D	351/396 (89%)	336 (96%)	14 (4%)	1 (0%)	36	56
All	All	1408/1584 (89%)	1348 (96%)	55 (4%)	5 (0%)	30	49

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	209	ALA
1	C	304	SER
1	B	304	SER
1	A	304	SER
1	D	304	SER

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	309/357 (87%)	289 (94%)	20 (6%)	15	33
1	B	313/357 (88%)	290 (93%)	23 (7%)	13	27
1	C	310/357 (87%)	290 (94%)	20 (6%)	15	33
1	D	310/357 (87%)	289 (93%)	21 (7%)	14	30
All	All	1242/1428 (87%)	1158 (93%)	84 (7%)	14	30

All (84) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	LEU
1	A	56	SER
1	A	66	SER
1	A	96	LYS
1	A	103	SER
1	A	111	LEU

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Mol	Chain	Res	Type
1	A	115	ILE
1	A	123	LEU
1	A	134	MET
1	A	138	LYS
1	A	144	LEU
1	A	157	LEU
1	A	185	ARG
1	A	193	ILE
1	A	198	ASP
1	A	237	LYS
1	A	339	LEU
1	A	356	LYS
1	A	363	LYS
1	A	370	LEU
1	B	52	LEU
1	B	56	SER
1	B	65	ILE
1	B	66	SER
1	B	103	SER
1	B	111	LEU
1	B	115	ILE
1	B	123	LEU
1	B	138	LYS
1	B	144	LEU
1	B	157	LEU
1	B	185	ARG
1	B	198	ASP
1	B	199	THR
1	B	208	ASP
1	B	211	ARG
1	B	237	LYS
1	B	241	ILE
1	B	339	LEU
1	B	350	GLU
1	B	356	LYS
1	B	363	LYS
1	B	370	LEU
1	C	52	LEU
1	C	56	SER
1	C	66	SER
1	C	86	ILE
1	C	96	LYS

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Mol	Chain	Res	Type
1	C	103	SER
1	C	111	LEU
1	C	115	ILE
1	C	123	LEU
1	C	138	LYS
1	C	144	LEU
1	C	157	LEU
1	C	181	ILE
1	C	185	ARG
1	C	198	ASP
1	C	237	LYS
1	C	339	LEU
1	C	353	LYS
1	C	363	LYS
1	C	370	LEU
1	D	52	LEU
1	D	56	SER
1	D	65	ILE
1	D	66	SER
1	D	96	LYS
1	D	111	LEU
1	D	115	ILE
1	D	123	LEU
1	D	144	LEU
1	D	157	LEU
1	D	185	ARG
1	D	198	ASP
1	D	199	THR
1	D	205	LYS
1	D	207	SER
1	D	213	ILE
1	D	237	LYS
1	D	339	LEU
1	D	356	LYS
1	D	363	LYS
1	D	370	LEU

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	151	ASN
1	A	161	ASN

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Mol	Chain	Res	Type
1	A	337	ASN
1	A	357	HIS
1	B	82	ASN
1	B	137	ASN
1	B	161	ASN
1	B	200	ASN
1	B	286	HIS
1	B	338	ASN
1	B	351	GLN
1	B	357	HIS
1	C	82	ASN
1	C	161	ASN
1	C	200	ASN
1	C	309	ASN
1	C	333	ASN
1	C	357	HIS
1	D	51	HIS
1	D	82	ASN
1	D	137	ASN
1	D	151	ASN
1	D	161	ASN
1	D	337	ASN
1	D	357	HIS

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](#)

Of 20 ligands modelled in this entry, 12 are monoatomic - leaving 8 for Mogul analysis.

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	$\# Z > 2$
4	SO4	D	3001	-	4,4,4	0.37	0	6,6,6	0.49	0
3	B73	C	2001	2	26,27,27	4.18	8 (30%)	32,36,36	2.20	10 (31%)
3	B73	D	2001	2	26,27,27	3.14	6 (23%)	32,36,36	2.46	11 (34%)
4	SO4	B	3001	-	4,4,4	0.37	0	6,6,6	0.32	0
3	B73	B	2001	2	26,27,27	3.45	8 (30%)	32,36,36	2.55	11 (34%)
3	B73	A	2001	2	26,27,27	3.19	6 (23%)	32,36,36	2.64	11 (34%)
4	SO4	C	3001	-	4,4,4	0.34	0	6,6,6	0.16	0
4	SO4	A	3001	-	4,4,4	0.47	0	6,6,6	0.35	0

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	B73	B	2001	2	-	14/26/28/28	0/1/1/1
3	B73	A	2001	2	-	18/26/28/28	0/1/1/1
3	B73	C	2001	2	-	19/26/28/28	0/1/1/1
3	B73	D	2001	2	-	14/26/28/28	0/1/1/1

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	2001	B73	PBA-OAF	16.19	1.76	1.49
3	B	2001	B73	PBA-OAF	11.77	1.69	1.49
3	A	2001	B73	PAZ-OAE	8.66	1.64	1.49
3	D	2001	B73	PBA-OAG	8.45	1.68	1.54
3	A	2001	B73	PBA-OAF	8.37	1.63	1.49
3	B	2001	B73	PAZ-OAE	7.86	1.62	1.49
3	D	2001	B73	PBA-OAF	7.75	1.62	1.49
3	D	2001	B73	PAZ-OAE	7.69	1.62	1.49
3	C	2001	B73	PBA-OAG	7.55	1.66	1.54
3	C	2001	B73	PAZ-OAD	7.53	1.66	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	2001	B73	PBA-OAG	7.36	1.66	1.54
3	B	2001	B73	PBA-OAG	6.92	1.65	1.54
3	C	2001	B73	PAZ-OAE	6.04	1.59	1.49
3	D	2001	B73	PAZ-OAD	5.80	1.64	1.54
3	A	2001	B73	PAZ-OAD	5.66	1.63	1.54
3	B	2001	B73	PAZ-OAD	4.85	1.62	1.54
3	A	2001	B73	PBA-OAC	-3.93	1.48	1.54
3	B	2001	B73	PBA-OAC	-3.67	1.49	1.54
3	A	2001	B73	PAZ-OAB	-3.56	1.49	1.54
3	D	2001	B73	PBA-OAC	-3.37	1.49	1.54
3	D	2001	B73	PAZ-OAB	-3.36	1.49	1.54
3	C	2001	B73	PBA-OAC	-3.31	1.49	1.54
3	C	2001	B73	CAV-NAY	3.24	1.50	1.47
3	B	2001	B73	PAZ-OAB	-2.73	1.50	1.54
3	C	2001	B73	PAZ-OAB	-2.57	1.50	1.54
3	C	2001	B73	PBA-CAW	-2.47	1.78	1.81
3	B	2001	B73	PBA-CAW	-2.18	1.78	1.81
3	B	2001	B73	PAZ-CAW	-2.12	1.78	1.81

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2001	B73	OAF-PBA-CAW	-7.35	91.43	112.29
3	B	2001	B73	OAF-PBA-CAW	-6.60	93.57	112.29
3	A	2001	B73	OAE-PAZ-CAW	-6.17	94.79	112.29
3	D	2001	B73	OAG-PBA-OAF	-5.74	99.05	113.45
3	C	2001	B73	CAV-NAY-CAI	-5.71	117.84	125.67
3	B	2001	B73	OAD-PAZ-OAE	-5.46	99.76	113.45
3	D	2001	B73	OAE-PAZ-CAW	-5.04	97.99	112.29
3	C	2001	B73	OAE-PAZ-CAW	-4.95	98.24	112.29
3	B	2001	B73	OAE-PAZ-CAW	-4.89	98.40	112.29
3	D	2001	B73	OAD-PAZ-OAE	-4.85	101.28	113.45
3	A	2001	B73	OAG-PBA-OAF	-4.72	101.61	113.45
3	D	2001	B73	CAV-NAY-CAI	-4.57	119.40	125.67
3	D	2001	B73	OAF-PBA-CAW	-4.57	99.33	112.29
3	B	2001	B73	CAV-NAY-CAI	-4.46	119.56	125.67
3	A	2001	B73	OAB-PAZ-CAW	4.43	120.76	106.88
3	C	2001	B73	OAF-PBA-CAW	-4.43	99.73	112.29
3	A	2001	B73	CAV-NAY-CAI	-4.34	119.72	125.67
3	B	2001	B73	OAB-PAZ-CAW	4.24	120.15	106.88
3	B	2001	B73	OAG-PBA-OAF	-4.15	103.04	113.45
3	D	2001	B73	OAB-PAZ-CAW	3.82	118.85	106.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2001	B73	OAC-PBA-CAW	3.78	118.70	106.88
3	C	2001	B73	OAG-PBA-OAF	-3.56	104.51	113.45
3	A	2001	B73	NAX-CAJ-NAY	-3.56	104.07	108.78
3	C	2001	B73	OAD-PAZ-OAE	-3.49	104.69	113.45
3	B	2001	B73	OAC-PBA-CAW	3.36	117.39	106.88
3	C	2001	B73	OAC-PBA-CAW	3.23	117.00	106.88
3	D	2001	B73	NAX-CAJ-NAY	-3.20	104.54	108.78
3	B	2001	B73	NAX-CAJ-NAY	-3.12	104.65	108.78
3	C	2001	B73	OAD-PAZ-OAB	2.97	115.65	107.58
3	A	2001	B73	OAD-PAZ-OAE	-2.92	106.12	113.45
3	D	2001	B73	CAU-NAX-CAH	-2.62	119.23	126.49
3	C	2001	B73	NAX-CAJ-NAY	-2.58	105.36	108.78
3	A	2001	B73	OAG-PBA-OAC	2.51	114.39	107.58
3	D	2001	B73	OAB-PAZ-OAE	2.48	119.65	113.45
3	A	2001	B73	CAH-NAX-CAJ	2.43	111.10	107.39
3	B	2001	B73	CAU-NAX-CAH	-2.43	119.77	126.49
3	D	2001	B73	OAG-PBA-OAC	2.39	114.06	107.58
3	B	2001	B73	OAD-PAZ-OAB	2.19	113.53	107.58
3	C	2001	B73	OAB-PAZ-CAW	2.16	113.63	106.88
3	D	2001	B73	OAC-PBA-CAW	2.12	113.51	106.88
3	C	2001	B73	CAU-NAX-CAH	-2.10	120.67	126.49
3	B	2001	B73	OAG-PBA-OAC	2.06	113.18	107.58
3	A	2001	B73	CAU-NAX-CAH	-2.01	120.93	126.49

There are no chirality outliers.

All (65) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	2001	B73	CAV-CAW-PAZ-OAB
3	A	2001	B73	CAV-CAW-PAZ-OAD
3	A	2001	B73	CAV-CAW-PAZ-OAE
3	A	2001	B73	PBA-CAW-PAZ-OAB
3	A	2001	B73	PBA-CAW-PAZ-OAE
3	A	2001	B73	CAV-CAW-PBA-OAC
3	A	2001	B73	CAV-CAW-PBA-OAF
3	A	2001	B73	PAZ-CAW-PBA-OAC
3	A	2001	B73	PAZ-CAW-PBA-OAF
3	B	2001	B73	CAV-CAW-PAZ-OAB
3	B	2001	B73	CAV-CAW-PAZ-OAE
3	B	2001	B73	PBA-CAW-PAZ-OAE
3	B	2001	B73	CAV-CAW-PBA-OAC
3	B	2001	B73	CAV-CAW-PBA-OAF

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Mol	Chain	Res	Type	Atoms
3	B	2001	B73	PAZ-CAW-PBA-OAC
3	B	2001	B73	PAZ-CAW-PBA-OAF
3	C	2001	B73	CAV-CAW-PAZ-OAB
3	C	2001	B73	CAV-CAW-PAZ-OAE
3	C	2001	B73	PBA-CAW-PAZ-OAE
3	C	2001	B73	CAV-CAW-PBA-OAC
3	C	2001	B73	CAV-CAW-PBA-OAF
3	C	2001	B73	PAZ-CAW-PBA-OAC
3	C	2001	B73	PAZ-CAW-PBA-OAF
3	D	2001	B73	CAV-CAW-PAZ-OAE
3	D	2001	B73	PBA-CAW-PAZ-OAE
3	D	2001	B73	CAV-CAW-PBA-OAC
3	D	2001	B73	CAV-CAW-PBA-OAF
3	D	2001	B73	PAZ-CAW-PBA-OAC
3	D	2001	B73	PAZ-CAW-PBA-OAF
3	C	2001	B73	CAM-CAN-CAO-CAP
3	C	2001	B73	CAK-CAL-CAM-CAN
3	A	2001	B73	CAO-CAP-CAQ-CAR
3	D	2001	B73	CAA-CAK-CAL-CAM
3	D	2001	B73	CAT-CAU-NAX-CAH
3	A	2001	B73	CAK-CAL-CAM-CAN
3	A	2001	B73	CAR-CAS-CAT-CAU
3	A	2001	B73	CAA-CAK-CAL-CAM
3	B	2001	B73	CAO-CAP-CAQ-CAR
3	C	2001	B73	CAA-CAK-CAL-CAM
3	C	2001	B73	PBA-CAW-PAZ-OAB
3	C	2001	B73	CAT-CAU-NAX-CAH
3	B	2001	B73	CAT-CAU-NAX-CAJ
3	C	2001	B73	CAT-CAU-NAX-CAJ
3	C	2001	B73	CAO-CAP-CAQ-CAR
3	D	2001	B73	CAT-CAU-NAX-CAJ
3	B	2001	B73	CAT-CAU-NAX-CAH
3	C	2001	B73	CAL-CAM-CAN-CAO
3	A	2001	B73	CAT-CAU-NAX-CAH
3	D	2001	B73	CAK-CAL-CAM-CAN
3	A	2001	B73	CAV-CAW-PBA-OAG
3	B	2001	B73	CAV-CAW-PAZ-OAD
3	B	2001	B73	CAV-CAW-PBA-OAG
3	C	2001	B73	CAW-CAV-NAY-CAI
3	C	2001	B73	CAV-CAW-PAZ-OAD
3	C	2001	B73	CAV-CAW-PBA-OAG
3	D	2001	B73	CAV-CAW-PAZ-OAD

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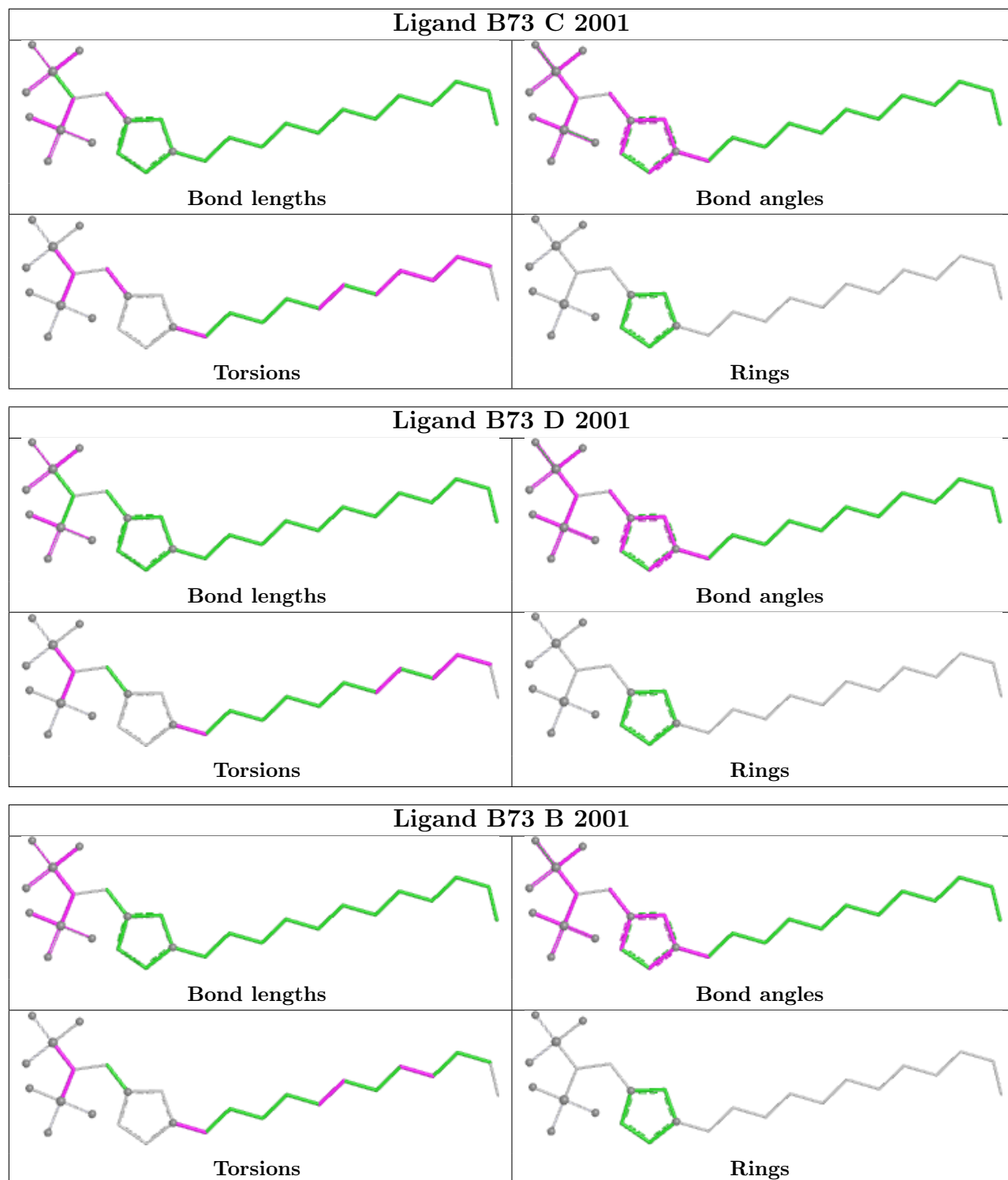
Mol	Chain	Res	Type	Atoms
3	D	2001	B73	CAV-CAW-PBA-OAG
3	A	2001	B73	CAT-CAU-NAX-CAJ
3	A	2001	B73	PBA-CAW-PAZ-OAD
3	B	2001	B73	PBA-CAW-PAZ-OAB
3	C	2001	B73	PAZ-CAW-PBA-OAG
3	A	2001	B73	CAN-CAO-CAP-CAQ
3	B	2001	B73	CAL-CAM-CAN-CAO
3	D	2001	B73	CAM-CAN-CAO-CAP
3	D	2001	B73	PBA-CAW-PAZ-OAB

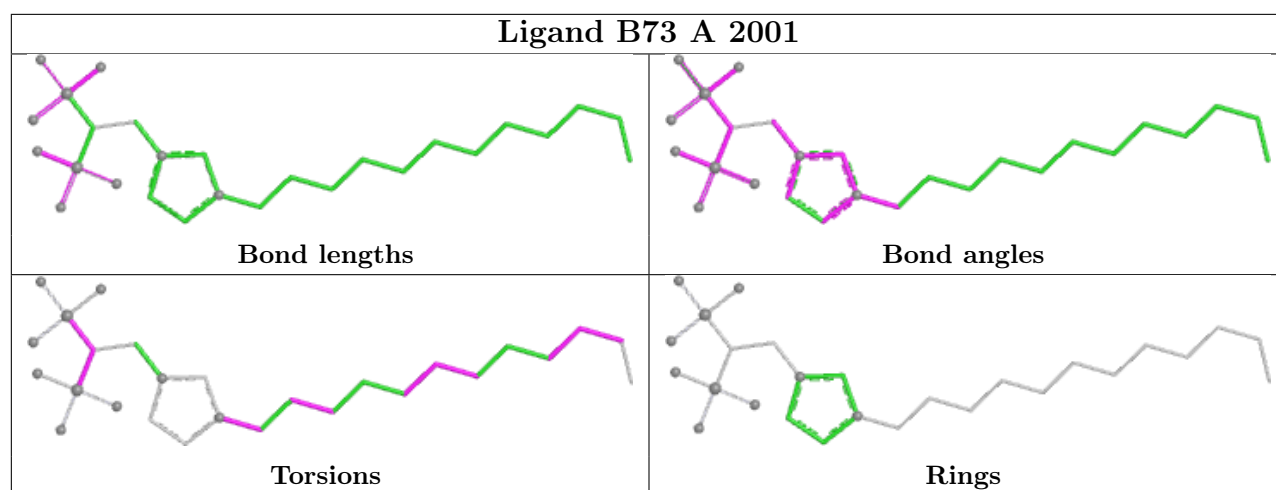
There are no ring outliers.

5 monomers are involved in 82 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	2001	B73	28	0
3	D	2001	B73	21	0
3	B	2001	B73	23	0
3	A	2001	B73	18	0
4	A	3001	SO4	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	355/396 (89%)	0.09	16 (4%) 38 33	17, 28, 53, 217	21 (5%)
1	B	362/396 (91%)	0.14	23 (6%) 25 21	17, 28, 53, 137	20 (5%)
1	C	356/396 (89%)	0.07	22 (6%) 26 22	17, 29, 59, 181	21 (5%)
1	D	357/396 (90%)	0.11	22 (6%) 26 22	17, 29, 58, 174	21 (5%)
All	All	1430/1584 (90%)	0.10	83 (5%) 29 24	17, 28, 57, 217	83 (5%)

All (83) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	34	LEU	7.9
1	D	34	LEU	7.7
1	C	34	LEU	7.7
1	A	37	PHE	6.6
1	A	36	PHE	6.5
1	B	34	LEU	6.3
1	A	35	ALA	5.9
1	A	38	ARG	5.8
1	D	40	MET	5.7
1	C	36	PHE	5.7
1	A	40	MET	5.5
1	C	35	ALA	5.5
1	C	37	PHE	5.4
1	B	36	PHE	4.9
1	D	35	ALA	4.8
1	D	37	PHE	4.7
1	C	38	ARG	4.6
1	D	38	ARG	4.5
1	C	40	MET	4.4
1	B	96	LYS	4.3
1	A	393	PHE	4.2

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Mol	Chain	Res	Type	RSRZ
1	B	40	MET	4.2
1	D	36	PHE	4.2
1	B	219	ASN	4.0
1	B	97	ASN	3.9
1	D	207	SER	3.9
1	C	220	VAL	3.8
1	C	396	VAL	3.6
1	D	219	ASN	3.5
1	B	38	ARG	3.4
1	A	185	ARG	3.4
1	C	221	PRO	3.3
1	C	223	GLN	3.3
1	B	37	PHE	3.3
1	B	220	VAL	3.2
1	B	35	ALA	3.2
1	B	209	ALA	3.2
1	B	95	VAL	3.1
1	D	394	THR	3.1
1	C	150	LYS	3.1
1	A	219	ASN	3.0
1	B	150	LYS	2.9
1	B	223	GLN	2.9
1	C	219	ASN	2.9
1	A	228	ILE	2.9
1	B	363	LYS	2.9
1	C	393	PHE	2.8
1	B	337	ASN	2.7
1	C	207	SER	2.6
1	D	206	TYR	2.6
1	A	97	ASN	2.6
1	B	396	VAL	2.6
1	B	98	ARG	2.6
1	D	377	HIS	2.6
1	B	221	PRO	2.6
1	D	157	LEU	2.5
1	B	208	ASP	2.5
1	C	339	LEU	2.5
1	D	264	VAL	2.5
1	D	39	ASN	2.4
1	B	261	GLY	2.4
1	B	207	SER	2.4
1	C	105	TRP	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	294	GLY	2.4
1	D	150[A]	LYS	2.3
1	D	300	GLY	2.3
1	A	150	LYS	2.3
1	C	363	LYS	2.3
1	A	39	ASN	2.2
1	D	97	ASN	2.2
1	D	101	ASN	2.2
1	D	185	ARG	2.2
1	A	223	GLN	2.2
1	D	395	GLY	2.2
1	C	222	GLU	2.2
1	D	100	ILE	2.2
1	B	262	ILE	2.1
1	D	225	VAL	2.1
1	C	392	LEU	2.1
1	A	225	VAL	2.1
1	C	265	ASP	2.0
1	C	60	GLU	2.0
1	C	96	LYS	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [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.

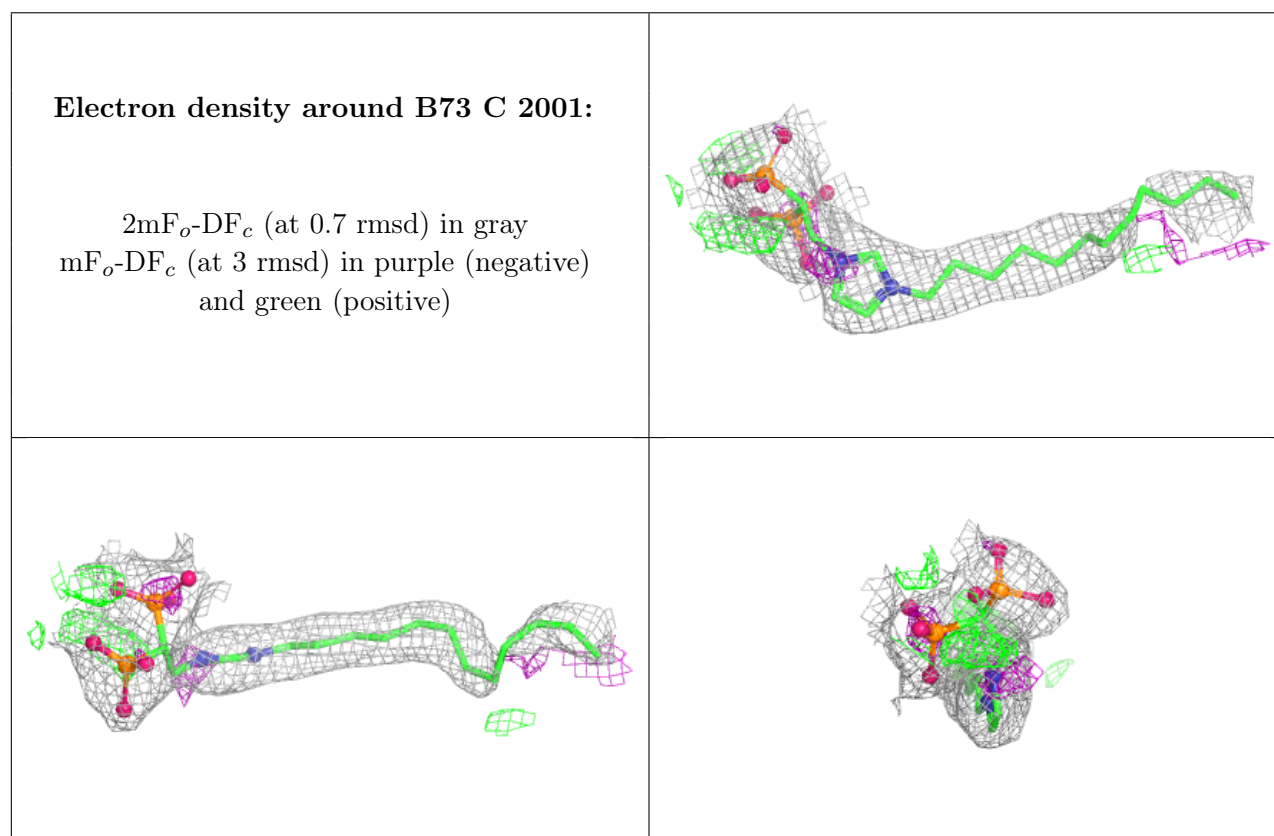
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MG	B	1002	1/1	0.92	0.06	20,20,20,20	0
2	MG	C	1003	1/1	0.94	0.04	3,3,3,3	0
2	MG	C	1001	1/1	0.95	0.13	20,20,20,20	0

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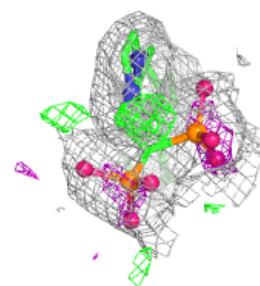
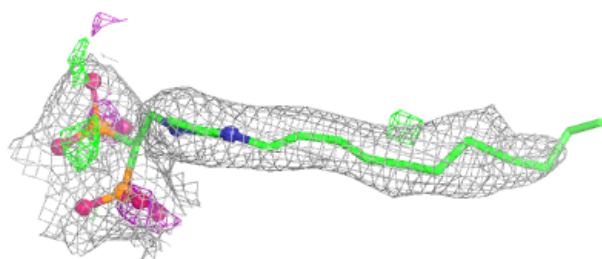
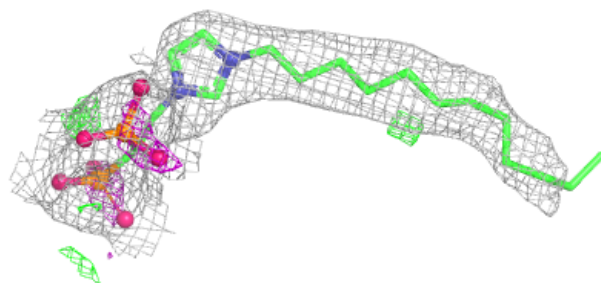
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MG	A	1003	1/1	0.96	0.07	4,4,4,4	0
3	B73	C	2001	27/27	0.96	0.09	2,8,30,34	0
2	MG	D	1003	1/1	0.97	0.04	8,8,8,8	0
3	B73	A	2001	27/27	0.97	0.09	2,8,41,52	0
3	B73	B	2001	27/27	0.97	0.10	2,11,49,60	0
2	MG	D	1001	1/1	0.97	0.04	18,18,18,18	0
3	B73	D	2001	27/27	0.97	0.08	5,10,47,57	0
4	SO4	A	3001	5/5	0.97	0.10	9,10,16,23	0
4	SO4	D	3001	5/5	0.97	0.10	14,15,22,24	0
2	MG	D	1002	1/1	0.98	0.06	19,19,19,19	0
4	SO4	B	3001	5/5	0.98	0.08	8,9,15,19	0
2	MG	B	1003	1/1	0.98	0.04	6,6,6,6	0
2	MG	C	1002	1/1	0.99	0.04	13,13,13,13	0
2	MG	B	1001	1/1	0.99	0.05	9,9,9,9	0
4	SO4	C	3001	5/5	0.99	0.10	16,17,24,26	0
2	MG	A	1002	1/1	0.99	0.08	16,16,16,16	0
2	MG	A	1001	1/1	1.00	0.06	12,12,12,12	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.

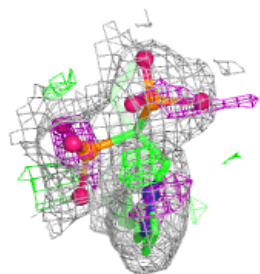
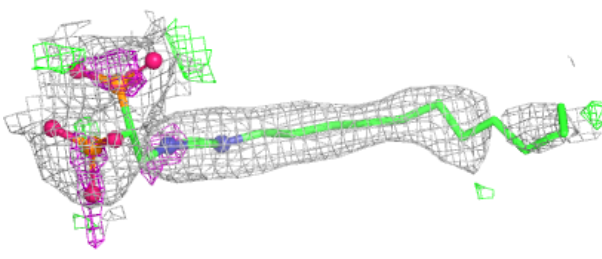
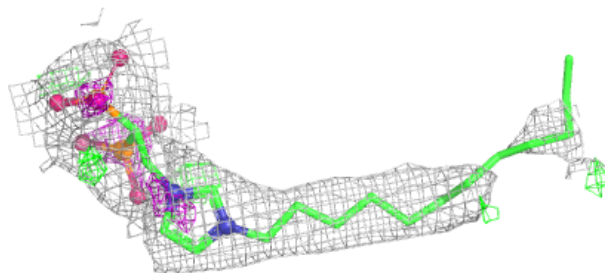


Electron density around B73 A 2001:

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

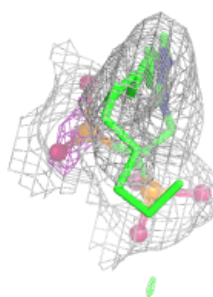
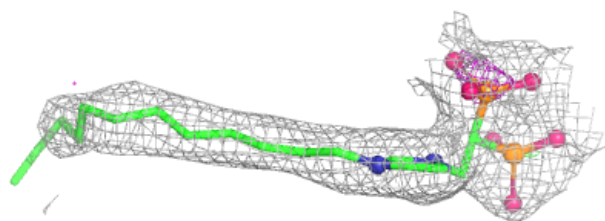
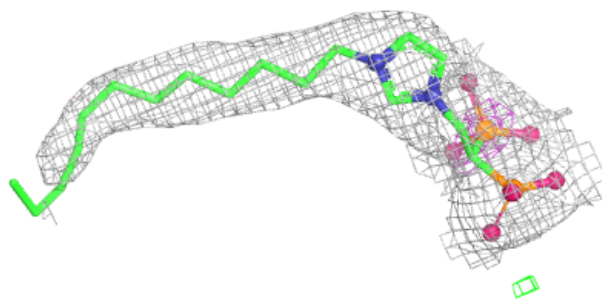
**Electron density around B73 B 2001:**

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



Electron density around B73 D 2001:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.