



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 1YIR / pdb_00001yir
Title : Crystal Structure of a Nicotinate Phosphoribosyltransferase
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Deposited on : 2005-01-12
Resolution : 2.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
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

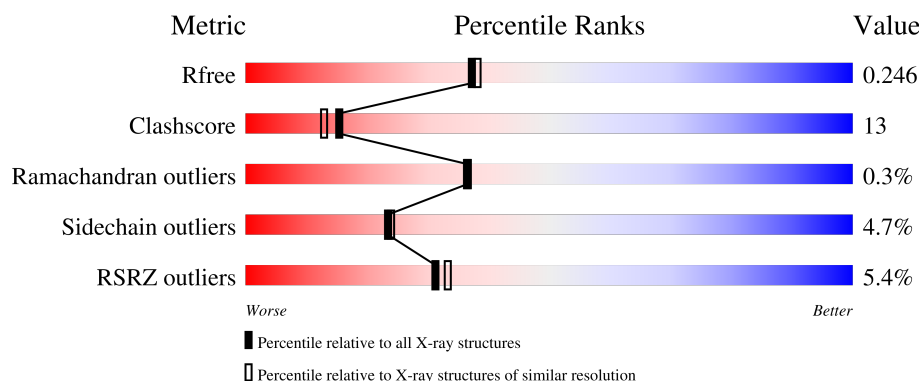
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	408	7% 69% 24% • •
1	B	408	5% 69% 24% • •
1	C	408	4% 67% 27% • •
1	D	408	5% 71% 22% • •

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	SO4	B	3002	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13436 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 Nicotinate phosphoribosyltransferase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	390	Total	C	N	O	S	0	0	0
			3165	2043	549	559	14			
1	B	390	Total	C	N	O	S	0	0	0
			3165	2043	549	559	14			
1	C	390	Total	C	N	O	S	0	0	0
			3165	2043	549	559	14			
1	D	390	Total	C	N	O	S	0	0	0
			3165	2043	549	559	14			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	cloning artifact	UNP Q9HW26
A	2	SER	-	cloning artifact	UNP Q9HW26
A	3	LEU	-	cloning artifact	UNP Q9HW26
A	401	GLU	-	expression tag	UNP Q9HW26
A	402	GLY	-	expression tag	UNP Q9HW26
A	403	HIS	-	expression tag	UNP Q9HW26
A	404	HIS	-	expression tag	UNP Q9HW26
A	405	HIS	-	expression tag	UNP Q9HW26
A	406	HIS	-	expression tag	UNP Q9HW26
A	407	HIS	-	expression tag	UNP Q9HW26
A	408	HIS	-	expression tag	UNP Q9HW26
B	1	MET	-	cloning artifact	UNP Q9HW26
B	2	SER	-	cloning artifact	UNP Q9HW26
B	3	LEU	-	cloning artifact	UNP Q9HW26
B	401	GLU	-	expression tag	UNP Q9HW26
B	402	GLY	-	expression tag	UNP Q9HW26
B	403	HIS	-	expression tag	UNP Q9HW26
B	404	HIS	-	expression tag	UNP Q9HW26
B	405	HIS	-	expression tag	UNP Q9HW26
B	406	HIS	-	expression tag	UNP Q9HW26
B	407	HIS	-	expression tag	UNP Q9HW26

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Chain	Residue	Modelled	Actual	Comment	Reference
B	408	HIS	-	expression tag	UNP Q9HW26
C	1	MET	-	cloning artifact	UNP Q9HW26
C	2	SER	-	cloning artifact	UNP Q9HW26
C	3	LEU	-	cloning artifact	UNP Q9HW26
C	401	GLU	-	expression tag	UNP Q9HW26
C	402	GLY	-	expression tag	UNP Q9HW26
C	403	HIS	-	expression tag	UNP Q9HW26
C	404	HIS	-	expression tag	UNP Q9HW26
C	405	HIS	-	expression tag	UNP Q9HW26
C	406	HIS	-	expression tag	UNP Q9HW26
C	407	HIS	-	expression tag	UNP Q9HW26
C	408	HIS	-	expression tag	UNP Q9HW26
D	1	MET	-	cloning artifact	UNP Q9HW26
D	2	SER	-	cloning artifact	UNP Q9HW26
D	3	LEU	-	cloning artifact	UNP Q9HW26
D	401	GLU	-	expression tag	UNP Q9HW26
D	402	GLY	-	expression tag	UNP Q9HW26
D	403	HIS	-	expression tag	UNP Q9HW26
D	404	HIS	-	expression tag	UNP Q9HW26
D	405	HIS	-	expression tag	UNP Q9HW26
D	406	HIS	-	expression tag	UNP Q9HW26
D	407	HIS	-	expression tag	UNP Q9HW26
D	408	HIS	-	expression tag	UNP Q9HW26

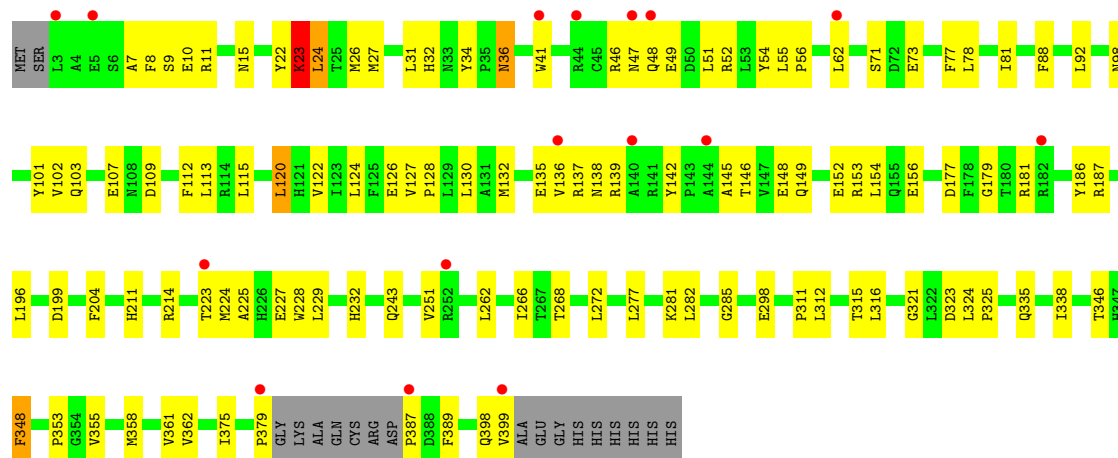
- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



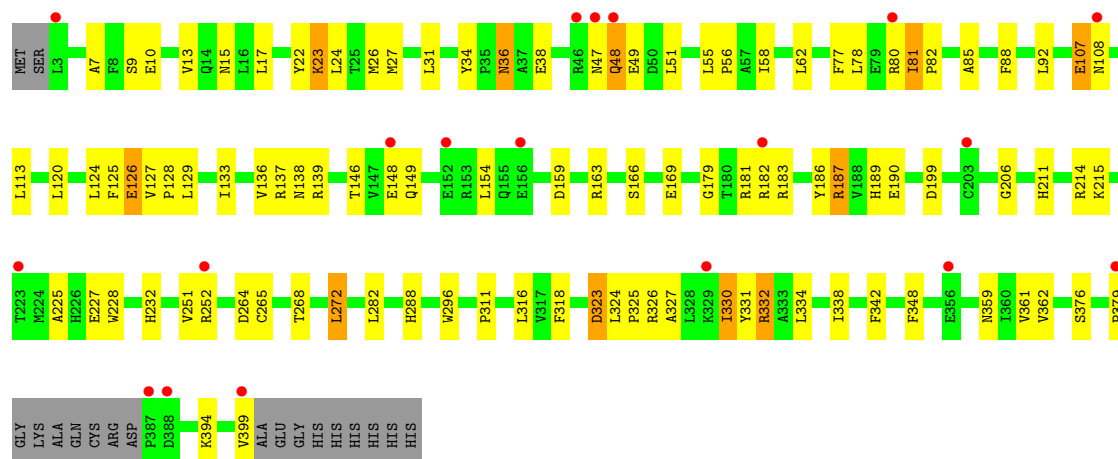
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	C	1	Total O S 5 4 1	0	0
2	C	1	Total O S 5 4 1	0	0
2	C	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	143	Total O 143 143	0	0
3	B	195	Total O 195 195	0	0
3	C	162	Total O 162 162	0	0
3	D	216	Total O 216 216	0	0



• Molecule 1: Nicotinate phosphoribosyltransferase 2



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	222.60Å 113.36Å 93.23Å 90.00° 104.07° 90.00°	Depositor
Resolution (Å)	48.03 – 2.10 48.03 – 2.10	Depositor EDS
% Data completeness (in resolution range)	94.2 (48.03-2.10) 94.2 (48.03-2.10)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.80 (at 2.10Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.213 , 0.247 0.213 , 0.246	Depositor DCC
R_{free} test set	12336 reflections (9.99%)	wwPDB-VP
Wilson B-factor (Å ²)	24.3	Xtriage
Anisotropy	0.185	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 37.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	13436	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.20% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	0.38	0/3244	0.91	9/4392 (0.2%)
1	B	0.39	0/3244	0.90	14/4392 (0.3%)
1	C	0.38	0/3244	0.88	8/4392 (0.2%)
1	D	0.56	2/3244 (0.1%)	1.02	20/4392 (0.5%)
All	All	0.43	2/12976 (0.0%)	0.93	51/17568 (0.3%)

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	D	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	107	GLU	C-N	-18.33	1.08	1.33
1	D	107	GLU	CB-CG	-11.05	1.19	1.52

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	107	GLU	O-C-N	-20.57	96.57	123.10
1	D	107	GLU	CA-C-N	12.65	145.69	121.54
1	D	107	GLU	C-N-CA	12.65	145.69	121.54
1	D	107	GLU	CA-CB-CG	11.66	137.43	114.10
1	C	181	ARG	N-CA-C	8.72	121.88	111.33
1	D	107	GLU	CB-CG-CD	-8.71	97.80	112.60
1	D	181	ARG	N-CA-C	8.18	121.23	111.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	48	GLN	N-CA-C	-8.14	101.43	113.40
1	A	181	ARG	N-CA-C	7.87	120.85	111.33
1	A	264	ASP	N-CA-C	6.97	121.10	112.59
1	B	181	ARG	N-CA-C	6.74	120.38	111.75
1	D	379	PRO	N-CA-CB	6.55	110.20	103.00
1	C	323	ASP	N-CA-C	-6.34	99.77	109.41
1	A	379	PRO	N-CA-CB	6.28	109.91	103.00
1	B	265	CYS	N-CA-C	-6.24	104.48	111.28
1	C	379	PRO	N-CA-CB	6.24	109.86	103.00
1	B	379	PRO	N-CA-CB	6.24	109.86	103.00
1	D	81	ILE	CA-C-N	6.09	127.45	119.84
1	D	81	ILE	C-N-CA	6.09	127.45	119.84
1	B	349	THR	N-CA-C	6.04	120.50	113.20
1	D	199	ASP	N-CA-C	5.91	122.34	114.12
1	B	223	THR	CA-C-O	5.84	121.33	117.94
1	B	164	GLU	N-CA-C	5.75	117.35	111.14
1	A	323	ASP	N-CA-C	-5.74	100.68	109.41
1	D	13	VAL	N-CA-C	-5.74	99.45	108.23
1	B	323	ASP	N-CA-C	-5.72	100.71	109.41
1	C	23	LYS	N-CA-C	-5.61	105.16	112.23
1	A	199	ASP	N-CA-C	5.60	119.76	111.87
1	B	14	GLN	N-CA-C	5.56	117.14	111.14
1	D	323	ASP	N-CA-C	-5.56	101.31	109.81
1	A	95	PHE	N-CA-C	5.50	118.21	110.23
1	D	265	CYS	N-CA-C	-5.46	105.41	111.36
1	D	206	GLY	N-CA-C	5.43	118.10	110.38
1	A	81	ILE	CA-C-N	5.37	125.69	119.47
1	A	81	ILE	C-N-CA	5.37	125.69	119.47
1	D	85	ALA	CA-C-N	5.34	124.97	119.05
1	D	85	ALA	C-N-CA	5.34	124.97	119.05
1	D	126	GLU	N-CA-C	5.33	122.16	110.80
1	B	95	PHE	N-CA-C	5.33	117.96	110.23
1	D	23	LYS	N-CA-C	-5.28	105.70	111.82
1	C	81	ILE	CA-C-N	5.23	125.28	119.32
1	C	81	ILE	C-N-CA	5.23	125.28	119.32
1	A	46	ARG	N-CA-C	5.23	119.28	113.01
1	B	142	TYR	CA-C-N	5.18	125.23	119.32
1	B	142	TYR	C-N-CA	5.18	125.23	119.32
1	B	223	THR	CB-CA-C	-5.16	109.64	117.07
1	D	179	GLY	N-CA-C	5.15	125.39	113.18
1	C	199	ASP	N-CA-C	5.15	121.33	113.61
1	B	48	GLN	N-CA-C	-5.13	106.97	113.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	179	GLY	N-CA-C	5.07	125.19	113.18
1	C	179	GLY	N-CA-C	5.04	125.13	113.18

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	107	GLU	Mainchain,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	3165	0	3142	88	0
1	B	3165	0	3142	84	0
1	C	3165	0	3142	99	0
1	D	3165	0	3141	73	0
2	A	15	0	0	0	0
2	B	15	0	0	2	0
2	C	15	0	0	1	0
2	D	15	0	0	0	0
3	A	143	0	0	5	0
3	B	195	0	0	5	0
3	C	162	0	0	9	0
3	D	216	0	0	7	0
All	All	13436	0	12567	341	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 13.

All (341) 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:C:26:MET:HE1	1:C:225:ALA:HB3	1.26	1.13
1:D:26:MET:HE1	1:D:225:ALA:HB3	1.38	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:26:MET:HE1	1:A:225:ALA:HB3	1.47	0.95
1:A:251:VAL:HG21	1:A:282:LEU:HD13	1.46	0.94
1:B:146:THR:H	1:B:149:GLN:HE21	1.01	0.94
1:D:137:ARG:HH21	1:D:138:ASN:HD21	1.09	0.94
1:B:137:ARG:HH21	1:B:138:ASN:HD21	1.08	0.93
1:C:146:THR:H	1:C:149:GLN:NE2	1.66	0.93
1:B:36:ASN:HD22	1:B:36:ASN:H	1.18	0.91
1:A:295:LEU:HD11	1:A:299:LYS:HE3	1.54	0.90
1:C:224:MET:HE3	1:C:229:LEU:HD11	1.53	0.89
1:C:146:THR:H	1:C:149:GLN:HE21	0.90	0.89
1:C:36:ASN:H	1:C:36:ASN:HD22	1.21	0.86
1:C:146:THR:N	1:C:149:GLN:HE21	1.73	0.86
1:B:55:LEU:HD22	1:B:59:ARG:HH12	1.39	0.85
1:C:251:VAL:HG11	1:C:282:LEU:HD13	1.59	0.84
1:D:36:ASN:HD22	1:D:36:ASN:H	1.22	0.83
1:A:137:ARG:HH21	1:A:138:ASN:HD21	1.26	0.83
1:A:130:LEU:HD21	1:A:362:VAL:HG23	1.60	0.82
1:B:49:GLU:OE1	1:B:137:ARG:HD2	1.81	0.80
1:B:251:VAL:HG11	1:B:282:LEU:HD13	1.61	0.79
1:B:146:THR:H	1:B:149:GLN:NE2	1.79	0.78
1:B:137:ARG:HH21	1:B:138:ASN:ND2	1.80	0.78
1:D:251:VAL:HG11	1:D:282:LEU:HD13	1.65	0.78
1:D:49:GLU:OE1	1:D:137:ARG:HD2	1.85	0.77
1:C:31:LEU:HD23	1:C:120:LEU:HD11	1.67	0.76
1:C:224:MET:HE2	1:C:262:LEU:H	1.50	0.76
1:A:146:THR:H	1:A:149:GLN:HE21	1.32	0.75
1:D:137:ARG:HH21	1:D:138:ASN:ND2	1.86	0.74
1:A:3:LEU:HD13	1:A:3:LEU:O	1.89	0.73
1:D:330:ILE:HD11	1:D:334:LEU:HD12	1.69	0.72
1:A:132:MET:O	1:A:136:VAL:HG13	1.90	0.72
1:A:49:GLU:OE1	1:A:137:ARG:HD2	1.89	0.72
1:D:190:GLU:OE2	1:D:215:LYS:HE2	1.90	0.72
1:A:27:MET:CE	1:A:92:LEU:HD21	2.19	0.71
1:A:27:MET:HE3	1:A:92:LEU:HD21	1.71	0.70
1:C:398:GLN:O	1:C:399:VAL:HG22	1.91	0.70
1:C:130:LEU:HD21	1:C:362:VAL:HG23	1.73	0.70
1:C:26:MET:CE	1:C:225:ALA:HB3	2.16	0.69
1:C:27:MET:HE3	1:C:88:PHE:CZ	2.27	0.69
1:B:145:ALA:HA	1:B:149:GLN:HE22	1.57	0.69
1:B:27:MET:HE3	1:B:88:PHE:CZ	2.28	0.69
1:B:55:LEU:HD22	1:B:59:ARG:NH1	2.08	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:47:ASN:HD21	1:D:359:ASN:H	1.42	0.68
1:B:146:THR:N	1:B:149:GLN:HE21	1.84	0.68
1:D:326:ARG:O	1:D:330:ILE:HG22	1.93	0.68
1:A:11:ARG:NH1	1:A:14:GLN:HA	2.10	0.67
1:C:55:LEU:HB3	1:C:56:PRO:HD3	1.77	0.66
1:A:11:ARG:HH12	1:A:14:GLN:HA	1.60	0.66
1:D:182:ARG:HD3	3:D:5089:HOH:O	1.95	0.66
1:A:4:ALA:HB1	1:A:148:GLU:HG3	1.78	0.66
1:D:47:ASN:ND2	1:D:359:ASN:H	1.95	0.65
1:B:190:GLU:OE2	1:B:215:LYS:HE2	1.97	0.65
1:C:137:ARG:HH21	1:C:138:ASN:HD21	1.42	0.65
1:A:228:TRP:O	1:A:232:HIS:HD2	1.80	0.65
1:A:127:VAL:HB	1:A:128:PRO:HD3	1.78	0.65
1:A:268:THR:HG22	1:A:272:LEU:HD22	1.79	0.64
1:D:15:ASN:HD21	1:D:211:HIS:CD2	2.14	0.64
1:A:394:LYS:O	1:A:399:VAL:N	2.28	0.63
1:D:36:ASN:HD22	1:D:36:ASN:N	1.88	0.63
1:B:361:VAL:HG22	1:B:362:VAL:N	2.14	0.62
1:B:147:VAL:HG11	1:B:187:ARG:HG2	1.80	0.62
1:D:228:TRP:O	1:D:232:HIS:HD2	1.83	0.62
1:A:36:ASN:H	1:A:36:ASN:HD22	1.46	0.62
1:B:36:ASN:HD22	1:B:36:ASN:N	1.91	0.62
1:B:6:SER:HB2	3:B:3149:HOH:O	1.99	0.61
1:C:145:ALA:HA	1:C:149:GLN:HE22	1.65	0.61
1:D:36:ASN:H	1:D:36:ASN:ND2	1.95	0.61
1:B:268:THR:HG22	1:B:272:LEU:HD22	1.80	0.61
1:A:26:MET:HE1	1:A:225:ALA:CB	2.27	0.61
1:D:58:ILE:O	1:D:62:LEU:HD23	2.01	0.61
1:C:107:GLU:HG3	1:C:112:PHE:CD2	2.36	0.61
1:B:146:THR:OG1	1:B:149:GLN:HG3	2.00	0.60
1:B:228:TRP:O	1:B:232:HIS:HD2	1.83	0.60
1:A:55:LEU:HB3	1:A:56:PRO:HD3	1.84	0.60
1:D:327:ALA:O	1:D:330:ILE:HG23	2.02	0.60
1:B:151:ARG:HD2	3:B:3021:HOH:O	2.01	0.60
1:D:182:ARG:NE	3:D:5099:HOH:O	2.34	0.60
1:C:298:GLU:CD	1:D:214:ARG:NH1	2.61	0.59
1:C:15:ASN:HD21	1:C:211:HIS:CD2	2.20	0.59
1:C:228:TRP:O	1:C:232:HIS:HD2	1.86	0.59
1:B:27:MET:HE3	1:B:88:PHE:HZ	1.63	0.59
1:C:127:VAL:HB	1:C:128:PRO:HD3	1.85	0.59
1:A:146:THR:OG1	1:A:149:GLN:HG3	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:27:MET:HE1	1:C:92:LEU:HD21	1.83	0.59
1:C:26:MET:HE1	1:C:225:ALA:CB	2.18	0.59
1:A:252:ARG:HG3	1:A:252:ARG:HH11	1.67	0.58
1:A:346:THR:HG22	1:A:350:CYS:HB3	1.85	0.58
1:C:31:LEU:HD13	1:C:31:LEU:C	2.27	0.58
1:C:268:THR:O	1:C:272:LEU:HD23	2.04	0.58
1:D:146:THR:OG1	1:D:149:GLN:HG3	2.03	0.58
1:C:146:THR:OG1	1:C:149:GLN:HG3	2.02	0.58
1:A:295:LEU:CD1	1:A:299:LYS:HE3	2.33	0.58
1:B:46:ARG:NH2	1:B:359:ASN:HD21	2.01	0.58
1:C:324:LEU:HD21	1:C:348:PHE:CE2	2.38	0.58
1:B:16:LEU:HD22	1:B:70:ILE:HB	1.85	0.57
1:C:324:LEU:HD21	1:C:348:PHE:HE2	1.68	0.57
1:A:49:GLU:O	1:A:51:LEU:HD13	2.04	0.57
1:B:363:LYS:NZ	1:B:363:LYS:HB3	2.19	0.57
1:D:252:ARG:HG3	1:D:252:ARG:HH11	1.70	0.57
1:A:137:ARG:HH21	1:A:138:ASN:ND2	1.98	0.57
1:B:27:MET:CE	1:B:92:LEU:HD21	2.34	0.57
1:A:146:THR:N	1:A:149:GLN:HE21	2.00	0.57
1:D:26:MET:CE	1:D:225:ALA:HB3	2.25	0.56
1:A:107:GLU:HG3	1:A:112:PHE:CE2	2.40	0.56
1:C:137:ARG:HH21	1:C:138:ASN:ND2	2.02	0.56
1:D:26:MET:HE2	3:D:5181:HOH:O	2.04	0.56
1:B:47:ASN:O	1:B:48:GLN:HB2	2.06	0.56
1:B:145:ALA:HA	1:B:149:GLN:NE2	2.21	0.56
1:D:394:LYS:O	1:D:399:VAL:N	2.38	0.55
1:C:34:TYR:OH	1:C:232:HIS:HE1	1.90	0.55
1:C:186:TYR:OH	1:C:211:HIS:HE1	1.90	0.55
1:A:223:THR:HG22	1:A:260:ILE:HB	1.88	0.55
1:A:324:LEU:HD21	1:A:348:PHE:CE2	2.42	0.55
1:B:36:ASN:H	1:B:36:ASN:ND2	1.98	0.55
1:C:153:ARG:HD2	1:C:353:PRO:HG3	1.89	0.55
1:D:49:GLU:O	1:D:51:LEU:HD13	2.06	0.55
1:B:53:LEU:HD12	1:B:53:LEU:N	2.22	0.54
1:B:147:VAL:CG1	1:B:187:ARG:HG2	2.37	0.54
1:A:71:SER:OG	1:A:73:GLU:HG2	2.07	0.54
1:C:27:MET:HE3	1:C:88:PHE:CE1	2.42	0.54
1:C:224:MET:CE	1:C:229:LEU:HD11	2.30	0.54
1:B:46:ARG:HH11	1:B:46:ARG:HG2	1.70	0.54
1:C:27:MET:CE	1:C:92:LEU:HD21	2.37	0.54
1:D:330:ILE:HD11	1:D:334:LEU:CD1	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:27:MET:CE	1:D:92:LEU:HD21	2.37	0.54
1:D:27:MET:HE3	1:D:88:PHE:CZ	2.43	0.54
1:A:4:ALA:HB1	1:A:148:GLU:CG	2.38	0.53
1:B:174:LYS:HD3	1:B:203:CYS:HB2	1.89	0.53
1:A:34:TYR:OH	1:A:232:HIS:HE1	1.91	0.53
1:C:132:MET:O	1:C:136:VAL:HG13	2.09	0.53
1:D:288:HIS:HB2	1:D:296:TRP:CE3	2.43	0.53
1:A:130:LEU:CD2	1:A:362:VAL:HG23	2.34	0.53
1:C:137:ARG:HD3	1:C:358:MET:SD	2.49	0.53
1:C:316:LEU:HG	1:C:338:ILE:HD13	1.90	0.53
1:A:137:ARG:HD3	1:A:358:MET:SD	2.50	0.52
1:D:252:ARG:HG3	1:D:252:ARG:NH1	2.25	0.52
1:C:73:GLU:HG2	3:C:4108:HOH:O	2.09	0.52
1:D:127:VAL:HB	1:D:128:PRO:HD3	1.92	0.52
1:D:159:ASP:O	1:D:163:ARG:HG3	2.09	0.52
1:A:36:ASN:HD22	1:A:36:ASN:N	2.03	0.52
1:A:113:LEU:HD23	1:A:113:LEU:C	2.33	0.52
1:C:54:TYR:CE2	1:C:137:ARG:HG3	2.44	0.52
1:C:387:PRO:N	3:C:4128:HOH:O	2.43	0.52
1:B:8:PHE:HB3	1:B:139:ARG:NH1	2.24	0.52
1:D:47:ASN:O	1:D:48:GLN:HB3	2.09	0.52
1:B:34:TYR:OH	1:B:232:HIS:HE1	1.92	0.51
1:C:113:LEU:C	1:C:113:LEU:HD23	2.35	0.51
1:C:36:ASN:H	1:C:36:ASN:ND2	1.99	0.51
1:B:137:ARG:NH2	1:B:138:ASN:HD21	1.92	0.51
1:C:8:PHE:CD2	1:C:139:ARG:HG2	2.46	0.51
1:A:27:MET:HE1	1:A:92:LEU:HD21	1.93	0.51
1:B:186:TYR:OH	1:B:211:HIS:HE1	1.94	0.51
1:D:34:TYR:OH	1:D:232:HIS:HE1	1.94	0.51
1:D:55:LEU:HB3	1:D:56:PRO:HD3	1.93	0.51
1:A:59:ARG:HE	1:A:104:THR:HG23	1.76	0.51
1:C:15:ASN:HD21	1:C:211:HIS:HD2	1.59	0.51
1:C:135:GLU:O	1:C:139:ARG:HG3	2.11	0.51
1:B:181:ARG:HG3	1:B:182:ARG:HG3	1.92	0.51
1:C:47:ASN:O	1:C:48:GLN:HB3	2.10	0.51
1:C:103:GLN:HG3	3:C:4137:HOH:O	2.10	0.51
1:C:98:ASN:HB3	1:C:101:TYR:CD2	2.46	0.50
1:C:31:LEU:HD12	1:C:32:HIS:CD2	2.47	0.50
1:A:47:ASN:ND2	1:A:359:ASN:HB3	2.27	0.50
1:A:153:ARG:HD2	1:A:353:PRO:HG3	1.94	0.50
1:A:394:LYS:HB3	1:A:399:VAL:HA	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:17:LEU:HD22	1:B:74:GLN:HG2	1.92	0.50
1:B:34:TYR:OH	1:B:232:HIS:CE1	2.65	0.50
1:D:361:VAL:CG1	1:D:362:VAL:N	2.75	0.50
1:B:46:ARG:HG2	1:B:46:ARG:NH1	2.27	0.50
1:B:175:MET:O	1:B:205:VAL:HG22	2.11	0.50
1:C:46:ARG:H	1:C:46:ARG:HD3	1.76	0.50
1:D:361:VAL:HG12	1:D:362:VAL:N	2.27	0.50
1:A:323:ASP:CG	1:A:325:PRO:HD2	2.36	0.50
1:C:10:GLU:HG3	3:C:4151:HOH:O	2.11	0.50
1:D:7:ALA:O	1:D:187:ARG:HB3	2.11	0.50
1:B:346:THR:HG22	2:B:3002:SO4:O3	2.11	0.50
1:A:324:LEU:HD21	1:A:348:PHE:HE2	1.78	0.49
1:B:46:ARG:CZ	1:B:359:ASN:HD21	2.25	0.49
1:C:298:GLU:CD	1:D:214:ARG:HH12	2.20	0.49
1:B:44:ARG:NH1	1:B:46:ARG:HD2	2.28	0.49
1:C:34:TYR:OH	1:C:232:HIS:CE1	2.65	0.49
1:B:361:VAL:HG23	3:B:3117:HOH:O	2.11	0.49
1:C:107:GLU:HG3	1:C:112:PHE:CE2	2.47	0.49
1:A:259:GLY:HA3	3:A:2140:HOH:O	2.13	0.49
1:B:27:MET:HE1	1:B:92:LEU:HD21	1.95	0.48
1:B:361:VAL:HG22	1:B:362:VAL:H	1.78	0.48
1:C:49:GLU:O	1:C:51:LEU:HD13	2.13	0.48
1:D:268:THR:HG22	1:D:272:LEU:HD22	1.94	0.48
1:A:46:ARG:HG2	1:A:46:ARG:HH11	1.79	0.48
1:D:316:LEU:HG	1:D:338:ILE:HD13	1.96	0.48
1:A:16:LEU:HD23	1:A:70:ILE:HB	1.96	0.47
1:C:36:ASN:HD22	1:C:36:ASN:N	1.91	0.47
1:C:324:LEU:HB2	1:C:325:PRO:HD3	1.95	0.47
1:A:196:LEU:HD13	1:A:204:PHE:CE1	2.50	0.47
1:B:53:LEU:HD13	1:B:54:TYR:CD1	2.49	0.47
1:D:27:MET:HE3	1:D:88:PHE:CE1	2.49	0.47
1:C:102:VAL:HG22	1:C:115:LEU:CD2	2.45	0.47
1:B:303:HIS:O	1:B:306:LYS:HG2	2.14	0.47
1:C:311:PRO:O	1:C:338:ILE:HG13	2.14	0.47
1:D:169:GLU:OE2	1:D:332:ARG:HD2	2.15	0.47
1:D:318:PHE:CZ	1:D:330:ILE:HD11	2.50	0.47
1:A:153:ARG:HD2	1:A:353:PRO:CD	2.45	0.47
1:B:53:LEU:HD12	1:B:53:LEU:H	1.78	0.47
1:D:34:TYR:OH	1:D:232:HIS:CE1	2.68	0.47
1:D:331:TYR:HB2	1:D:342:PHE:CZ	2.50	0.47
1:C:399:VAL:O	1:C:399:VAL:HG23	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:98:ASN:HB3	1:B:101:TYR:CD2	2.51	0.46
1:A:36:ASN:H	1:A:36:ASN:ND2	2.11	0.46
1:A:324:LEU:N	1:A:324:LEU:HD22	2.31	0.46
1:B:102:VAL:HG22	1:B:115:LEU:CD2	2.46	0.46
1:B:323:ASP:CG	1:B:325:PRO:HD2	2.40	0.46
1:D:23:LYS:HE3	1:D:126:GLU:OE1	2.15	0.46
1:D:77:PHE:HA	1:D:80:ARG:NH2	2.30	0.46
1:A:252:ARG:HG3	1:A:252:ARG:NH1	2.29	0.46
1:B:9:SER:HB3	1:B:187:ARG:HD3	1.97	0.46
1:C:27:MET:HE3	1:C:88:PHE:HZ	1.76	0.46
1:D:323:ASP:OD2	1:D:326:ARG:HB2	2.15	0.46
1:A:40:GLU:HG2	1:A:116:LYS:HG3	1.97	0.45
1:A:252:ARG:HD3	3:A:2007:HOH:O	2.16	0.45
1:C:31:LEU:HD13	1:C:31:LEU:O	2.16	0.45
1:C:145:ALA:HA	1:C:149:GLN:NE2	2.30	0.45
1:D:26:MET:SD	1:D:227:GLU:HG3	2.56	0.45
1:C:389:PHE:HB3	3:C:4128:HOH:O	2.16	0.45
1:B:24:LEU:N	1:B:24:LEU:HD22	2.31	0.45
1:C:26:MET:SD	1:C:227:GLU:HG3	2.57	0.45
1:C:298:GLU:OE2	1:D:214:ARG:NH1	2.49	0.45
1:A:227:GLU:HG3	1:A:364:MET:HE3	1.99	0.45
1:C:8:PHE:O	1:C:187:ARG:NH2	2.50	0.45
1:C:48:GLN:O	1:C:48:GLN:HG2	2.17	0.45
1:C:196:LEU:HD13	1:C:204:PHE:CE1	2.51	0.45
1:B:10:GLU:HG3	1:B:11:ARG:H	1.82	0.45
1:B:40:GLU:HG2	1:B:116:LYS:HG3	1.99	0.45
1:B:41:TRP:HB2	1:B:115:LEU:HB2	1.97	0.45
1:D:133:ILE:O	1:D:136:VAL:HG22	2.17	0.45
1:A:27:MET:HE3	1:A:88:PHE:CZ	2.52	0.45
1:A:361:VAL:HG22	1:A:362:VAL:N	2.32	0.45
1:C:130:LEU:CD2	1:C:362:VAL:HG23	2.44	0.45
1:B:133:ILE:O	1:B:136:VAL:HG22	2.17	0.45
1:C:224:MET:HB2	3:C:4131:HOH:O	2.17	0.45
1:D:183:ARG:HD2	1:D:189:HIS:HB2	1.98	0.45
1:A:264:ASP:O	1:A:376:SER:HA	2.17	0.44
1:B:182:ARG:NH1	2:B:3002:SO4:O2	2.50	0.44
1:A:16:LEU:HD13	1:A:68:LEU:HB3	1.99	0.44
1:A:34:TYR:OH	1:A:232:HIS:CE1	2.70	0.44
1:A:54:TYR:CE2	1:A:137:ARG:HG3	2.52	0.44
1:B:27:MET:HG2	1:B:88:PHE:HE1	1.81	0.44
1:B:172:GLY:HA2	1:B:174:LYS:NZ	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:137:ARG:HD3	1:B:358:MET:SD	2.58	0.44
1:D:330:ILE:CD1	1:D:334:LEU:HD12	2.43	0.44
1:A:16:LEU:HD12	1:A:16:LEU:HA	1.87	0.44
1:D:166:SER:OG	1:D:169:GLU:HG2	2.17	0.44
1:B:398:GLN:O	1:B:399:VAL:HG22	2.18	0.44
1:D:324:LEU:HB3	1:D:325:PRO:HD3	1.99	0.44
1:A:36:ASN:ND2	3:A:2100:HOH:O	2.50	0.44
1:B:252:ARG:NH1	3:B:3031:HOH:O	2.51	0.44
1:B:361:VAL:CG2	1:B:362:VAL:N	2.80	0.44
1:D:186:TYR:OH	1:D:211:HIS:HE1	2.00	0.44
1:A:23:LYS:NZ	1:A:126:GLU:OE1	2.51	0.43
1:C:361:VAL:HG22	1:C:362:VAL:N	2.34	0.43
1:D:264:ASP:O	1:D:376:SER:HA	2.18	0.43
1:A:81:ILE:HA	1:A:82:PRO:HD2	1.85	0.43
1:C:224:MET:HE3	1:C:229:LEU:CD1	2.36	0.43
1:D:252:ARG:HG3	3:D:5137:HOH:O	2.17	0.43
1:A:46:ARG:HG2	1:A:46:ARG:NH1	2.32	0.43
1:B:26:MET:SD	1:B:227:GLU:HG3	2.59	0.43
1:C:103:GLN:O	1:C:113:LEU:HA	2.17	0.43
1:C:268:THR:HG22	1:C:272:LEU:HD23	2.00	0.43
1:D:23:LYS:HE3	1:D:126:GLU:CD	2.43	0.43
1:B:288:HIS:HB2	1:B:296:TRP:CE3	2.54	0.43
1:C:389:PHE:N	3:C:4128:HOH:O	2.51	0.43
1:A:112:PHE:CD1	1:A:112:PHE:C	2.96	0.43
1:C:243:GLN:HB3	3:C:4019:HOH:O	2.18	0.43
1:C:46:ARG:HD3	1:C:46:ARG:N	2.34	0.43
1:D:182:ARG:HG2	3:D:5099:HOH:O	2.18	0.43
1:A:47:ASN:HD21	1:A:359:ASN:CB	2.31	0.42
1:B:12:ILE:HG21	1:B:132:MET:HA	2.01	0.42
1:B:41:TRP:CE3	1:B:362:VAL:HG12	2.55	0.42
1:C:146:THR:N	1:C:149:GLN:NE2	2.47	0.42
1:A:153:ARG:HD3	1:A:351:ASP:O	2.19	0.42
1:C:152:GLU:O	1:C:156:GLU:HB2	2.19	0.42
1:C:285:GLY:HA3	1:C:315:THR:O	2.19	0.42
1:A:113:LEU:HD23	1:A:114:ARG:N	2.34	0.42
1:A:243:GLN:HB3	3:A:2024:HOH:O	2.19	0.42
1:B:8:PHE:HB3	1:B:139:ARG:CZ	2.50	0.42
1:B:399:VAL:HG23	1:B:399:VAL:O	2.18	0.42
1:C:277:LEU:HG	1:C:281:LYS:HE3	2.01	0.42
1:D:27:MET:HE1	1:D:92:LEU:HD21	2.00	0.42
1:A:295:LEU:C	1:A:295:LEU:HD13	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:7:ALA:O	1:C:187:ARG:HB3	2.20	0.42
1:C:122:VAL:O	1:C:122:VAL:HG12	2.19	0.42
1:B:288:HIS:HB2	1:B:296:TRP:CZ3	2.54	0.41
1:B:41:TRP:HZ2	1:B:227:GLU:OE1	2.03	0.41
1:A:7:ALA:O	1:A:187:ARG:HB3	2.20	0.41
1:A:41:TRP:HB2	1:A:115:LEU:HB2	2.02	0.41
1:B:324:LEU:H	1:B:324:LEU:HD22	1.84	0.41
1:B:359:ASN:C	1:B:359:ASN:HD22	2.29	0.41
1:D:47:ASN:O	1:D:48:GLN:CB	2.68	0.41
1:A:348:PHE:HD2	1:A:348:PHE:HA	1.75	0.41
1:B:183:ARG:HD2	1:B:189:HIS:HB2	2.03	0.41
1:D:113:LEU:C	1:D:113:LEU:HD23	2.46	0.41
1:A:226:HIS:CD2	1:A:374:LYS:HD2	2.56	0.41
1:C:10:GLU:HG3	1:C:11:ARG:H	1.85	0.41
1:B:226:HIS:CD2	1:B:374:LYS:HD2	2.56	0.41
1:B:264:ASP:O	1:B:376:SER:HA	2.21	0.41
1:D:9:SER:O	1:D:139:ARG:NH2	2.52	0.41
1:D:311:PRO:O	1:D:338:ILE:HG13	2.21	0.41
1:D:330:ILE:HG23	1:D:342:PHE:CE2	2.55	0.41
1:A:27:MET:HG2	1:A:88:PHE:HE1	1.86	0.41
1:D:182:ARG:CD	3:D:5099:HOH:O	2.69	0.41
1:A:154:LEU:HD22	1:A:158:PHE:CE1	2.56	0.41
1:A:223:THR:CG2	1:A:260:ILE:HB	2.50	0.41
1:B:27:MET:HE3	1:B:92:LEU:HD21	2.01	0.41
1:C:77:PHE:CG	1:C:214:ARG:HD3	2.56	0.41
1:C:321:GLY:HA2	2:C:4002:SO4:O1	2.20	0.41
1:C:9:SER:O	1:C:139:ARG:NH2	2.54	0.41
1:C:24:LEU:HD12	1:C:27:MET:HE2	2.03	0.41
1:C:41:TRP:CH2	1:C:126:GLU:CD	2.99	0.41
1:C:266:ILE:HG23	1:C:375:ILE:HD12	2.02	0.41
1:D:27:MET:HE3	1:D:92:LEU:HD21	2.01	0.41
1:D:81:ILE:HA	1:D:82:PRO:HD3	1.86	0.41
1:A:10:GLU:HG3	1:A:11:ARG:N	2.36	0.40
1:A:22:TYR:CE1	1:A:225:ALA:HB2	2.56	0.40
1:A:153:ARG:HD2	1:A:353:PRO:HD3	2.04	0.40
1:C:52:ARG:NH1	1:C:109:ASP:HB3	2.35	0.40
1:A:137:ARG:HD3	1:A:358:MET:HE3	2.03	0.40
1:B:214:ARG:NH2	3:B:3162:HOH:O	2.53	0.40
1:A:98:ASN:HB3	1:A:101:TYR:CD2	2.56	0.40
1:A:285:GLY:HA3	1:A:315:THR:O	2.22	0.40
1:B:54:TYR:CE2	1:B:137:ARG:HG3	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:71:SER:OG	1:C:73:GLU:HG3	2.21	0.40
1:A:36:ASN:N	1:A:36:ASN:ND2	2.69	0.40
1:A:332:ARG:HD2	3:A:2131:HOH:O	2.20	0.40
1:C:23:LYS:HE2	1:C:227:GLU:OE2	2.21	0.40
1:C:142:TYR:CE2	1:C:355:VAL:HG13	2.56	0.40
1:D:125:PHE:O	1:D:129:LEU:HG	2.22	0.40
1:B:394:LYS:O	1:B:399:VAL:N	2.49	0.40
1:C:112:PHE:CD1	1:C:112:PHE:C	2.99	0.40
1:C:312:LEU:HD23	1:C:312:LEU:HA	1.93	0.40
1:C:387:PRO:CD	3:C:4128:HOH:O	2.70	0.40
1:D:148:GLU:HB3	3:D:5052:HOH:O	2.20	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	386/408 (95%)	368 (95%)	16 (4%)	2 (0%)	24	22
1	B	386/408 (95%)	370 (96%)	16 (4%)	0	100	100
1	C	386/408 (95%)	370 (96%)	15 (4%)	1 (0%)	36	36
1	D	386/408 (95%)	369 (96%)	16 (4%)	1 (0%)	36	36
All	All	1544/1632 (95%)	1477 (96%)	63 (4%)	4 (0%)	36	36

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	108	ASN
1	A	164	GLU
1	A	223	THR
1	C	223	THR

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	334/349 (96%)	320 (96%)	14 (4%)	26	28
1	B	334/349 (96%)	315 (94%)	19 (6%)	18	17
1	C	334/349 (96%)	320 (96%)	14 (4%)	26	28
1	D	334/349 (96%)	318 (95%)	16 (5%)	23	23
All	All	1336/1396 (96%)	1273 (95%)	63 (5%)	23	24

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	LEU
1	A	22	TYR
1	A	31	LEU
1	A	36	ASN
1	A	38	GLU
1	A	62	LEU
1	A	78	LEU
1	A	120	LEU
1	A	124	LEU
1	A	154	LEU
1	A	177	ASP
1	A	272	LEU
1	A	335	GLN
1	A	348	PHE
1	B	22	TYR
1	B	31	LEU
1	B	36	ASN
1	B	47	ASN
1	B	51	LEU
1	B	53	LEU
1	B	68	LEU
1	B	78	LEU
1	B	120	LEU
1	B	124	LEU

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Mol	Chain	Res	Type
1	B	151	ARG
1	B	153	ARG
1	B	154	LEU
1	B	187	ARG
1	B	272	LEU
1	B	295	LEU
1	B	348	PHE
1	B	352	LEU
1	B	363	LYS
1	C	22	TYR
1	C	23	LYS
1	C	24	LEU
1	C	36	ASN
1	C	62	LEU
1	C	78	LEU
1	C	120	LEU
1	C	124	LEU
1	C	148	GLU
1	C	154	LEU
1	C	177	ASP
1	C	335	GLN
1	C	346	THR
1	C	348	PHE
1	D	10	GLU
1	D	17	LEU
1	D	22	TYR
1	D	24	LEU
1	D	31	LEU
1	D	36	ASN
1	D	38	GLU
1	D	78	LEU
1	D	120	LEU
1	D	124	LEU
1	D	154	LEU
1	D	187	ARG
1	D	272	LEU
1	D	330	ILE
1	D	332	ARG
1	D	348	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (38) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	36	ASN
1	A	47	ASN
1	A	48	GLN
1	A	61	GLN
1	A	138	ASN
1	A	149	GLN
1	A	211	HIS
1	A	232	HIS
1	A	243	GLN
1	A	347	HIS
1	A	359	ASN
1	A	391	HIS
1	B	36	ASN
1	B	61	GLN
1	B	138	ASN
1	B	149	GLN
1	B	155	GLN
1	B	211	HIS
1	B	232	HIS
1	B	339	ASN
1	B	359	ASN
1	C	36	ASN
1	C	47	ASN
1	C	61	GLN
1	C	138	ASN
1	C	149	GLN
1	C	211	HIS
1	C	232	HIS
1	C	359	ASN
1	D	36	ASN
1	D	47	ASN
1	D	61	GLN
1	D	108	ASN
1	D	138	ASN
1	D	211	HIS
1	D	232	HIS
1	D	339	ASN
1	D	347	HIS

5.3.3 RNA ⓘ

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](#)

12 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	SO4	C	4002	-	4,4,4	0.36	0	6,6,6	0.09	0
2	SO4	D	5000	-	4,4,4	0.32	0	6,6,6	0.07	0
2	SO4	D	5001	-	4,4,4	0.36	0	6,6,6	0.10	0
2	SO4	A	2001	-	4,4,4	0.32	0	6,6,6	0.12	0
2	SO4	C	4003	-	4,4,4	0.34	0	6,6,6	0.22	0
2	SO4	A	2002	-	4,4,4	0.41	0	6,6,6	0.10	0
2	SO4	D	5002	-	4,4,4	0.36	0	6,6,6	0.16	0
2	SO4	C	4001	-	4,4,4	0.39	0	6,6,6	0.09	0
2	SO4	B	3000	-	4,4,4	0.42	0	6,6,6	0.05	0
2	SO4	A	2000	-	4,4,4	0.43	0	6,6,6	0.14	0
2	SO4	B	3001	-	4,4,4	0.33	0	6,6,6	0.14	0
2	SO4	B	3002	-	4,4,4	0.37	0	6,6,6	0.19	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	4002	SO4	1	0
2	B	3002	SO4	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	D	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	107:GLU	C	108:ASN	N	1.08

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	390/408 (95%)	0.47	29 (7%) 20 22	15, 28, 46, 56	0
1	B	390/408 (95%)	0.19	21 (5%) 31 33	15, 24, 37, 76	0
1	C	390/408 (95%)	0.28	16 (4%) 41 43	16, 25, 44, 65	0
1	D	390/408 (95%)	0.05	19 (4%) 35 37	13, 21, 37, 59	0
All	All	1560/1632 (95%)	0.25	85 (5%) 31 33	13, 24, 42, 76	0

All (85) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	4	ALA	8.8
1	B	3	LEU	7.6
1	B	399	VAL	6.9
1	C	3	LEU	6.7
1	D	379	PRO	6.4
1	C	399	VAL	6.3
1	D	399	VAL	6.1
1	B	5	GLU	6.0
1	D	3	LEU	5.9
1	C	379	PRO	5.6
1	A	387	PRO	5.1
1	D	387	PRO	5.1
1	A	3	LEU	4.9
1	A	399	VAL	4.8
1	A	379	PRO	4.7
1	B	387	PRO	4.7
1	D	47	ASN	4.3
1	B	379	PRO	4.3
1	A	47	ASN	4.0
1	C	47	ASN	4.0
1	B	47	ASN	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	252	ARG	3.6
1	D	329	LYS	3.5
1	C	387	PRO	3.4
1	D	388	ASP	3.4
1	A	4	ALA	3.3
1	A	223	THR	3.3
1	A	156	GLU	3.2
1	D	156	GLU	3.2
1	B	198	GLU	3.1
1	B	306	LYS	3.1
1	A	165	ALA	3.1
1	B	163	ARG	3.0
1	A	153	ARG	2.9
1	A	163	ARG	2.9
1	A	108	ASN	2.9
1	C	252	ARG	2.8
1	D	148	GLU	2.8
1	B	362	VAL	2.8
1	A	162	ARG	2.7
1	B	41	TRP	2.7
1	C	48	GLN	2.6
1	D	223	THR	2.6
1	D	48	GLN	2.5
1	B	48	GLN	2.5
1	A	361	VAL	2.5
1	A	44	ARG	2.5
1	C	62	LEU	2.5
1	D	108	ASN	2.5
1	B	199	ASP	2.4
1	D	152	GLU	2.4
1	A	109	ASP	2.4
1	D	203	CYS	2.4
1	A	171	ALA	2.4
1	D	80	ARG	2.4
1	C	223	THR	2.4
1	D	252	ARG	2.4
1	C	182	ARG	2.4
1	A	100	ARG	2.3
1	B	73	GLU	2.3
1	B	46	ARG	2.3
1	A	126	GLU	2.3
1	A	46	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	203	CYS	2.3
1	D	46	ARG	2.3
1	C	140	ALA	2.3
1	A	142	TYR	2.3
1	A	136	VAL	2.2
1	B	182	ARG	2.2
1	B	139	ARG	2.2
1	D	356	GLU	2.1
1	A	148	GLU	2.1
1	B	378	THR	2.1
1	C	136	VAL	2.1
1	D	182	ARG	2.1
1	A	140	ALA	2.1
1	C	5	GLU	2.1
1	A	48	GLN	2.1
1	A	182	ARG	2.1
1	C	44	ARG	2.1
1	C	41	TRP	2.1
1	C	144	ALA	2.1
1	B	168	GLU	2.1
1	A	150	ALA	2.1
1	A	168	GLU	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	SO4	B	3000	5/5	0.84	0.22	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	SO4	C	4001	5/5	0.85	0.21	47,47,47,47	0
2	SO4	A	2000	5/5	0.89	0.16	47,47,47,47	0
2	SO4	B	3002	5/5	0.90	0.14	47,47,47,47	0
2	SO4	A	2002	5/5	0.92	0.11	47,47,47,47	0
2	SO4	A	2001	5/5	0.92	0.10	47,47,47,47	0
2	SO4	C	4003	5/5	0.93	0.13	47,47,47,47	0
2	SO4	D	5001	5/5	0.93	0.11	47,47,47,47	0
2	SO4	D	5002	5/5	0.93	0.12	47,47,47,47	0
2	SO4	C	4002	5/5	0.94	0.11	47,47,47,47	0
2	SO4	B	3001	5/5	0.94	0.11	47,47,47,47	0
2	SO4	D	5000	5/5	0.97	0.14	47,47,47,47	0

6.5 Other polymers [i](#)

There are no such residues in this entry.