



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:19 AM UTC

PDB ID : 1D9E / pdb_00001d9e
Title : STRUCTURE OF E. COLI KDO8P SYNTHASE
Authors : Radaev, S.; Dastidar, P.; Patel, M.; Woodard, R.W.; Gatti, D.L.
Deposited on : 1999-10-27
Resolution : 2.40 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

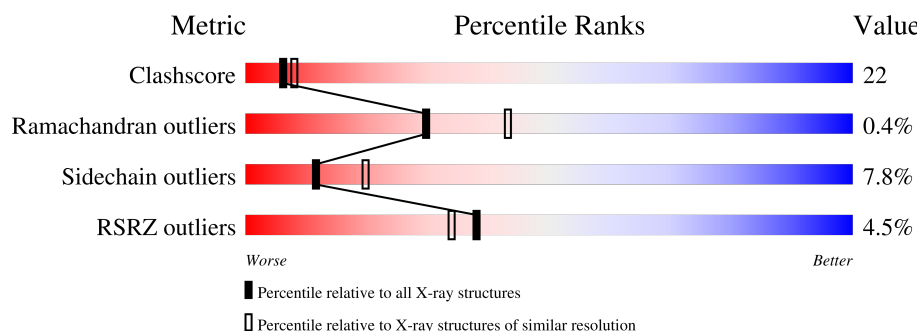
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	284	
1	B	284	
1	C	284	
1	D	284	

2 Entry composition [i](#)

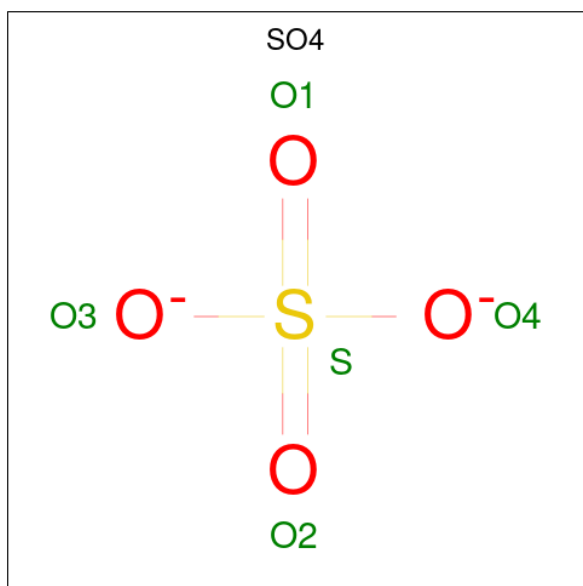
There are 3 unique types of molecules in this entry. The entry contains 8618 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 3-DEOXY-D-MANNO-OCTULOSONATE 8-PHOSPHATE SYNTHASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	266	Total	C	N	O	S	0	0	0
			2040	1305	344	379	12			
1	B	266	Total	C	N	O	S	0	0	0
			2040	1305	344	379	12			
1	C	266	Total	C	N	O	S	0	0	0
			2040	1305	344	379	12			
1	D	264	Total	C	N	O	S	0	0	0
			2024	1295	342	375	12			

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



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

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

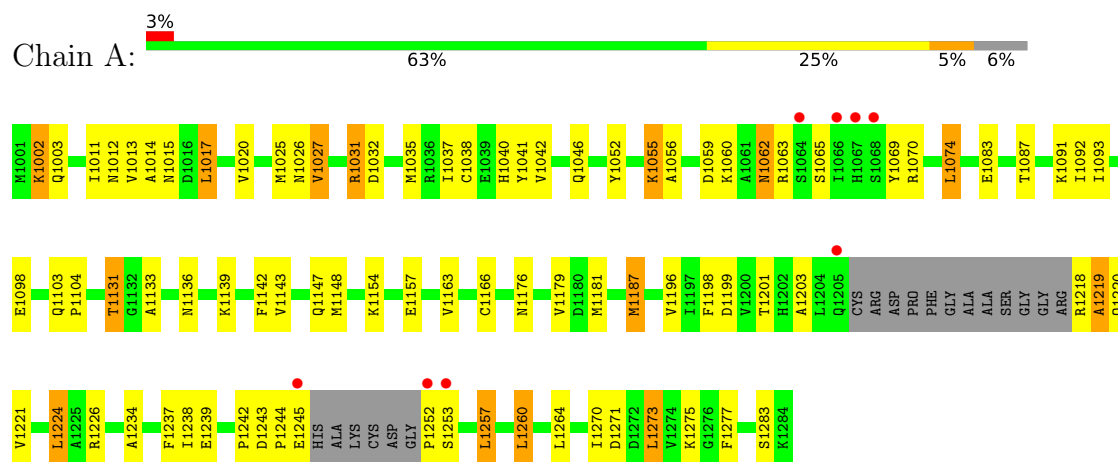
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	143	Total	O	0	0
			143	143		
3	B	122	Total	O	0	0
			122	122		
3	C	119	Total	O	0	0
			119	119		
3	D	40	Total	O	0	0
			40	40		

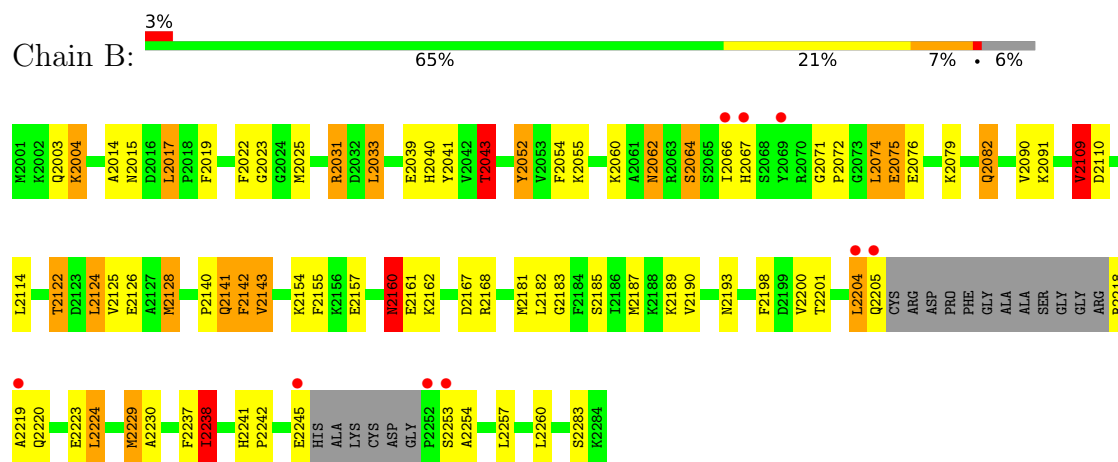
3 Residue-property plots

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.

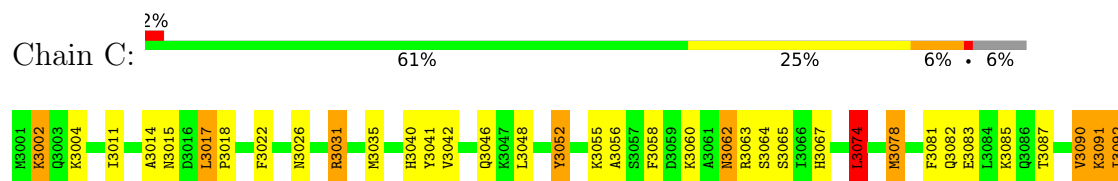
• Molecule 1: 3-DEOXY-D-MANNO-OCTULOSONATE 8-PHOSPHATE SYNTHASE

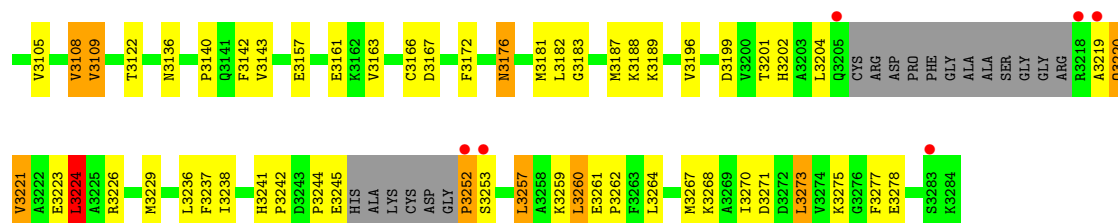


• Molecule 1: 3-DEOXY-D-MANNO-OCTULOSONATE 8-PHOSPHATE SYNTHASE

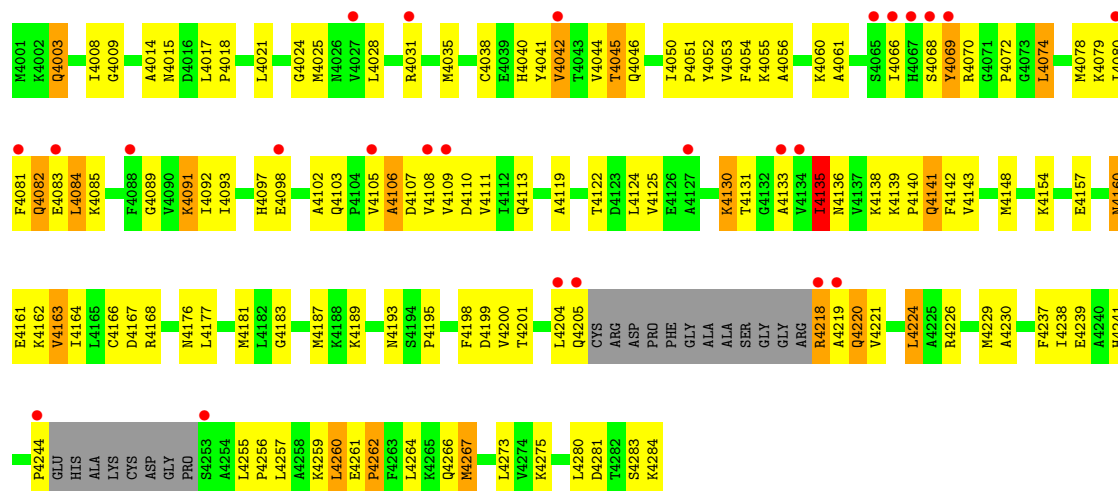


• Molecule 1: 3-DEOXY-D-MANNO-OCTULOSONATE 8-PHOSPHATE SYNTHASE





● Molecule 1: 3-DEOXY-D-MANNO-OCTULOSONATE 8-PHOSPHATE SYNTHASE



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 3	Depositor
Cell constants a, b, c, α , β , γ	228.62Å 228.62Å 228.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	22.86 – 2.40 22.86 – 2.40	Depositor EDS
% Data completeness (in resolution range)	(Not available) (22.86-2.40) 99.2 (22.86-2.40)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.04 (at 2.41Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.199 , 0.239 0.211 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	45.6	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 47.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.046 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8618	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.23% 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	0.72	1/2075 (0.0%)	1.06	3/2796 (0.1%)
1	B	0.67	4/2075 (0.2%)	1.07	12/2796 (0.4%)
1	C	0.70	1/2075 (0.0%)	1.08	14/2796 (0.5%)
1	D	0.59	0/2058	1.07	7/2773 (0.3%)
All	All	0.67	6/8283 (0.1%)	1.07	36/11161 (0.3%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1187	MET	SD-CE	-7.78	1.60	1.79
1	C	3078	MET	SD-CE	-6.00	1.64	1.79
1	B	2128	MET	SD-CE	-5.71	1.65	1.79
1	B	2043	THR	CA-CB	5.28	1.62	1.53
1	B	2229	MET	SD-CE	-5.25	1.66	1.79
1	B	2238	ILE	CA-CB	5.02	1.62	1.55

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	4084	LEU	N-CA-C	-8.43	102.58	113.12
1	B	2090	VAL	CB-CA-C	-7.35	101.48	111.63
1	A	1163	VAL	N-CA-C	6.79	118.08	108.36
1	B	2109	VAL	N-CA-C	6.65	118.69	109.45
1	D	4163	VAL	N-CA-C	6.52	117.69	108.36
1	C	3074	LEU	N-CA-C	6.40	117.92	111.07
1	C	3163	VAL	N-CA-C	6.32	117.40	108.36
1	A	1092	ILE	N-CA-C	6.28	117.74	108.45
1	C	3189	LYS	N-CA-C	6.14	117.97	111.28
1	C	3221	VAL	N-CA-C	-6.03	104.47	110.62
1	A	1219	ALA	N-CA-C	-5.88	106.15	113.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	3278	GLU	N-CA-C	-5.88	102.24	110.35
1	B	2091	LYS	N-CA-C	-5.87	101.79	110.48
1	D	4189	LYS	N-CA-C	5.79	118.37	111.71
1	B	2052	TYR	N-CA-C	5.76	118.85	109.06
1	C	3122	THR	N-CA-C	5.65	118.17	111.33
1	C	3058	PHE	N-CA-C	-5.61	106.27	113.23
1	B	2064	SER	N-CA-C	5.53	117.31	111.28
1	B	2160	ASN	N-CA-C	5.51	117.50	108.52
1	C	3108	VAL	CB-CA-C	-5.39	106.32	111.06
1	C	3092	ILE	N-CA-C	5.36	116.45	108.46
1	C	3052	TYR	N-CA-C	5.35	118.15	109.06
1	B	2067	HIS	N-CA-C	5.33	119.78	113.28
1	C	3090	VAL	CB-CA-C	-5.32	104.29	111.63
1	B	2142	PHE	N-CA-C	5.28	119.83	113.17
1	B	2090	VAL	N-CA-C	5.27	116.82	109.55
1	D	4262	PRO	N-CA-C	-5.26	106.21	113.53
1	C	3224	LEU	N-CA-C	-5.18	105.55	111.14
1	C	3090	VAL	N-CA-C	5.17	116.68	109.55
1	D	4119	ALA	N-CA-C	5.12	119.01	112.87
1	D	4091	LYS	N-CA-C	-5.06	102.79	110.28
1	D	4135	ILE	N-CA-C	5.05	115.75	108.48
1	C	3091	LYS	N-CA-C	-5.03	103.04	110.48
1	B	2071	GLY	CA-C-N	5.02	125.09	119.87
1	B	2071	GLY	C-N-CA	5.02	125.09	119.87
1	B	2254	ALA	N-CA-C	5.01	117.41	109.50

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2040	0	2081	68	0
1	B	2040	0	2081	86	0
1	C	2040	0	2081	85	0
1	D	2024	0	2067	155	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	10	0	0	0	0
2	B	15	0	0	0	0
2	C	15	0	0	1	0
2	D	10	0	0	1	0
3	A	143	0	0	1	0
3	B	122	0	0	5	0
3	C	119	0	0	5	0
3	D	40	0	0	5	0
All	All	8618	0	8310	370	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 22.

All (370) 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:2141:GLN:H	1:B:2141:GLN:NE2	1.40	1.19
1:B:2141:GLN:HE21	1:B:2141:GLN:N	1.46	1.09
1:D:4078:MET:HE3	1:D:4108:VAL:HB	1.29	1.09
1:D:4045:THR:HG21	1:D:4052:TYR:HB2	1.41	1.02
1:A:1218:ARG:HH11	1:A:1253:SER:HB3	1.24	1.01
1:C:3078:MET:HE3	1:C:3108:VAL:HB	1.41	1.01
1:D:4003:GLN:HE21	1:D:4015:ASN:HD22	1.04	1.00
1:C:3078:MET:HE2	1:C:3105:VAL:HA	1.46	0.98
1:D:4028:LEU:HB2	1:D:4072:PRO:HG2	1.45	0.96
1:C:3002:LYS:H	1:C:3002:LYS:HD3	1.30	0.94
1:D:4078:MET:HE2	1:D:4105:VAL:HA	1.50	0.93
1:B:2114:LEU:HD13	1:B:2128:MET:HE1	1.47	0.92
1:D:4141:GLN:H	1:D:4141:GLN:NE2	1.68	0.92
1:A:1201:THR:HG21	1:A:1239:GLU:H	1.35	0.91
1:D:4167:ASP:HB2	1:D:4187:MET:HE1	1.52	0.91
1:B:2124:LEU:HD22	1:B:2128:MET:HE2	1.52	0.89
1:D:4168:ARG:HH22	1:D:4205:GLN:NE2	1.70	0.89
1:D:4141:GLN:HE21	1:D:4141:GLN:N	1.70	0.89
1:D:4078:MET:HE3	1:D:4108:VAL:CB	2.01	0.88
1:B:2185:SER:O	1:B:2189:LYS:HD3	1.73	0.87
1:D:4003:GLN:NE2	1:D:4015:ASN:HD22	1.74	0.85
1:D:4160:ASN:ND2	1:D:4162:LYS:H	1.73	0.85
1:D:4025:MET:HE2	1:D:4054:PHE:HZ	1.43	0.84
1:D:4267:MET:HE3	1:D:4267:MET:HA	1.59	0.83
1:C:3002:LYS:HD3	1:C:3002:LYS:N	1.93	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3220:GLN:HG3	1:C:3223:GLU:CD	2.03	0.83
1:D:4131:THR:HG22	1:D:4133:ALA:H	1.44	0.82
1:D:4082:GLN:HA	1:D:4082:GLN:HE21	1.40	0.82
1:B:2223:GLU:HG3	3:B:24:HOH:O	1.78	0.82
1:D:4160:ASN:C	1:D:4160:ASN:HD22	1.88	0.82
1:D:4082:GLN:HA	1:D:4082:GLN:NE2	1.94	0.81
1:A:1015:ASN:HD21	1:A:1196:VAL:H	1.28	0.81
1:C:3204:LEU:HD11	1:C:3221:VAL:HG22	1.62	0.80
1:D:4078:MET:CE	1:D:4105:VAL:HA	2.12	0.80
1:D:4226:ARG:HA	1:D:4267:MET:HE1	1.64	0.79
1:B:2204:LEU:HD22	1:B:2220:GLN:HE21	1.46	0.79
1:B:2014:ALA:HB3	1:B:2017:LEU:HD22	1.64	0.79
1:D:4103:GLN:HG2	1:D:4130:LYS:HE2	1.65	0.79
1:A:1014:ALA:HB3	1:A:1017:LEU:HD22	1.65	0.77
1:D:4168:ARG:HH22	1:D:4205:GLN:HE22	1.33	0.77
1:A:1218:ARG:NH1	1:A:1253:SER:HB3	2.00	0.77
1:A:1131:THR:CG2	1:A:1133:ALA:H	1.98	0.76
1:C:3015:ASN:HD21	1:C:3196:VAL:H	1.31	0.75
1:A:1055:LYS:HB2	1:A:1093:ILE:HG23	1.67	0.75
1:B:2122:THR:HG22	1:B:2154:LYS:NZ	2.02	0.74
1:D:4055:LYS:C	1:D:4055:LYS:HD3	2.12	0.74
1:C:3229:MET:CE	1:C:3236:LEU:HD13	2.17	0.74
1:D:4074:LEU:O	1:D:4078:MET:HG2	1.87	0.74
1:B:2168:ARG:HG3	1:B:2168:ARG:HH11	1.49	0.74
1:C:3002:LYS:H	1:C:3002:LYS:CD	1.93	0.74
1:B:2003:GLN:NE2	1:B:2015:ASN:HD22	1.86	0.73
1:D:4081:PHE:O	1:D:4085:LYS:HG3	1.87	0.73
1:B:2075:GLU:CD	1:B:2075:GLU:H	1.97	0.73
1:B:2160:ASN:ND2	1:B:2162:LYS:H	1.86	0.73
1:D:4160:ASN:HD22	1:D:4161:GLU:N	1.85	0.73
1:D:4078:MET:CE	1:D:4108:VAL:HB	2.16	0.73
1:C:3220:GLN:OE1	1:C:3223:GLU:HG2	1.89	0.72
1:A:1148:MET:HG3	1:A:1187:MET:HE3	1.71	0.72
1:C:3204:LEU:HD12	1:C:3253:SER:OG	1.88	0.72
1:B:2114:LEU:HD13	1:B:2128:MET:CE	2.20	0.72
1:D:4218:ARG:HG2	1:D:4220:GLN:OE1	1.90	0.71
1:B:2140:PRO:HB2	1:B:2143:VAL:HG13	1.72	0.71
1:B:2160:ASN:HD22	1:B:2162:LYS:H	1.39	0.71
1:C:3060:LYS:HE2	1:C:3060:LYS:HA	1.73	0.70
1:D:4082:GLN:HE21	1:D:4082:GLN:CA	2.02	0.70
1:D:4014:ALA:HB3	1:D:4017:LEU:HD22	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:4003:GLN:HE21	1:D:4015:ASN:ND2	1.85	0.70
1:D:4038:CYS:O	1:D:4042:VAL:HG23	1.92	0.69
1:D:4183:GLY:HA3	3:D:133:HOH:O	1.91	0.68
1:B:2124:LEU:HD22	1:B:2128:MET:CE	2.23	0.68
1:C:3078:MET:HE3	1:C:3108:VAL:CB	2.21	0.68
1:D:4054:PHE:HB3	1:D:4092:ILE:HD13	1.74	0.68
1:D:4198:PHE:CE2	1:D:4200:VAL:HG22	2.28	0.68
1:D:4241:HIS:O	1:D:4244:PRO:HD3	1.93	0.68
1:C:3055:LYS:C	1:C:3055:LYS:HD3	2.19	0.67
1:C:3261:GLU:HB3	1:C:3262:PRO:HD3	1.76	0.66
1:A:1038:CYS:O	1:A:1042:VAL:HG23	1.95	0.66
1:D:4025:MET:HE2	1:D:4054:PHE:CZ	2.28	0.65
1:C:3201:THR:HG23	1:C:3238:ILE:HG13	1.78	0.65
1:D:4042:VAL:O	1:D:4046:GLN:HB2	1.97	0.65
1:A:1199:ASP:HA	1:A:1237:PHE:HB3	1.77	0.65
1:C:3031:ARG:O	1:C:3035:MET:HG2	1.96	0.65
1:B:2205:GLN:HB2	1:B:2220:GLN:HE22	1.62	0.65
1:A:1040:HIS:ND1	1:A:1257:LEU:HD22	2.12	0.64
1:B:2204:LEU:HD22	1:B:2220:GLN:NE2	2.11	0.64
1:B:2204:LEU:HD21	1:B:2220:GLN:HG3	1.79	0.64
1:B:2223:GLU:OE1	3:B:511:HOH:O	2.15	0.64
1:D:4003:GLN:CG	1:D:4015:ASN:HB2	2.27	0.64
1:A:1131:THR:HG23	1:A:1133:ALA:H	1.61	0.64
1:A:1025:MET:O	1:A:1055:LYS:HE3	1.98	0.64
1:D:4135:ILE:HD13	1:D:4136:ASN:N	2.13	0.64
1:B:2218:ARG:HB3	1:B:2220:GLN:HG2	1.80	0.63
1:C:3078:MET:CE	1:C:3105:VAL:HA	2.25	0.63
1:D:4176:ASN:HD22	1:D:4177:LEU:H	1.45	0.63
1:C:3078:MET:CE	1:C:3108:VAL:HB	2.24	0.62
1:A:1136:ASN:HD21	1:A:1166:CYS:HB2	1.64	0.62
1:D:4097:HIS:O	1:D:4098:GLU:HG3	1.99	0.62
1:B:2124:LEU:CD2	1:B:2128:MET:HE2	2.27	0.62
1:D:4008:ILE:O	1:D:4091:LYS:NZ	2.29	0.62
1:D:4141:GLN:H	1:D:4141:GLN:HE21	0.84	0.62
1:A:1219:ALA:HB2	1:B:2283:SER:OG	1.99	0.62
1:D:4045:THR:HG22	1:D:4050:ILE:HB	1.82	0.62
1:D:4135:ILE:HD13	1:D:4135:ILE:C	2.25	0.62
1:B:2072:PRO:HB2	1:B:2076:GLU:HB3	1.81	0.61
1:C:3229:MET:HE3	1:C:3236:LEU:HD13	1.80	0.61
1:D:4109:VAL:HG12	1:D:4110:ASP:N	2.16	0.60
1:D:4122:THR:HG22	1:D:4154:LYS:NZ	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:4218:ARG:O	1:D:4221:VAL:HG23	2.01	0.60
1:A:1181:MET:HE3	1:B:2181:MET:HG3	1.83	0.60
1:A:1220:GLN:NE2	1:B:2182:LEU:HD22	2.17	0.60
1:D:4015:ASN:O	1:D:4275:LYS:HE2	2.01	0.60
1:A:1042:VAL:O	1:A:1046:GLN:HB2	2.01	0.60
1:D:4168:ARG:NH2	1:D:4205:GLN:NE2	2.48	0.60
1:D:4055:LYS:HB2	1:D:4093:ILE:CG2	2.33	0.59
1:A:1131:THR:HG22	1:A:1133:ALA:H	1.66	0.59
1:C:3267:MET:HE3	1:C:3267:MET:HA	1.83	0.59
1:D:4168:ARG:HD2	2:D:4999:SO4:O4	2.03	0.59
1:A:1062:ASN:H	1:A:1062:ASN:HD22	1.48	0.59
1:C:3042:VAL:O	1:C:3046:GLN:HB2	2.02	0.59
1:C:3229:MET:HE1	1:C:3236:LEU:HD13	1.84	0.58
1:B:2055:LYS:C	1:B:2055:LYS:HD3	2.27	0.58
1:D:4176:ASN:ND2	1:D:4177:LEU:H	2.02	0.58
1:D:4160:ASN:HD21	1:D:4162:LYS:H	1.50	0.58
1:D:4054:PHE:O	1:D:4093:ILE:HG22	2.04	0.58
1:B:2122:THR:HB	1:B:2154:LYS:HE3	1.86	0.58
1:B:2122:THR:HG22	1:B:2154:LYS:HZ2	1.68	0.57
1:C:3055:LYS:HD3	1:C:3056:ALA:N	2.20	0.57
1:D:4135:ILE:CG2	1:D:4163:VAL:HG22	2.33	0.57
1:D:4055:LYS:HD3	1:D:4056:ALA:N	2.19	0.57
1:D:4102:ALA:HB3	3:D:119:HOH:O	2.05	0.57
1:D:4140:PRO:HD2	1:D:4143:VAL:CG2	2.35	0.57
1:C:3220:GLN:HG3	1:C:3223:GLU:OE2	2.05	0.57
1:B:2060:LYS:HE2	1:B:2060:LYS:HA	1.87	0.56
1:B:2241:HIS:ND1	1:B:2242:PRO:HD2	2.19	0.56
1:A:1201:THR:CG2	1:A:1238:ILE:HG13	2.35	0.56
1:A:1031:ARG:HD3	1:A:1032:ASP:N	2.20	0.56
1:B:2114:LEU:CD1	1:B:2128:MET:HE1	2.30	0.56
1:A:1218:ARG:O	1:A:1221:VAL:HG23	2.06	0.56
1:D:4044:VAL:HG13	1:D:4261:GLU:HG3	1.88	0.56
1:B:2190:VAL:HG22	1:B:2190:VAL:O	2.06	0.56
1:C:3136:ASN:HD21	1:C:3166:CYS:HB2	1.71	0.56
1:B:2039:GLU:O	1:B:2043:THR:HG23	2.05	0.56
1:C:3092:ILE:HG22	1:C:3109:VAL:HG22	1.86	0.56
1:D:4229:MET:CG	1:D:4267:MET:HE2	2.35	0.56
1:C:3035:MET:HE1	1:C:3087:THR:HG21	1.87	0.55
1:D:4140:PRO:HD2	1:D:4143:VAL:HG21	1.87	0.55
1:D:4045:THR:HG22	1:D:4050:ILE:O	2.07	0.55
1:D:4003:GLN:NE2	1:D:4193:ASN:HB3	2.20	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1063:ARG:NH1	1:A:1069:TYR:O	2.35	0.55
1:A:1181:MET:HG3	1:B:2181:MET:HE3	1.89	0.55
1:D:4009:GLY:HA3	1:D:4091:LYS:NZ	2.20	0.55
1:D:4109:VAL:CG1	1:D:4110:ASP:N	2.70	0.55
1:A:1031:ARG:HD3	1:A:1031:ARG:C	2.32	0.55
1:A:1055:LYS:HD2	1:A:1056:ALA:N	2.22	0.54
1:C:3167:ASP:HB2	1:C:3187:MET:HE1	1.88	0.54
1:C:3048:LEU:O	1:C:3268:LYS:HE3	2.07	0.54
1:C:3031:ARG:HD3	1:C:3083:GLU:OE2	2.07	0.54
1:C:3219:ALA:CB	1:D:4283:SER:HB3	2.38	0.54
1:C:3140:PRO:HB2	1:C:3143:VAL:HG23	1.90	0.53
1:D:4130:LYS:HD2	1:D:4131:THR:N	2.23	0.53
1:B:2168:ARG:HG3	1:B:2168:ARG:NH1	2.22	0.53
1:D:4102:ALA:O	1:D:4106:ALA:HB2	2.08	0.53
1:D:4160:ASN:HD22	1:D:4162:LYS:H	1.52	0.53
1:B:2074:LEU:HD13	1:B:2074:LEU:C	2.34	0.53
1:D:4031:ARG:HD3	1:D:4083:GLU:OE2	2.08	0.53
1:D:4176:ASN:ND2	1:D:4177:LEU:N	2.56	0.53
1:D:4052:TYR:CD1	1:D:4053:VAL:N	2.76	0.52
1:D:4122:THR:HG22	1:D:4154:LYS:HZ2	1.74	0.52
1:D:4201:THR:HG21	1:D:4239:GLU:HB2	1.90	0.52
1:A:1060:LYS:HE2	1:A:1060:LYS:HA	1.92	0.52
1:A:1062:ASN:HD22	1:A:1062:ASN:N	2.05	0.52
1:B:2031:ARG:HG2	3:B:287:HOH:O	2.09	0.52
1:C:3181:MET:HE3	1:D:4181:MET:HG3	1.92	0.52
1:D:4260:LEU:O	1:D:4260:LEU:HD23	2.10	0.52
1:A:1226:ARG:HD2	1:B:2230:ALA:O	2.09	0.52
1:D:4140:PRO:HB2	1:D:4143:VAL:HG13	1.92	0.52
1:A:1002:LYS:HG3	1:A:1003:GLN:O	2.10	0.52
1:A:1226:ARG:HG2	1:A:1270:ILE:CD1	2.40	0.52
1:D:4261:GLU:HB2	3:D:66:HOH:O	2.10	0.52
1:D:4199:ASP:OD1	1:D:4199:ASP:C	2.53	0.51
1:A:1027:VAL:HG22	1:A:1060:LYS:HD2	1.91	0.51
1:B:2039:GLU:OE1	1:B:2043:THR:HG21	2.10	0.51
1:C:3260:LEU:HD22	1:C:3264:LEU:HG	1.92	0.51
1:A:1143:VAL:CG1	1:A:1147:GLN:HB2	2.40	0.51
1:A:1154:LYS:HD2	1:C:3064:SER:O	2.09	0.51
1:B:2168:ARG:HG3	1:B:2168:ARG:O	2.11	0.51
1:D:4260:LEU:HD23	1:D:4264:LEU:HG	1.93	0.51
1:C:3022:PHE:O	1:C:3237:PHE:HA	2.11	0.51
1:B:2142:PHE:CD2	1:D:4142:PHE:CD2	2.99	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:4074:LEU:O	1:D:4074:LEU:HD13	2.10	0.51
1:D:4113:GLN:HB3	1:D:4136:ASN:HB3	1.92	0.51
1:D:4199:ASP:HA	1:D:4237:PHE:HB3	1.93	0.50
1:A:1059:ASP:HA	1:A:1070:ARG:O	2.11	0.50
1:A:1198:PHE:HZ	1:A:1224:LEU:HD13	1.76	0.50
1:B:2066:ILE:HG13	1:D:4154:LYS:HG3	1.92	0.50
1:D:4093:ILE:HA	1:D:4111:VAL:O	2.12	0.50
1:D:4031:ARG:HD3	1:D:4083:GLU:CD	2.37	0.50
1:D:4092:ILE:HG22	1:D:4093:ILE:N	2.27	0.50
1:A:1026:ASN:OD1	1:A:1060:LYS:HD2	2.11	0.50
1:A:1011:ILE:HG22	1:A:1012:ASN:N	2.27	0.49
1:A:1035:MET:HE1	1:A:1087:THR:HG21	1.93	0.49
1:B:2125:VAL:HG13	1:B:2155:PHE:CE1	2.47	0.49
1:B:2218:ARG:C	1:B:2220:GLN:H	2.19	0.49
1:C:3273:LEU:HD12	1:D:4273:LEU:HD22	1.94	0.49
1:D:4028:LEU:O	1:D:4072:PRO:HG3	2.12	0.49
1:D:4204:LEU:CD1	1:D:4221:VAL:HG22	2.41	0.49
1:B:2019:PHE:CG	1:B:2229:MET:HE1	2.47	0.49
1:C:3273:LEU:CD2	1:C:3277:PHE:CE1	2.95	0.49
1:A:1074:LEU:CD1	1:A:1074:LEU:C	2.86	0.49
1:D:4259:LYS:O	1:D:4262:PRO:HD2	2.13	0.49
1:D:4040:HIS:O	1:D:4044:VAL:HG23	2.13	0.49
1:D:4003:GLN:HG2	1:D:4015:ASN:HB2	1.94	0.49
1:B:2154:LYS:HG3	1:D:4066:ILE:HD12	1.94	0.49
1:B:2218:ARG:CB	1:B:2220:GLN:HG2	2.43	0.49
1:C:3188:LYS:HE2	3:C:353:HOH:O	2.11	0.49
1:D:4226:ARG:CA	1:D:4267:MET:HE1	2.39	0.49
1:D:4025:MET:HE3	1:D:4028:LEU:HD23	1.95	0.49
1:D:4135:ILE:HD13	1:D:4136:ASN:C	2.38	0.49
1:C:3273:LEU:HD22	1:C:3277:PHE:CZ	2.48	0.49
1:A:1142:PHE:CD1	1:C:3142:PHE:CD2	3.01	0.48
1:C:3015:ASN:HD21	1:C:3196:VAL:N	2.05	0.48
1:D:4074:LEU:HD21	1:D:4105:VAL:HG23	1.95	0.48
1:C:3015:ASN:ND2	1:C:3196:VAL:H	2.07	0.48
1:A:1015:ASN:ND2	1:A:1196:VAL:H	2.05	0.48
1:C:3219:ALA:HB1	1:D:4283:SER:HB3	1.96	0.48
1:C:3074:LEU:O	1:C:3078:MET:HG2	2.13	0.48
1:D:4009:GLY:HA3	1:D:4091:LYS:HZ1	1.79	0.48
1:B:2074:LEU:C	1:B:2074:LEU:CD1	2.86	0.48
1:B:2124:LEU:HD22	1:B:2128:MET:HG3	1.96	0.48
1:A:1074:LEU:C	1:A:1074:LEU:HD12	2.39	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2200:VAL:HG12	1:B:2238:ILE:HG22	1.94	0.48
1:A:1065:SER:HB2	1:C:3157:GLU:OE2	2.13	0.48
1:D:4260:LEU:CD2	1:D:4264:LEU:HG	2.43	0.47
1:D:4160:ASN:ND2	1:D:4160:ASN:C	2.60	0.47
1:B:2003:GLN:HE21	1:B:2015:ASN:HD22	1.61	0.47
1:D:4068:SER:O	1:D:4069:TYR:C	2.57	0.47
1:B:2198:PHE:HZ	1:B:2224:LEU:HD13	1.80	0.47
1:D:4017:LEU:O	1:D:4018:PRO:C	2.57	0.47
1:D:4025:MET:CE	1:D:4054:PHE:HZ	2.21	0.47
1:D:4229:MET:HG3	1:D:4267:MET:HE2	1.97	0.46
1:B:2004:LYS:HB2	1:B:2193:ASN:O	2.15	0.46
1:A:1041:TYR:HB3	1:A:1052:TYR:CZ	2.51	0.46
1:B:2062:ASN:N	1:B:2062:ASN:HD22	2.12	0.46
1:D:4041:TYR:HB3	1:D:4052:TYR:CZ	2.51	0.46
1:D:4125:VAL:HG11	1:D:4154:LYS:HG2	1.98	0.46
1:B:2025:MET:CE	1:B:2033:LEU:HD13	2.45	0.46
1:B:2141:GLN:NE2	1:B:2141:GLN:N	2.26	0.46
1:C:3259:LYS:NZ	1:D:4281:ASP:O	2.46	0.46
1:A:1062:ASN:N	1:A:1062:ASN:ND2	2.63	0.46
1:C:3031:ARG:HD3	1:C:3083:GLU:CD	2.41	0.46
1:C:3181:MET:HG3	1:D:4181:MET:HE3	1.98	0.46
1:A:1139:LYS:HE2	3:A:68:HOH:O	2.15	0.45
1:B:2022:PHE:O	1:B:2237:PHE:HA	2.16	0.45
1:B:2154:LYS:HG3	1:D:4066:ILE:CD1	2.46	0.45
1:C:3011:ILE:HD12	1:C:3091:LYS:HD2	1.97	0.45
1:D:4092:ILE:CG2	1:D:4093:ILE:N	2.79	0.45
1:D:4041:TYR:O	1:D:4045:THR:OG1	2.33	0.45
1:B:2201:THR:HB	1:B:2253:SER:O	2.16	0.45
1:C:3182:LEU:HD22	1:D:4220:GLN:HB3	1.99	0.45
1:D:4080:ILE:O	1:D:4084:LEU:HG	2.16	0.45
1:A:1015:ASN:HD21	1:A:1196:VAL:N	2.05	0.45
1:D:4226:ARG:HD3	1:D:4266:GLN:OE1	2.17	0.45
1:B:2204:LEU:CD2	1:B:2220:GLN:HE21	2.23	0.45
1:D:4136:ASN:HD21	1:D:4166:CYS:HB2	1.82	0.45
1:A:1260:LEU:HD22	1:A:1264:LEU:HG	1.98	0.45
1:B:2160:ASN:HD22	1:B:2160:ASN:C	2.25	0.45
1:C:3040:HIS:ND1	1:C:3257:LEU:HD22	2.31	0.45
1:D:4218:ARG:N	1:D:4221:VAL:HG23	2.32	0.45
1:B:2122:THR:HG23	1:D:4061:ALA:O	2.17	0.45
1:B:2241:HIS:CE1	1:B:2242:PRO:HD2	2.52	0.45
1:C:3244:PRO:O	1:C:3245:GLU:HB2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3201:THR:CG2	1:C:3238:ILE:HG13	2.47	0.44
1:D:4021:LEU:HD11	1:D:4238:ILE:HG22	1.99	0.44
1:D:4176:ASN:HD22	1:D:4177:LEU:N	2.09	0.44
1:A:1271:ASP:O	1:A:1275:LYS:HB2	2.17	0.44
1:A:1103:GLN:HB3	1:A:1104:PRO:HD3	1.99	0.44
1:C:3226:ARG:HA	1:C:3267:MET:HE1	1.99	0.44
1:D:4229:MET:HG2	1:D:4267:MET:HE2	1.99	0.44
1:A:1013:VAL:HG22	1:A:1020:VAL:HG21	1.97	0.44
1:B:2041:TYR:HB3	1:B:2052:TYR:CZ	2.52	0.44
1:D:4070:ARG:HD3	3:D:415:HOH:O	2.17	0.44
1:D:4255:LEU:HD12	1:D:4256:PRO:HD2	1.98	0.44
1:B:2039:GLU:OE1	1:B:2043:THR:CG2	2.66	0.44
1:C:3085:LYS:HD2	1:C:3090:VAL:O	2.18	0.44
1:D:4050:ILE:O	1:D:4051:PRO:C	2.59	0.44
1:D:4085:LYS:O	1:D:4089:GLY:HA2	2.18	0.44
1:C:3226:ARG:HG2	1:C:3270:ILE:CD1	2.48	0.44
1:D:4135:ILE:HG21	1:D:4163:VAL:HG22	1.99	0.44
1:B:2183:GLY:HA3	3:B:73:HOH:O	2.17	0.44
1:B:2062:ASN:HD22	1:B:2062:ASN:H	1.66	0.44
1:C:3204:LEU:HD23	1:C:3204:LEU:HA	1.85	0.44
1:C:3202:HIS:CD2	1:C:3252:PRO:HD2	2.52	0.43
1:D:4079:LYS:O	1:D:4083:GLU:HG2	2.18	0.43
1:D:4092:ILE:C	1:D:4109:VAL:HG13	2.43	0.43
1:C:3014:ALA:HB3	1:C:3017:LEU:HD22	1.99	0.43
1:C:3031:ARG:HD2	3:C:346:HOH:O	2.17	0.43
1:C:3260:LEU:HD22	1:C:3264:LEU:CD1	2.48	0.43
1:D:4052:TYR:CG	1:D:4053:VAL:N	2.86	0.43
1:B:2079:LYS:HA	1:B:2082:GLN:HG3	2.00	0.43
1:D:4003:GLN:HG3	1:D:4015:ASN:HB2	2.00	0.43
1:A:1037:ILE:HD11	1:A:1242:PRO:HD3	1.99	0.43
1:B:2064:SER:O	1:D:4154:LYS:HD3	2.18	0.43
1:C:3026:ASN:HD21	1:C:3060:LYS:NZ	2.16	0.43
1:C:3062:ASN:H	1:C:3062:ASN:HD22	1.66	0.43
1:C:3271:ASP:O	1:C:3275:LYS:HB2	2.18	0.43
1:C:3092:ILE:CG2	1:C:3109:VAL:HG22	2.49	0.43
1:D:4164:ILE:HG12	1:D:4195:PRO:HG2	2.01	0.43
1:B:2109:VAL:CG1	1:B:2110:ASP:N	2.82	0.43
1:A:1198:PHE:CZ	1:A:1224:LEU:HD13	2.54	0.43
1:C:3017:LEU:O	1:C:3018:PRO:C	2.59	0.43
1:D:4139:LYS:HB2	1:D:4148:MET:HE2	1.99	0.43
1:B:2122:THR:CB	1:B:2154:LYS:HE3	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2167:ASP:HB2	1:B:2187:MET:HE1	1.99	0.43
1:A:1176:ASN:HD22	1:A:1176:ASN:HA	1.68	0.43
1:A:1283:SER:HB3	1:B:2219:ALA:HB2	2.01	0.43
1:C:3226:ARG:NH1	1:D:4230:ALA:O	2.51	0.43
1:D:4113:GLN:CB	1:D:4136:ASN:HB3	2.48	0.43
1:B:2062:ASN:N	1:B:2062:ASN:ND2	2.67	0.43
1:D:4031:ARG:O	1:D:4035:MET:HB2	2.19	0.43
1:B:2124:LEU:HD13	1:B:2128:MET:HE2	2.00	0.42
1:C:3241:HIS:ND1	1:C:3242:PRO:HD2	2.34	0.42
1:C:3241:HIS:CE1	1:C:3242:PRO:HD2	2.54	0.42
1:D:4113:GLN:NE2	1:D:4138:LYS:HD2	2.34	0.42
1:A:1148:MET:HG3	1:A:1187:MET:CE	2.45	0.42
1:B:2003:GLN:NE2	1:B:2015:ASN:HB2	2.33	0.42
1:C:3067:HIS:HB2	3:C:403:HOH:O	2.18	0.42
1:A:1055:LYS:HB2	1:A:1093:ILE:CG2	2.44	0.42
1:B:2154:LYS:O	1:B:2157:GLU:HG2	2.19	0.42
1:C:3041:TYR:HB3	1:C:3052:TYR:CZ	2.54	0.42
1:D:4280:LEU:HB3	3:D:188:HOH:O	2.19	0.42
1:D:4055:LYS:CB	1:D:4093:ILE:HG23	2.49	0.42
1:C:3172:PHE:O	1:C:3176:ASN:HB3	2.19	0.42
1:A:1015:ASN:ND2	1:A:1234:ALA:HB2	2.35	0.42
1:B:2124:LEU:HD13	1:B:2128:MET:CE	2.49	0.42
1:D:4106:ALA:HB1	1:D:4131:THR:HG23	2.01	0.42
1:A:1011:ILE:HG13	1:A:1091:LYS:HE2	2.00	0.42
1:D:4014:ALA:CB	1:D:4017:LEU:HD22	2.47	0.42
1:C:3062:ASN:HD22	1:C:3062:ASN:N	2.17	0.42
1:A:1179:VAL:CG2	1:A:1203:ALA:HB1	2.49	0.42
1:B:2023:GLY:O	1:B:2054:PHE:HA	2.20	0.42
1:D:4078:MET:HE1	1:D:4105:VAL:HG13	2.02	0.42
1:C:3257:LEU:O	1:C:3260:LEU:HB2	2.19	0.41
1:D:4218:ARG:HE	1:D:4220:GLN:CD	2.28	0.41
1:A:1154:LYS:O	1:A:1157:GLU:HB2	2.20	0.41
1:C:3063:ARG:HB3	2:C:3777:SO4:O1	2.20	0.41
1:A:1273:LEU:HD22	1:A:1277:PHE:CE1	2.55	0.41
1:D:4201:THR:OG1	1:D:4238:ILE:HA	2.20	0.41
1:D:4260:LEU:O	1:D:4260:LEU:CD2	2.68	0.41
1:C:3183:GLY:HA3	3:C:150:HOH:O	2.20	0.41
1:C:3199:ASP:HA	1:C:3237:PHE:HB3	2.01	0.41
1:B:2141:GLN:H	1:B:2141:GLN:HE21	0.62	0.41
1:A:1015:ASN:HD22	1:A:1234:ALA:HB2	1.84	0.41
1:A:1243:ASP:C	1:A:1245:GLU:H	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:4154:LYS:O	1:D:4157:GLU:HG2	2.20	0.41
1:D:4218:ARG:O	1:D:4220:GLN:N	2.54	0.41
1:C:3004:LYS:NZ	1:C:3161:GLU:HB3	2.36	0.41
1:C:3253:SER:HA	3:C:296:HOH:O	2.20	0.41
1:A:1014:ALA:CB	1:A:1017:LEU:HD22	2.45	0.41
1:D:4224:LEU:HD23	1:D:4224:LEU:HA	1.92	0.41
1:B:2126:GLU:HG3	1:D:4066:ILE:HG12	2.03	0.41
1:B:2218:ARG:HD3	1:B:2218:ARG:HA	1.75	0.41
1:C:3026:ASN:HD21	1:C:3060:LYS:HZ3	1.67	0.41
1:D:4024:GLY:HA3	1:D:4055:LYS:O	2.21	0.41
1:C:3229:MET:HE2	1:C:3229:MET:CA	2.51	0.40
1:C:3081:PHE:O	1:C:3085:LYS:HG2	2.20	0.40
1:D:4131:THR:HG22	1:D:4133:ALA:N	2.25	0.40
1:B:2040:HIS:HD2	3:B:148:HOH:O	2.04	0.40
1:C:3224:LEU:HD23	1:C:3224:LEU:HA	1.90	0.40
1:A:1031:ARG:HH21	1:A:1083:GLU:CD	2.29	0.40
1:B:2004:LYS:NZ	1:B:2161:GLU:O	2.41	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	260/284 (92%)	253 (97%)	6 (2%)	1 (0%)	30	43
1	B	260/284 (92%)	247 (95%)	13 (5%)	0	100	100
1	C	260/284 (92%)	251 (96%)	9 (4%)	0	100	100
1	D	258/284 (91%)	241 (93%)	14 (5%)	3 (1%)	10	16
All	All	1038/1136 (91%)	992 (96%)	42 (4%)	4 (0%)	30	43

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	4219	ALA
1	D	4069	TYR
1	D	4106	ALA
1	A	1244	PRO

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	222/233 (95%)	208 (94%)	14 (6%)	16	29
1	B	222/233 (95%)	201 (90%)	21 (10%)	8	13
1	C	222/233 (95%)	207 (93%)	15 (7%)	14	25
1	D	220/233 (94%)	201 (91%)	19 (9%)	10	16
All	All	886/932 (95%)	817 (92%)	69 (8%)	11	20

All (69) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1002	LYS
1	A	1017	LEU
1	A	1027	VAL
1	A	1031	ARG
1	A	1055	LYS
1	A	1062	ASN
1	A	1074	LEU
1	A	1098	GLU
1	A	1131	THR
1	A	1224	LEU
1	A	1252	PRO
1	A	1257	LEU
1	A	1260	LEU
1	A	1273	LEU
1	B	2004	LYS
1	B	2017	LEU
1	B	2031	ARG
1	B	2033	LEU

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Mol	Chain	Res	Type
1	B	2043	THR
1	B	2062	ASN
1	B	2074	LEU
1	B	2075	GLU
1	B	2082	GLN
1	B	2109	VAL
1	B	2122	THR
1	B	2124	LEU
1	B	2141	GLN
1	B	2143	VAL
1	B	2160	ASN
1	B	2204	LEU
1	B	2224	LEU
1	B	2238	ILE
1	B	2245	GLU
1	B	2257	LEU
1	B	2260	LEU
1	C	3002	LYS
1	C	3017	LEU
1	C	3031	ARG
1	C	3062	ASN
1	C	3065	SER
1	C	3074	LEU
1	C	3082	GLN
1	C	3109	VAL
1	C	3176	ASN
1	C	3220	GLN
1	C	3224	LEU
1	C	3252	PRO
1	C	3257	LEU
1	C	3260	LEU
1	C	3273	LEU
1	D	4003	GLN
1	D	4042	VAL
1	D	4045	THR
1	D	4060	LYS
1	D	4074	LEU
1	D	4082	GLN
1	D	4107	ASP
1	D	4124	LEU
1	D	4130	LYS
1	D	4135	ILE

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Mol	Chain	Res	Type
1	D	4141	GLN
1	D	4160	ASN
1	D	4218	ARG
1	D	4220	GLN
1	D	4224	LEU
1	D	4257	LEU
1	D	4260	LEU
1	D	4267	MET
1	D	4284	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1015	ASN
1	A	1062	ASN
1	A	1113	GLN
1	A	1136	ASN
1	A	1150	ASN
1	A	1176	ASN
1	B	2003	GLN
1	B	2040	HIS
1	B	2062	ASN
1	B	2103	GLN
1	B	2121	GLN
1	B	2136	ASN
1	B	2141	GLN
1	B	2147	GLN
1	B	2150	ASN
1	B	2160	ASN
1	B	2220	GLN
1	C	3015	ASN
1	C	3026	ASN
1	C	3062	ASN
1	C	3086	GLN
1	C	3113	GLN
1	C	3136	ASN
1	C	3150	ASN
1	C	3176	ASN
1	D	4003	GLN
1	D	4026	ASN
1	D	4082	GLN
1	D	4136	ASN

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Mol	Chain	Res	Type
1	D	4141	GLN
1	D	4160	ASN
1	D	4176	ASN
1	D	4205	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

10 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	A	1999	-	4,4,4	0.48	0	6,6,6	0.40	0
2	SO4	A	1777	-	4,4,4	0.37	0	6,6,6	0.20	0
2	SO4	C	3777	-	4,4,4	0.34	0	6,6,6	0.19	0
2	SO4	B	2888	-	4,4,4	0.34	0	6,6,6	0.21	0
2	SO4	D	4999	-	4,4,4	0.46	0	6,6,6	0.28	0
2	SO4	C	3999	-	4,4,4	0.34	0	6,6,6	0.24	0
2	SO4	C	3888	-	4,4,4	0.36	0	6,6,6	0.12	0
2	SO4	B	2777	-	4,4,4	0.36	0	6,6,6	0.09	0
2	SO4	D	4777	-	4,4,4	0.36	0	6,6,6	0.12	0
2	SO4	B	2999	-	4,4,4	0.41	0	6,6,6	0.26	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 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	3777	SO4	1	0
2	D	4999	SO4	1	0

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	266/284 (93%)	-0.43	8 (3%)	52	48	25, 36, 66, 89	0
1	B	266/284 (93%)	-0.31	9 (3%)	48	44	26, 40, 75, 93	0
1	C	266/284 (93%)	-0.36	6 (2%)	61	57	24, 38, 73, 95	0
1	D	264/284 (92%)	0.78	25 (9%)	14	11	31, 64, 90, 95	0
All	All	1062/1136 (93%)	-0.08	48 (4%)	38	34	24, 42, 84, 95	0

All (48) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	2205	GLN	4.4
1	A	1252	PRO	4.3
1	B	2252	PRO	4.0
1	A	1067	HIS	4.0
1	B	2219	ALA	3.7
1	C	3252	PRO	3.7
1	A	1066	ILE	3.3
1	C	3219	ALA	3.2
1	D	4253	SER	3.1
1	D	4134	VAL	3.0
1	D	4218	ARG	3.0
1	D	4205	GLN	3.0
1	D	4031	ARG	2.9
1	C	3218	ARG	2.9
1	A	1253	SER	2.9
1	C	3253	SER	2.8
1	B	2253	SER	2.8
1	B	2067	HIS	2.7
1	D	4067	HIS	2.7
1	B	2066	ILE	2.7
1	D	4042	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
1	D	4066	ILE	2.7
1	C	3283	SER	2.7
1	D	4069	TYR	2.7
1	B	2245	GLU	2.6
1	A	1205	GLN	2.6
1	B	2204	LEU	2.6
1	D	4244	PRO	2.5
1	A	1068	SER	2.5
1	D	4080	ILE	2.5
1	D	4108	VAL	2.5
1	A	1064	SER	2.4
1	D	4109	VAL	2.4
1	D	4083	GLU	2.4
1	D	4068	SER	2.3
1	D	4219	ALA	2.3
1	D	4027	VAL	2.3
1	D	4098	GLU	2.3
1	D	4081	PHE	2.2
1	D	4133	ALA	2.2
1	C	3205	GLN	2.2
1	D	4105	VAL	2.1
1	D	4088	PHE	2.1
1	D	4127	ALA	2.1
1	A	1245	GLU	2.1
1	B	2069	TYR	2.1
1	D	4065	SER	2.1
1	D	4204	LEU	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	D	4777	5/5	0.66	0.21	88,90,91,91	5
2	SO4	A	1777	5/5	0.81	0.16	47,56,59,61	5
2	SO4	B	2777	5/5	0.90	0.15	69,70,72,73	5
2	SO4	C	3777	5/5	0.94	0.17	44,53,57,57	5
2	SO4	B	2888	5/5	0.94	0.08	53,59,66,71	0
2	SO4	D	4999	5/5	0.95	0.08	59,63,67,70	0
2	SO4	C	3888	5/5	0.95	0.13	57,59,62,63	5
2	SO4	B	2999	5/5	0.97	0.06	53,56,58,60	0
2	SO4	A	1999	5/5	0.99	0.04	27,28,34,35	0
2	SO4	C	3999	5/5	0.99	0.04	27,32,37,39	0

6.5 Other polymers [i](#)

There are no such residues in this entry.