



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 09:24 PM UTC

PDB ID : 1EWE / pdb_00001ewe
Title : Fructose 1,6-Bisphosphate Aldolase from Rabbit Muscle
Authors : Maurady, A.; Sygusch, J.
Deposited on : 2000-04-25
Resolution : 2.60 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

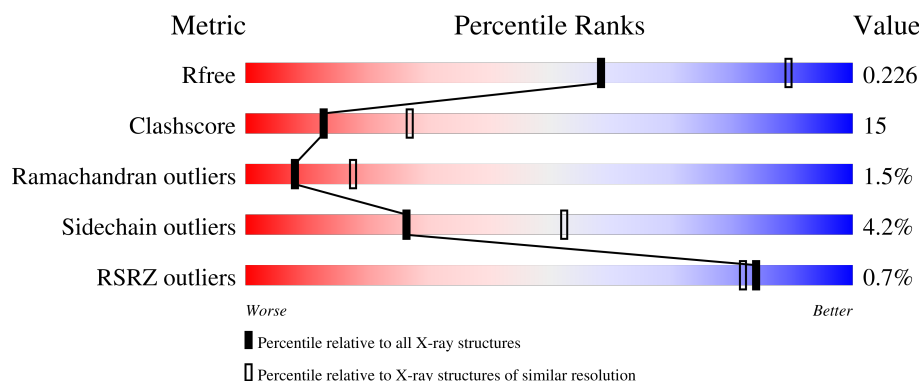
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	363	66% 32%
1	B	363	67% 30%
1	C	363	68% 28%
1	D	363	65% 31%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13475 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.

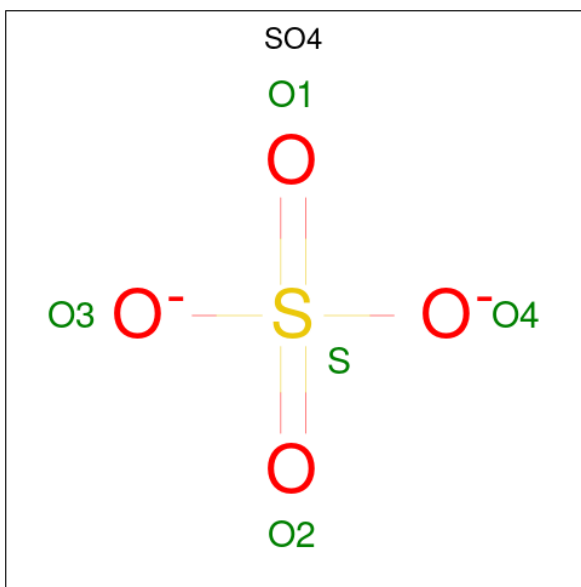
- Molecule 1 is a protein called FRUCTOSE 1,6-BISPHOSPHATE ALDOLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	363	Total	C	N	O	S	0	0	0
			2757	1732	488	525	12			
1	B	363	Total	C	N	O	S	0	0	0
			2757	1732	488	525	12			
1	C	363	Total	C	N	O	S	0	0	0
			2757	1732	488	525	12			
1	D	363	Total	C	N	O	S	0	0	0
			2757	1732	488	525	12			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	229	MET	LYS	engineered mutation	UNP P00883
B	229	MET	LYS	engineered mutation	UNP P00883
C	229	MET	LYS	engineered mutation	UNP P00883
D	229	MET	LYS	engineered mutation	UNP P00883

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



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

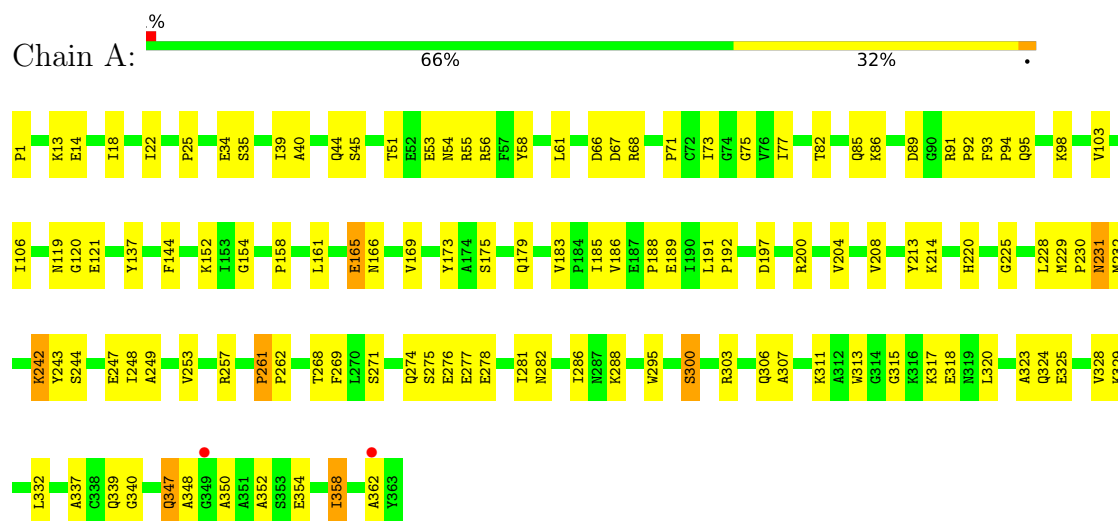
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	420	Total	O	0	0
			420	420		
3	B	430	Total	O	0	0
			430	430		
3	C	867	Total	O	0	0
			867	867		
3	D	720	Total	O	0	0
			720	720		

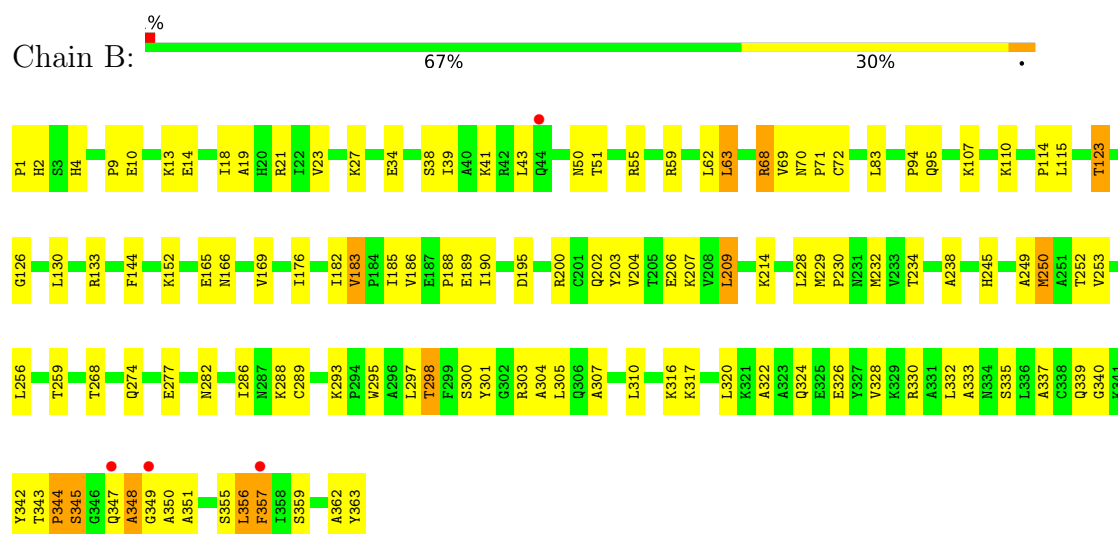
3 Residue-property plots

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: FRUCTOSE 1,6-BISPHOSPHATE ALDOLASE

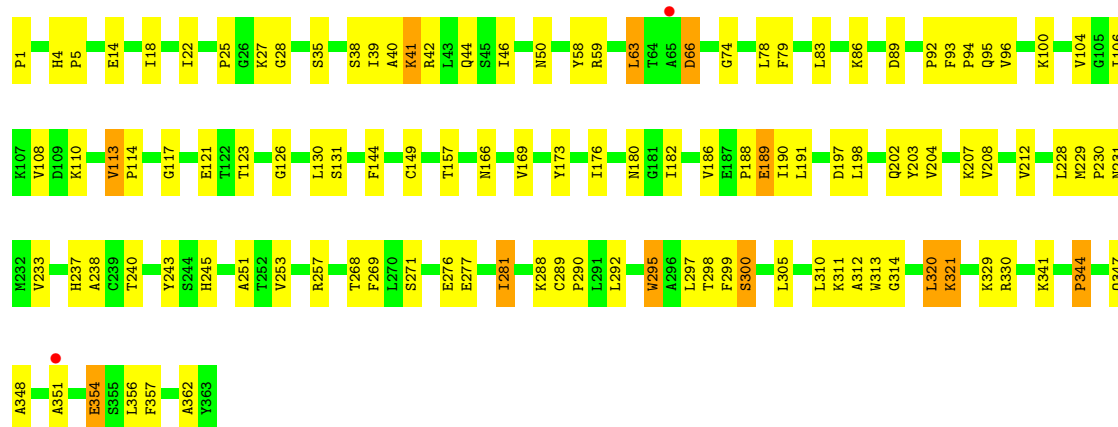


• Molecule 1: FRUCTOSE 1,6-BISPHOSPHATE ALDOLASE

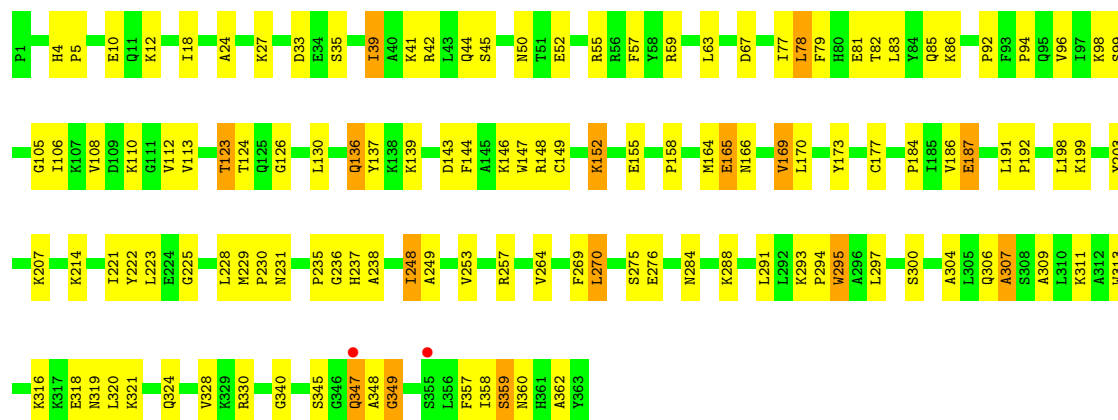


• Molecule 1: FRUCTOSE 1,6-BISPHOSPHATE ALDOLASE





● Molecule 1: FRUCTOSE 1,6-BISPHOSPHATE ALDOLASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	164.24Å 57.41Å 85.05Å 90.00° 102.65° 90.00°	Depositor
Resolution (Å)	10.00 – 2.60 10.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	8.0 (10.00-2.60) 70.6 (10.00-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.36 (at 2.61Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.166 , 0.237 0.157 , 0.226	Depositor DCC
R_{free} test set	2796 reflections (8.04%)	wwPDB-VP
Wilson B-factor (Å ²)	16.2	Xtriage
Anisotropy	0.913	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.22 , 122.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.032 for -h-l,-k,l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	13475	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.80% 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	0.45	0/2811	0.93	10/3809 (0.3%)
1	B	0.43	0/2811	0.98	7/3809 (0.2%)
1	C	0.45	0/2811	0.94	10/3809 (0.3%)
1	D	0.43	0/2811	0.95	8/3809 (0.2%)
All	All	0.44	0/11244	0.95	35/15236 (0.2%)

There are no bond length outliers.

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	191	LEU	N-CA-C	7.36	118.99	109.64
1	B	214	LYS	N-CA-C	-7.25	103.46	111.36
1	B	356	LEU	N-CA-C	6.84	117.07	108.45
1	D	347	GLN	N-CA-C	6.28	122.30	113.56
1	C	271	SER	N-CA-C	6.22	118.14	111.36
1	A	248	ILE	N-CA-C	-6.20	104.47	110.42
1	A	300	SER	N-CA-C	-6.15	97.71	110.80
1	D	148	ARG	N-CA-C	5.95	118.43	108.73
1	B	123	THR	N-CA-C	-5.94	100.29	109.14
1	B	63	LEU	N-CA-C	5.71	119.06	111.75
1	C	189	GLU	N-CA-C	5.57	117.80	108.23
1	D	123	THR	N-CA-C	-5.54	100.70	108.96
1	A	261	PRO	CA-C-N	5.54	125.63	119.32
1	A	261	PRO	C-N-CA	5.54	125.63	119.32
1	B	68	ARG	N-CA-C	-5.47	105.87	112.54
1	C	108	VAL	N-CA-C	5.42	116.29	111.90
1	C	231	ASN	N-CA-C	-5.42	102.50	110.52
1	B	351	ALA	N-CA-C	5.39	122.29	110.80
1	A	73	ILE	N-CA-C	5.33	115.77	107.99
1	D	223	LEU	N-CA-C	5.31	117.75	111.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	187	GLU	N-CA-C	5.27	118.74	108.21
1	C	63	LEU	N-CA-C	5.24	116.68	111.07
1	A	214	LYS	N-CA-C	-5.19	105.31	111.69
1	D	96	VAL	N-CA-C	-5.16	105.30	110.30
1	B	345	SER	N-CA-C	-5.15	105.25	112.25
1	A	189	GLU	N-CA-C	5.12	116.82	108.63
1	C	300	SER	N-CA-C	-5.11	99.91	110.80
1	A	313	TRP	N-CA-C	-5.11	107.00	113.43
1	A	269	PHE	N-CA-C	5.10	117.11	110.43
1	C	4	HIS	CA-C-N	5.08	126.19	119.84
1	C	4	HIS	C-N-CA	5.08	126.19	119.84
1	D	214	LYS	N-CA-C	-5.07	106.27	112.90
1	C	113	VAL	CA-C-N	5.02	124.78	119.76
1	C	113	VAL	C-N-CA	5.02	124.78	119.76
1	D	300	SER	N-CA-C	-5.01	100.12	110.80

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	2757	0	2772	91	0
1	B	2757	0	2772	84	0
1	C	2757	0	2772	75	0
1	D	2757	0	2772	92	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
3	A	420	0	0	21	0
3	B	430	0	0	11	0
3	C	867	0	0	17	0
3	D	720	0	0	19	0
All	All	13475	0	11088	333	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 15.

All (333) 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:D:45:SER:HA	3:D:6089:HOH:O	1.73	0.89
1:C:320:LEU:HA	3:C:4074:HOH:O	1.73	0.88
1:D:235:PRO:HA	3:D:5422:HOH:O	1.73	0.87
1:D:83:LEU:HG	3:D:5443:HOH:O	1.74	0.87
1:A:185:ILE:HG21	1:A:229:MET:HE3	1.56	0.86
1:D:82:THR:HA	1:D:85:GLN:HE21	1.41	0.86
1:B:357:PHE:HA	3:B:2660:HOH:O	1.78	0.83
1:C:348:ALA:HB1	1:C:351:ALA:O	1.81	0.81
1:A:228:LEU:HG	1:A:230:PRO:HD3	1.62	0.79
1:A:1:PRO:HB3	3:A:1725:HOH:O	1.84	0.77
1:B:27:LYS:O	1:B:298:THR:HG21	1.84	0.77
1:C:228:LEU:HG	1:C:230:PRO:HD3	1.66	0.77
1:D:228:LEU:HG	1:D:230:PRO:HD3	1.64	0.77
1:C:354:GLU:HB3	1:C:356:LEU:HD22	1.67	0.76
1:C:276:GLU:HB3	1:C:330:ARG:HD2	1.67	0.76
1:B:228:LEU:HG	1:B:230:PRO:HD3	1.69	0.75
1:A:242:LYS:HD3	1:A:242:LYS:H	1.51	0.74
1:C:281:ILE:HD12	3:C:4091:HOH:O	1.88	0.72
1:C:344:PRO:HA	3:C:3822:HOH:O	1.90	0.72
1:D:41:LYS:HB2	3:D:5553:HOH:O	1.88	0.72
1:D:137:TYR:HD2	3:D:5417:HOH:O	1.72	0.72
1:A:317:LYS:H	1:A:317:LYS:HD3	1.53	0.71
1:A:1:PRO:HD2	1:D:158:PRO:HD2	1.73	0.70
1:B:274:GLN:HE22	1:B:282:ASN:HD22	1.40	0.70
1:B:277:GLU:CB	1:B:350:ALA:HB2	2.22	0.69
1:A:192:PRO:HB3	3:A:1487:HOH:O	1.92	0.69
1:B:277:GLU:HB3	1:B:350:ALA:HB2	1.75	0.68
1:A:325:GLU:HG3	3:A:1417:HOH:O	1.93	0.68
1:D:275:SER:HB2	3:D:5872:HOH:O	1.92	0.68
1:A:1:PRO:HB2	1:D:203:TYR:CE2	2.29	0.67
1:A:14:GLU:O	1:A:18:ILE:HG12	1.94	0.67
1:A:268:THR:HB	1:A:300:SER:HB2	1.76	0.66
1:C:66:ASP:O	1:C:100:LYS:NZ	2.28	0.66
1:B:41:LYS:HE3	1:B:363:TYR:HB2	1.76	0.66
1:B:342:TYR:O	1:B:344:PRO:HD3	1.96	0.66
1:D:229:MET:HE2	1:D:270:LEU:HD23	1.77	0.65
1:A:98:LYS:HG2	3:A:1462:HOH:O	1.96	0.65
1:B:10:GLU:HB3	3:B:2754:HOH:O	1.97	0.64
1:D:284:ASN:OD1	1:D:340:GLY:HA2	1.98	0.64
1:D:324:GLN:O	1:D:328:VAL:HG23	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:46:ILE:HB	1:C:314:GLY:HA2	1.80	0.63
1:D:124:THR:CG2	1:D:149:CYS:SG	2.87	0.63
1:C:329:LYS:HD2	3:C:3539:HOH:O	1.98	0.63
1:D:349:GLY:HA2	3:D:5399:HOH:O	2.00	0.62
1:A:1:PRO:HB2	1:D:203:TYR:HE2	1.64	0.62
1:C:186:VAL:HG12	1:C:188:PRO:HD3	1.82	0.62
1:B:186:VAL:O	1:B:188:PRO:HD3	1.99	0.61
1:D:110:LYS:HG2	1:D:126:GLY:HA2	1.83	0.61
1:B:152:LYS:HE2	3:B:2460:HOH:O	2.00	0.61
1:C:238:ALA:HB2	3:C:3754:HOH:O	2.01	0.61
1:C:198:LEU:HD21	1:C:251:ALA:HB2	1.83	0.60
1:D:248:ILE:HG13	1:D:249:ALA:N	2.15	0.60
1:B:130:LEU:HB3	1:B:176:ILE:HG21	1.83	0.60
1:B:95:GLN:HG3	3:B:2498:HOH:O	2.00	0.60
1:D:316:LYS:HB3	1:D:318:GLU:HG2	1.83	0.60
1:B:249:ALA:O	1:B:253:VAL:HG23	2.01	0.60
1:D:83:LEU:HD22	1:D:106:ILE:HD13	1.84	0.59
1:D:152:LYS:HD3	1:D:191:LEU:HD12	1.83	0.59
1:B:34:GLU:HB3	1:B:38:SER:HB2	1.85	0.59
1:D:198:LEU:HD13	1:D:235:PRO:HD3	1.84	0.59
1:A:45:SER:HA	3:A:1395:HOH:O	2.01	0.59
1:A:166:ASN:O	1:A:169:VAL:HG12	2.03	0.59
1:C:312:ALA:HB1	3:C:4034:HOH:O	2.03	0.59
1:C:237:HIS:HB2	3:C:4107:HOH:O	2.02	0.59
1:B:322:ALA:O	1:B:326:GLU:HG2	2.03	0.59
1:A:120:GLY:O	1:A:152:LYS:HE3	2.03	0.58
1:A:34:GLU:HB3	1:A:39:ILE:HB	1.85	0.58
1:C:240:THR:HG22	1:C:357:PHE:O	2.02	0.58
1:D:55:ARG:O	1:D:59:ARG:HG2	2.03	0.58
1:A:161:LEU:O	1:A:165:GLU:HB2	2.03	0.58
1:B:274:GLN:HE22	1:B:282:ASN:ND2	2.00	0.58
1:A:204:VAL:O	1:A:208:VAL:HG23	2.04	0.58
1:C:288:LYS:HE3	3:C:4068:HOH:O	2.03	0.58
1:A:91:ARG:HH21	1:A:95:GLN:HG3	1.69	0.57
1:A:51:THR:HB	1:A:54:ASN:OD1	2.03	0.57
1:C:14:GLU:O	1:C:18:ILE:HG13	2.03	0.57
1:A:61:LEU:HD21	1:A:323:ALA:HB1	1.86	0.57
1:A:253:VAL:O	1:A:257:ARG:HG3	2.05	0.57
1:D:81:GLU:O	1:D:85:GLN:HG3	2.05	0.57
1:A:39:ILE:HG21	1:A:55:ARG:HD2	1.87	0.57
1:D:94:PRO:O	1:D:98:LYS:HG2	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:274:GLN:OE1	1:A:282:ASN:ND2	2.38	0.56
1:D:137:TYR:CD2	3:D:5417:HOH:O	2.52	0.56
1:D:147:TRP:HB3	1:D:173:TYR:CE2	2.41	0.56
1:B:324:GLN:O	1:B:328:VAL:HG23	2.06	0.55
1:D:124:THR:HG22	1:D:149:CYS:SG	2.46	0.55
1:C:245:HIS:HD2	1:C:347:GLN:HA	1.71	0.55
1:B:301:TYR:HB2	1:B:305:LEU:HG	1.88	0.55
1:A:303:ARG:NH2	1:A:354:GLU:HG2	2.22	0.55
1:C:27:LYS:HD3	1:C:74:GLY:HA2	1.89	0.55
1:A:94:PRO:HG2	3:A:1604:HOH:O	2.07	0.55
1:C:18:ILE:O	1:C:22:ILE:HG13	2.06	0.55
1:B:166:ASN:O	1:B:169:VAL:HG22	2.08	0.54
1:D:57:PHE:HE2	1:D:313:TRP:HE1	1.53	0.54
1:D:86:LYS:HA	1:D:92:PRO:HA	1.90	0.54
1:D:358:ILE:HG21	3:D:5411:HOH:O	2.06	0.54
1:B:317:LYS:O	1:B:320:LEU:HD22	2.07	0.54
1:A:318:GLU:C	1:A:320:LEU:H	2.16	0.54
1:B:277:GLU:HB2	1:B:350:ALA:HB2	1.90	0.53
1:C:41:LYS:HA	1:C:44:GLN:HE21	1.73	0.53
1:D:39:ILE:HD13	1:D:42:ARG:HB2	1.90	0.53
1:D:184:PRO:HD2	1:D:225:GLY:O	2.09	0.53
1:B:19:ALA:O	1:B:23:VAL:HG22	2.09	0.53
1:D:57:PHE:CZ	1:D:320:LEU:HD13	2.44	0.53
1:D:82:THR:HA	1:D:85:GLN:NE2	2.18	0.53
1:D:345:SER:HB2	3:D:5399:HOH:O	2.08	0.53
1:B:200:ARG:O	1:B:204:VAL:HG23	2.09	0.53
1:C:46:ILE:HG22	1:C:311:LYS:HA	1.89	0.53
1:D:276:GLU:HB3	1:D:330:ARG:HD2	1.90	0.53
1:C:63:LEU:O	1:C:100:LYS:HE2	2.08	0.52
1:C:295:TRP:O	1:C:297:LEU:HD12	2.09	0.52
1:D:253:VAL:O	1:D:257:ARG:HG3	2.09	0.52
1:B:68:ARG:NH2	1:B:328:VAL:HG11	2.24	0.52
1:A:186:VAL:O	1:A:188:PRO:HD3	2.09	0.52
1:B:14:GLU:O	1:B:18:ILE:HG13	2.10	0.52
1:C:166:ASN:HA	1:C:169:VAL:HG12	1.92	0.52
1:C:245:HIS:CD2	1:C:347:GLN:HA	2.44	0.52
1:C:277:GLU:HG3	1:C:281:ILE:HD13	1.92	0.52
1:A:13:LYS:HE3	3:A:1511:HOH:O	2.09	0.52
1:A:18:ILE:O	1:A:22:ILE:HG13	2.10	0.52
1:A:51:THR:HG23	3:A:1653:HOH:O	2.10	0.52
1:B:250:MET:HE2	1:B:289:CYS:SG	2.50	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:347:GLN:O	1:D:347:GLN:HG2	2.10	0.52
1:A:92:PRO:HB2	1:A:94:PRO:HD2	1.91	0.51
1:D:124:THR:HG21	1:D:149:CYS:SG	2.50	0.51
1:B:185:ILE:CG2	1:B:229:MET:HB2	2.41	0.51
1:B:203:TYR:HE2	1:C:1:PRO:HB2	1.76	0.51
1:B:41:LYS:HG3	1:B:363:TYR:HD2	1.75	0.51
1:A:68:ARG:O	1:A:71:PRO:HD2	2.10	0.51
1:C:321:LYS:H	1:C:321:LYS:HD3	1.76	0.51
1:D:155:GLU:HA	3:D:5456:HOH:O	2.11	0.51
1:D:18:ILE:HD13	1:D:143:ASP:HB3	1.91	0.50
1:A:61:LEU:HD21	1:A:323:ALA:CB	2.42	0.50
1:A:183:VAL:HG13	1:A:225:GLY:O	2.11	0.50
1:A:311:LYS:HD3	1:A:352:ALA:CB	2.42	0.50
1:B:301:TYR:HB3	1:B:304:ALA:HB3	1.92	0.50
1:B:288:LYS:HE2	1:B:340:GLY:O	2.12	0.50
1:C:42:ARG:HE	1:C:310:LEU:HD22	1.76	0.50
1:A:303:ARG:HH21	1:A:354:GLU:HG2	1.75	0.50
1:B:110:LYS:HE3	1:B:133:ARG:NH2	2.26	0.50
1:B:303:ARG:NH1	1:B:307:ALA:HA	2.26	0.50
1:D:35:SER:HA	1:D:79:PHE:CZ	2.46	0.50
1:B:39:ILE:O	1:B:43:LEU:HG	2.11	0.49
1:C:130:LEU:HB3	1:C:176:ILE:HG21	1.93	0.49
1:B:326:GLU:HA	3:B:2628:HOH:O	2.11	0.49
1:D:170:LEU:HD13	1:D:186:VAL:CG1	2.43	0.49
1:D:359:SER:HB2	3:D:5552:HOH:O	2.12	0.49
1:B:1:PRO:HA	3:B:2681:HOH:O	2.12	0.49
1:B:144:PHE:HA	1:B:182:ILE:HG23	1.95	0.49
1:A:204:VAL:HG12	3:A:1767:HOH:O	2.13	0.49
1:B:72:CYS:SG	1:B:335:SER:HB2	2.53	0.49
1:C:28:GLY:HA3	1:C:299:PHE:CE1	2.48	0.49
1:B:72:CYS:SG	1:B:332:LEU:HD23	2.53	0.49
1:C:204:VAL:O	1:C:208:VAL:HG23	2.13	0.49
1:A:61:LEU:HD11	1:A:323:ALA:HB3	1.95	0.48
1:B:347:GLN:O	1:B:348:ALA:HB3	2.12	0.48
1:D:170:LEU:HD13	1:D:186:VAL:HG13	1.95	0.48
1:A:324:GLN:O	1:A:328:VAL:HG23	2.13	0.48
1:A:262:PRO:HG3	1:D:294:PRO:HG2	1.95	0.48
1:A:93:PHE:CE1	3:A:1747:HOH:O	2.56	0.48
1:A:320:LEU:HB2	3:A:1683:HOH:O	2.14	0.48
1:B:115:LEU:HD21	1:B:123:THR:HB	1.96	0.48
1:B:277:GLU:HG2	1:B:349:GLY:O	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:113:VAL:HG23	1:C:123:THR:CG2	2.44	0.48
1:A:119:ASN:OD1	1:B:4:HIS:NE2	2.47	0.48
1:B:83:LEU:HD12	1:B:94:PRO:HG3	1.96	0.48
1:C:28:GLY:HA3	1:C:299:PHE:CZ	2.49	0.48
1:C:46:ILE:HG21	1:C:310:LEU:O	2.13	0.48
1:A:61:LEU:HD13	1:A:320:LEU:HD12	1.96	0.48
1:A:311:LYS:HD3	1:A:352:ALA:HB1	1.96	0.48
1:A:86:LYS:HA	1:A:92:PRO:HA	1.95	0.47
1:B:1:PRO:HG3	3:C:2612:HOH:O	2.13	0.47
1:A:175:SER:O	1:A:179:GLN:HB2	2.14	0.47
1:A:197:ASP:HB2	1:A:243:TYR:OH	2.14	0.47
3:A:2390:HOH:O	1:B:114:PRO:HB3	2.13	0.47
1:A:66:ASP:OD1	1:A:68:ARG:HD3	2.14	0.47
1:B:252:THR:HG21	1:B:286:ILE:HD13	1.96	0.47
1:D:166:ASN:HA	1:D:169:VAL:HG23	1.96	0.47
1:A:277:GLU:HG2	3:A:1735:HOH:O	2.14	0.47
1:D:288:LYS:HD2	3:D:5739:HOH:O	2.13	0.47
1:D:146:LYS:HE3	1:D:187:GLU:OE2	2.13	0.47
1:D:293:LYS:HD3	1:D:297:LEU:CD1	2.45	0.47
1:A:91:ARG:NH2	1:A:95:GLN:HG3	2.30	0.47
1:D:321:LYS:HB2	3:D:5636:HOH:O	2.14	0.47
1:C:121:GLU:CD	1:C:157:THR:HG22	2.39	0.47
1:A:249:ALA:HA	1:A:286:ILE:HG12	1.96	0.47
1:A:40:ALA:O	1:A:44:GLN:HG2	2.15	0.47
1:A:350:ALA:HB3	3:A:1662:HOH:O	2.16	0.46
1:B:293:LYS:HD3	1:B:297:LEU:HD12	1.97	0.46
1:D:33:ASP:HB3	1:D:77:ILE:HG22	1.97	0.46
1:A:93:PHE:HE1	3:A:1747:HOH:O	1.97	0.46
1:A:325:GLU:O	1:A:329:LYS:HG3	2.16	0.46
1:A:229:MET:HE2	1:A:300:SER:OG	2.15	0.46
1:D:203:TYR:O	1:D:207:LYS:HG2	2.16	0.46
1:B:51:THR:O	1:B:55:ARG:HG3	2.16	0.46
1:A:58:TYR:OH	1:A:306:GLN:HB3	2.16	0.46
3:A:2649:HOH:O	1:B:114:PRO:HD3	2.15	0.46
1:D:99:SER:HB3	3:D:5535:HOH:O	2.16	0.46
1:A:220:HIS:HD2	1:D:207:LYS:NZ	2.13	0.46
1:B:343:THR:O	1:B:345:SER:N	2.49	0.46
1:C:189:GLU:HG3	3:C:4188:HOH:O	2.16	0.46
1:D:41:LYS:HE2	3:D:5553:HOH:O	2.15	0.46
1:A:56:ARG:HB2	1:A:85:GLN:NE2	2.31	0.46
1:D:136:GLN:O	1:D:139:LYS:HG2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:40:ALA:O	1:C:44:GLN:HG3	2.15	0.45
1:B:253:VAL:HG22	1:B:286:ILE:HG23	1.97	0.45
1:B:209:LEU:HD22	3:B:2779:HOH:O	2.16	0.45
1:A:94:PRO:O	1:A:98:LYS:HE2	2.17	0.45
1:C:46:ILE:HD12	1:C:313:TRP:O	2.16	0.45
1:D:264:VAL:O	1:D:295:TRP:HB3	2.17	0.45
1:B:330:ARG:HA	1:B:330:ARG:NE	2.32	0.45
1:C:229:MET:HE1	3:C:4086:HOH:O	2.15	0.45
1:D:105:GLY:HA2	1:D:144:PHE:O	2.17	0.45
1:A:106:ILE:HG12	1:A:137:TYR:CE2	2.52	0.45
1:A:204:VAL:CG1	3:A:1767:HOH:O	2.64	0.45
1:A:220:HIS:HD2	1:D:207:LYS:HZ1	1.64	0.45
1:B:203:TYR:O	1:B:207:LYS:HG2	2.17	0.45
1:D:136:GLN:OE1	1:D:139:LYS:HD2	2.17	0.45
1:B:39:ILE:HG21	1:B:55:ARG:CD	2.46	0.45
1:A:347:GLN:HB2	1:A:348:ALA:H	1.55	0.45
1:B:70:ASN:N	1:B:71:PRO:HD2	2.31	0.45
1:D:12:LYS:HD2	1:D:222:TYR:CD1	2.52	0.44
1:D:318:GLU:HG3	1:D:319:ASN:N	2.32	0.44
1:D:347:GLN:O	1:D:347:GLN:CG	2.66	0.44
1:C:269:PHE:HE2	1:C:297:LEU:HB3	1.83	0.44
1:C:58:TYR:CE2	3:C:4017:HOH:O	2.70	0.44
1:D:173:TYR:CE1	1:D:177:CYS:SG	3.11	0.44
1:B:9:PRO:O	1:B:13:LYS:HB2	2.18	0.44
1:A:213:TYR:OH	1:A:228:LEU:HD22	2.17	0.44
1:C:86:LYS:HE2	1:C:92:PRO:HG3	1.98	0.44
1:A:77:ILE:HD11	1:A:229:MET:HE1	1.99	0.44
1:B:200:ARG:HG2	1:B:200:ARG:HH11	1.83	0.44
1:A:328:VAL:O	1:A:332:LEU:HG	2.18	0.43
1:B:355:SER:HB2	1:B:356:LEU:HD23	2.00	0.43
1:C:298:THR:HG21	3:C:3389:HOH:O	2.17	0.43
1:B:259:THR:HG22	3:B:2782:HOH:O	2.18	0.43
1:D:293:LYS:HD3	1:D:297:LEU:HD11	2.00	0.43
1:B:186:VAL:C	1:B:188:PRO:HD3	2.42	0.43
1:C:35:SER:HA	1:C:79:PHE:CE2	2.54	0.43
1:C:131:SER:HA	1:C:180:ASN:HD21	1.83	0.43
1:D:165:GLU:O	1:D:169:VAL:HG23	2.17	0.43
1:B:69:VAL:CG2	1:B:328:VAL:HG22	2.49	0.43
1:B:190:ILE:N	1:B:190:ILE:HD12	2.33	0.43
1:C:149:CYS:O	1:C:189:GLU:HB3	2.19	0.43
1:B:245:HIS:ND1	1:B:282:ASN:OD1	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:59:ARG:O	1:B:63:LEU:HD13	2.18	0.43
1:C:39:ILE:HD12	1:C:59:ARG:CZ	2.49	0.43
1:C:92:PRO:HB2	1:C:95:GLN:HG2	2.00	0.43
1:C:110:LYS:HG2	1:C:126:GLY:HA2	2.00	0.43
1:C:268:THR:HB	1:C:300:SER:HB2	2.01	0.43
1:D:357:PHE:HA	1:D:362:ALA:HB2	2.01	0.43
1:A:121:GLU:OE1	1:A:158:PRO:HA	2.19	0.43
1:C:117:GLY:HA2	1:D:4:HIS:O	2.19	0.43
1:C:83:LEU:HD22	1:C:106:ILE:HD12	2.01	0.43
1:C:269:PHE:CZ	1:C:297:LEU:HD23	2.54	0.43
1:D:269:PHE:HE2	1:D:297:LEU:HB3	1.83	0.43
1:C:78:LEU:HD13	1:C:104:VAL:HG13	2.00	0.42
1:D:291:LEU:O	1:D:293:LYS:HG3	2.19	0.42
1:A:75:GLY:HA2	1:A:103:VAL:O	2.19	0.42
1:C:357:PHE:HA	1:C:362:ALA:HB2	2.00	0.42
1:D:112:VAL:HG12	3:D:5769:HOH:O	2.18	0.42
1:D:348:ALA:O	1:D:349:GLY:C	2.62	0.42
1:C:144:PHE:HA	1:C:182:ILE:HG23	2.01	0.42
1:A:231:ASN:HD22	1:A:232:MET:N	2.18	0.42
1:B:110:LYS:HD2	1:B:126:GLY:HA2	2.01	0.42
1:B:144:PHE:CB	1:B:183:VAL:HG22	2.49	0.42
1:C:35:SER:HA	1:C:79:PHE:CZ	2.53	0.42
1:C:190:ILE:HD13	1:C:204:VAL:HG23	2.02	0.42
1:C:203:TYR:O	1:C:207:LYS:HG2	2.19	0.42
1:A:58:TYR:O	1:A:61:LEU:HB3	2.19	0.42
1:A:271:SER:O	1:A:274:GLN:HG3	2.19	0.42
1:A:95:GLN:HA	1:A:98:LYS:HE3	2.01	0.42
1:C:253:VAL:O	1:C:257:ARG:HG3	2.19	0.42
1:C:289:CYS:HA	1:C:290:PRO:HD3	1.85	0.42
1:D:113:VAL:HG23	1:D:123:THR:HG22	2.01	0.42
1:D:199:LYS:HA	1:D:199:LYS:HD3	1.85	0.42
1:B:69:VAL:HG23	1:B:328:VAL:HG13	2.01	0.42
1:C:44:GLN:HG2	3:C:4015:HOH:O	2.19	0.42
1:B:337:ALA:C	1:B:339:GLN:H	2.28	0.42
1:D:57:PHE:HE2	1:D:313:TRP:NE1	2.17	0.42
1:D:306:GLN:O	1:D:309:ALA:N	2.53	0.42
1:A:277:GLU:O	1:A:281:ILE:HG13	2.20	0.42
1:A:337:ALA:C	1:A:339:GLN:H	2.28	0.42
1:B:21:ARG:HB3	3:B:2689:HOH:O	2.20	0.42
1:C:197:ASP:HB2	1:C:243:TYR:OH	2.19	0.42
1:D:24:ALA:HB3	1:D:27:LYS:HD2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:40:ALA:HB2	1:C:50:ASN:ND2	2.35	0.42
1:D:306:GLN:O	1:D:307:ALA:C	2.62	0.42
1:A:93:PHE:CD1	3:A:1747:HOH:O	2.73	0.41
1:C:348:ALA:HB2	3:C:3378:HOH:O	2.19	0.41
1:B:202:GLN:O	1:B:206:GLU:HG3	2.19	0.41
1:C:27:LYS:HD3	1:C:74:GLY:CA	2.50	0.41
1:D:108:VAL:HB	1:D:130:LEU:HD11	2.01	0.41
1:D:192:PRO:HD3	1:D:231:ASN:ND2	2.34	0.41
1:B:256:LEU:HD12	3:B:2779:HOH:O	2.20	0.41
1:D:311:LYS:HB3	1:D:311:LYS:HE2	1.81	0.41
1:A:35:SER:O	1:A:39:ILE:HG22	2.21	0.41
1:C:93:PHE:N	1:C:94:PRO:HD2	2.36	0.41
1:D:78:LEU:HD12	3:D:5850:HOH:O	2.19	0.41
1:B:130:LEU:HA	1:B:130:LEU:HD23	1.88	0.41
1:A:244:SER:OG	1:A:247:GLU:HG3	2.21	0.41
1:B:165:GLU:O	1:B:169:VAL:HG13	2.20	0.41
1:B:195:ASP:HB3	1:B:238:ALA:HB3	2.02	0.41
1:A:51:THR:HG22	1:A:53:GLU:H	1.86	0.41
1:B:268:THR:HB	1:B:300:SER:HB2	2.03	0.41
1:D:77:ILE:HG12	1:D:144:PHE:HE1	1.85	0.41
1:A:51:THR:HA	3:A:1653:HOH:O	2.19	0.41
1:C:288:LYS:NZ	3:C:3860:HOH:O	2.53	0.41
1:A:261:PRO:HA	1:A:262:PRO:HD3	1.92	0.41
1:A:288:LYS:HE2	1:A:340:GLY:O	2.21	0.41
1:B:232:MET:O	1:B:234:THR:HG23	2.21	0.41
1:D:77:ILE:HD13	1:D:146:LYS:HD2	2.03	0.41
1:D:152:LYS:HB3	1:D:152:LYS:NZ	2.36	0.41
1:A:277:GLU:CG	3:A:1735:HOH:O	2.69	0.40
1:C:202:GLN:HB2	1:C:233:VAL:HG11	2.03	0.40
1:D:236:GLY:O	1:D:238:ALA:N	2.54	0.40
1:A:154:GLY:O	1:A:200:ARG:NH2	2.54	0.40
1:A:276:GLU:CD	1:A:307:ALA:HB3	2.46	0.40
1:B:333:ALA:HB1	1:B:342:TYR:CE1	2.57	0.40
1:D:124:THR:CG2	1:D:147:TRP:HE1	2.34	0.40
1:D:276:GLU:HG2	1:D:304:ALA:HA	2.03	0.40
1:A:358:ILE:HG12	3:A:1764:HOH:O	2.20	0.40
1:C:166:ASN:O	1:C:169:VAL:HG12	2.22	0.40
1:C:212:VAL:HG13	3:C:3476:HOH:O	2.21	0.40
1:D:27:LYS:HE2	3:D:5837:HOH:O	2.20	0.40
1:A:144:PHE:CD1	1:A:185:ILE:HD11	2.56	0.40
1:C:113:VAL:HA	1:C:114:PRO:HD3	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:275:SER:OG	1:A:278:GLU:HB2	2.22	0.40
1:B:43:LEU:CD1	1:B:50:ASN:HA	2.52	0.40
1:B:209:LEU:CD2	3:B:2779:HOH:O	2.69	0.40
1:B:274:GLN:NE2	1:B:282:ASN:HD22	2.12	0.40
1:B:277:GLU:OE2	1:B:342:TYR:HE2	2.04	0.40
1:D:249:ALA:O	1:D:253:VAL:HG23	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	361/363 (99%)	329 (91%)	28 (8%)	4 (1%)	11	25
1	B	361/363 (99%)	323 (90%)	34 (9%)	4 (1%)	11	25
1	C	361/363 (99%)	329 (91%)	27 (8%)	5 (1%)	9	19
1	D	361/363 (99%)	324 (90%)	29 (8%)	8 (2%)	5	10
All	All	1444/1452 (99%)	1305 (90%)	118 (8%)	21 (2%)	8	18

All (21) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	349	GLY
1	D	359	SER
1	A	67	ASP
1	B	348	ALA
1	C	354	GLU
1	D	67	ASP
1	D	237	HIS
1	A	362	ALA
1	D	5	PRO

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Mol	Chain	Res	Type
1	D	50	ASN
1	D	307	ALA
1	B	362	ALA
1	C	5	PRO
1	C	320	LEU
1	D	360	ASN
1	A	315	GLY
1	B	344	PRO
1	B	357	PHE
1	A	25	PRO
1	C	25	PRO
1	C	344	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	291/291 (100%)	282 (97%)	9 (3%)	35	63
1	B	291/291 (100%)	279 (96%)	12 (4%)	27	54
1	C	291/291 (100%)	278 (96%)	13 (4%)	24	50
1	D	291/291 (100%)	276 (95%)	15 (5%)	21	44
All	All	1164/1164 (100%)	1115 (96%)	49 (4%)	26	52

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	82	THR
1	A	89	ASP
1	A	165	GLU
1	A	173	TYR
1	A	231	ASN
1	A	242	LYS
1	A	295	TRP
1	A	347	GLN
1	A	358	ILE

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Mol	Chain	Res	Type
1	B	2	HIS
1	B	62	LEU
1	B	107	LYS
1	B	183	VAL
1	B	189	GLU
1	B	209	LEU
1	B	250	MET
1	B	295	TRP
1	B	298	THR
1	B	310	LEU
1	B	316	LYS
1	B	359	SER
1	C	38	SER
1	C	41	LYS
1	C	66	ASP
1	C	89	ASP
1	C	96	VAL
1	C	173	TYR
1	C	191	LEU
1	C	281	ILE
1	C	292	LEU
1	C	295	TRP
1	C	305	LEU
1	C	321	LYS
1	C	341	LYS
1	D	10	GLU
1	D	39	ILE
1	D	44	GLN
1	D	52	GLU
1	D	63	LEU
1	D	78	LEU
1	D	136	GLN
1	D	152	LYS
1	D	164	MET
1	D	165	GLU
1	D	169	VAL
1	D	221	ILE
1	D	248	ILE
1	D	270	LEU
1	D	295	TRP

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	50	ASN
1	A	220	HIS
1	A	241	GLN
1	A	324	GLN
1	B	119	ASN
1	B	179	GLN
1	B	274	GLN
1	C	44	GLN
1	C	54	ASN
1	C	70	ASN
1	C	119	ASN
1	C	180	ASN
1	C	237	HIS
1	C	241	GLN
1	C	319	ASN
1	C	339	GLN
1	D	2	HIS
1	D	20	HIS
1	D	44	GLN
1	D	54	ASN
1	D	85	GLN
1	D	202	GLN
1	D	241	GLN
1	D	287	ASN
1	D	324	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](#)

2 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	D	5664	-	4,4,4	0.44	0	6,6,6	0.33	0
2	SO4	C	2799	-	4,4,4	0.46	0	6,6,6	0.17	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.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	363/363 (100%)	-0.59	2 (0%) 85 83	2, 11, 71, 112	0
1	B	363/363 (100%)	-0.67	4 (1%) 78 74	2, 8, 58, 119	0
1	C	363/363 (100%)	-0.67	2 (0%) 85 83	2, 10, 56, 88	0
1	D	363/363 (100%)	-0.65	2 (0%) 85 83	2, 11, 57, 95	0
All	All	1452/1452 (100%)	-0.64	10 (0%) 84 82	2, 10, 63, 119	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	347	GLN	4.3
1	B	349	GLY	3.1
1	A	362	ALA	2.9
1	B	357	PHE	2.8
1	C	351	ALA	2.5
1	B	44	GLN	2.4
1	D	347	GLN	2.3
1	D	355	SER	2.3
1	C	65	ALA	2.2
1	A	349	GLY	2.2

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	5664	5/5	0.87	0.10	76,77,78,78	0
2	SO4	C	2799	5/5	0.95	0.07	58,60,61,61	0

6.5 Other polymers [i](#)

There are no such residues in this entry.