Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 01:46 PM GMT

PDB ID	:	3UYS
Title	:	Crystal structure of apo human ck1d
Authors	:	Huang, X.
Deposited on	:	2011-12-06
Resolution	:	2.30 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

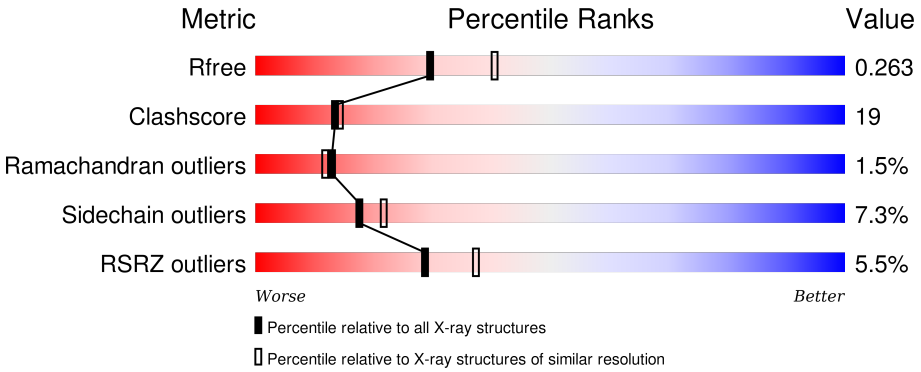
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	91344	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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 on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. 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 <=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	296	3% 60% 31% • 5%
1	B	296	5% 59% 28% 5% • 6%
1	C	296	5% 67% 26% • •
1	D	296	7% 60% 32% • •

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9619 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.

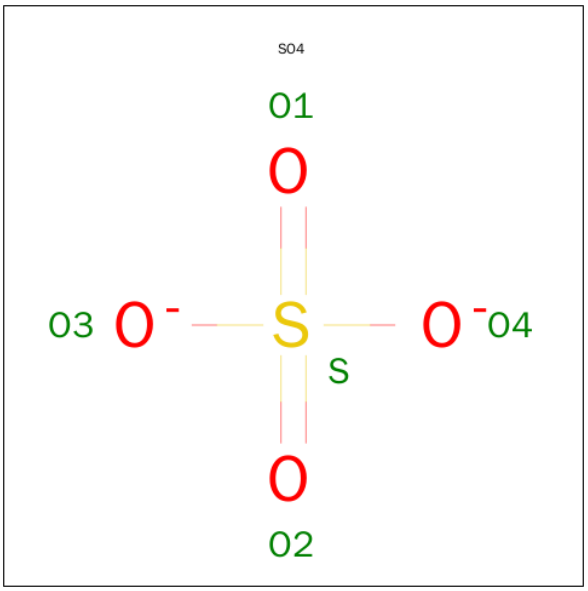
- Molecule 1 is a protein called Casein kinase I isoform delta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	281	Total	C	N	O	S	0	0	0
			2271	1459	390	408	14			
1	B	279	Total	C	N	O	S	0	0	0
			2267	1454	394	405	14			
1	C	286	Total	C	N	O	S	0	0	0
			2265	1454	388	409	14			
1	D	284	Total	C	N	O	S	0	0	0
			2293	1471	396	412	14			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	EXPRESSION TAG	UNP P48730
A	0	SER	-	EXPRESSION TAG	UNP P48730
B	-1	GLY	-	EXPRESSION TAG	UNP P48730
B	0	SER	-	EXPRESSION TAG	UNP P48730
C	-1	GLY	-	EXPRESSION TAG	UNP P48730
C	0	SER	-	EXPRESSION TAG	UNP P48730
D	-1	GLY	-	EXPRESSION TAG	UNP P48730
D	0	SER	-	EXPRESSION TAG	UNP P48730

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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	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	120	Total O 120 120	0	0
3	B	118	Total O 118 118	0	0

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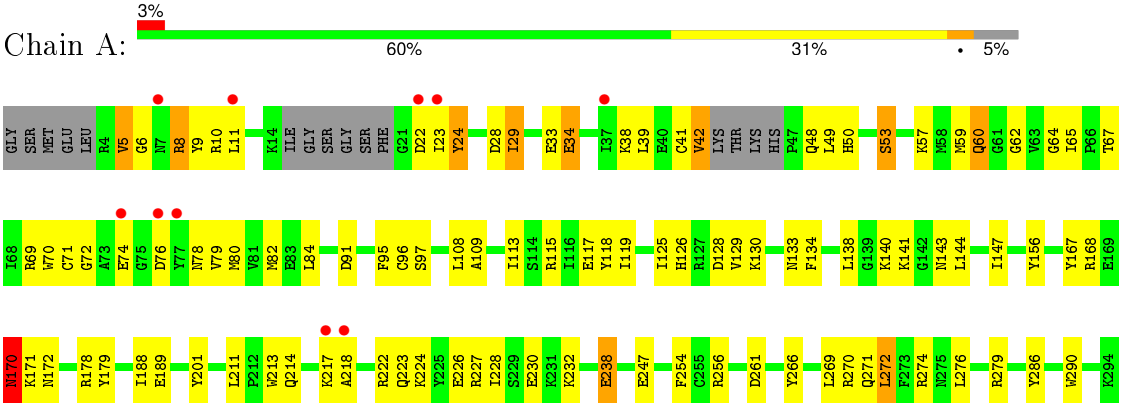
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	126	Total O 126 126	0	0
3	D	109	Total O 109 109	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

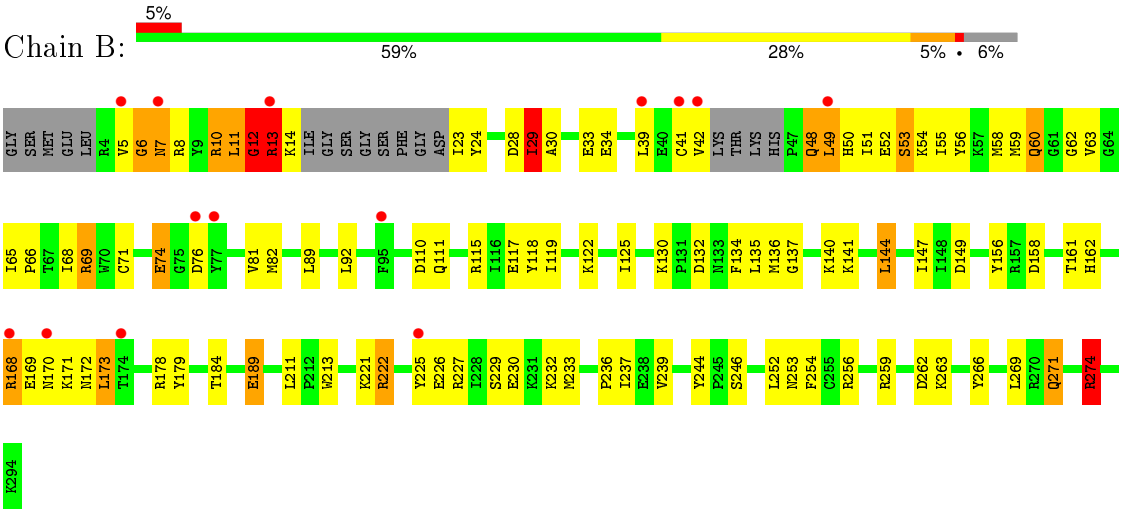
- Molecule 1: Casein kinase I isoform delta

Chain A:



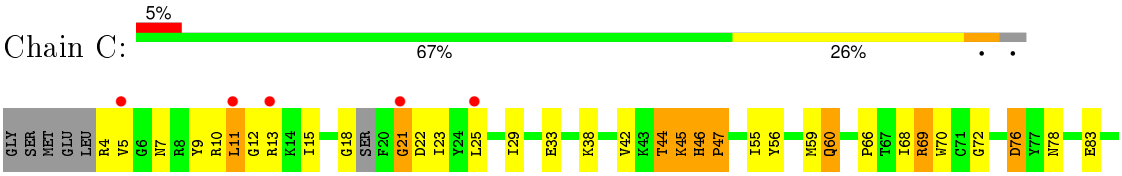
- Molecule 1: Casein kinase I isoform delta

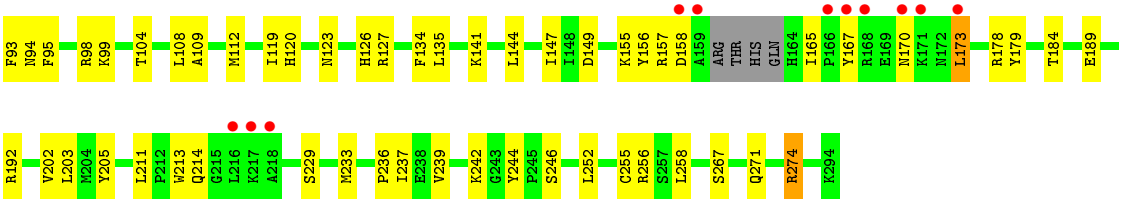
Chain B:



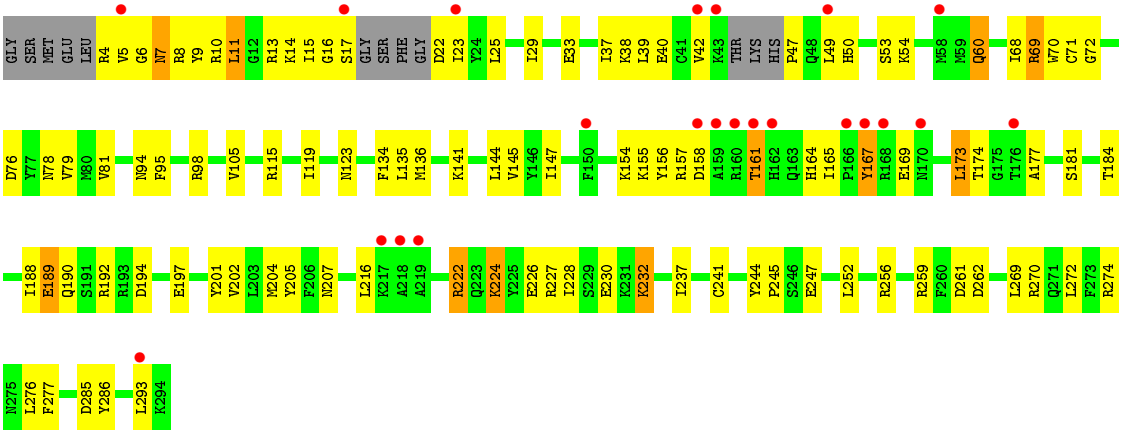
- Molecule 1: Casein kinase I isoform delta

Chain C:





- Molecule 1: Casein kinase I isoform delta



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	49.77Å 85.16Å 89.12Å 70.19° 73.86° 86.15°	Depositor
Resolution (Å)	50.00 – 2.30 49.21 – 2.21	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.30) 86.1 (49.21-2.21)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.72 (at 2.20Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.238 , 0.276 0.231 , 0.263	Depositor DCC
R_{free} test set	2905 reflections (5.10%)	DCC
Wilson B-factor (Å^2)	42.5	Xtriage
Anisotropy	0.322	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 40.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Outliers	0 of 63519 reflections	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	9619	wwPDB-VP
Average B, all atoms (Å^2)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.87% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0.51	0/2322	0.73	2/3123 (0.1%)
1	B	0.52	0/2317	0.81	8/3114 (0.3%)
1	C	0.51	0/2314	0.72	1/3118 (0.0%)
1	D	0.53	0/2343	0.74	3/3151 (0.1%)
All	All	0.52	0/9296	0.75	14/12506 (0.1%)

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

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

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	10	ARG	NE-CZ-NH1	11.06	125.83	120.30
1	A	5	VAL	N-CA-C	7.61	131.56	111.00
1	D	16	GLY	N-CA-C	7.25	131.21	113.10
1	C	21	GLY	N-CA-C	7.19	131.06	113.10
1	B	168	ARG	CB-CG-CD	6.46	128.41	111.60
1	D	6	GLY	N-CA-C	6.11	128.38	113.10
1	B	10	ARG	NE-CZ-NH2	-5.97	117.32	120.30
1	B	274	ARG	NE-CZ-NH1	5.50	123.05	120.30
1	A	256	ARG	NE-CZ-NH1	5.46	123.03	120.30
1	B	6	GLY	CA-C-N	-5.46	105.18	117.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	78	ASN	N-CA-C	-5.33	96.61	111.00
1	B	6	GLY	N-CA-C	5.16	126.00	113.10
1	B	5	VAL	N-CA-C	5.04	124.62	111.00
1	B	12	GLY	N-CA-C	5.04	125.69	113.10

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	244	TYR	Sidechain
1	B	6	GLY	Mainchain
1	C	244	TYR	Sidechain

5.2 Too-close contacts (i)

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	2271	0	2239	91	0
1	B	2267	0	2249	97	0
1	C	2265	0	2206	69	0
1	D	2293	0	2263	84	0
2	A	15	0	0	2	0
2	B	15	0	0	0	0
2	C	10	0	0	2	0
2	D	10	0	0	0	0
3	A	120	0	0	10	0
3	B	118	0	0	14	0
3	C	126	0	0	4	0
3	D	109	0	0	6	0
All	All	9619	0	8957	338	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 19.

All (338) 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:222:ARG:HG2	1:B:222:ARG:HH11	1.00	1.09
1:A:60:GLN:HA	1:A:60:GLN:HE21	1.25	1.01
1:B:23:ILE:HG22	1:B:24:TYR:H	1.20	1.00
1:A:170:ASN:O	1:B:222:ARG:NH1	1.97	0.97
1:B:222:ARG:CG	1:B:222:ARG:HH11	1.77	0.96
1:C:141:LYS:HD2	1:C:144:LEU:HD12	1.46	0.96
1:B:23:ILE:HG22	1:B:24:TYR:N	1.82	0.95
1:A:223:GLN:O	1:A:227:ARG:HG3	1.66	0.95
1:D:69:ARG:HH11	1:D:69:ARG:HB3	1.32	0.93
1:B:222:ARG:NH1	1:B:222:ARG:HG2	1.84	0.92
1:B:59:MET:HA	3:B:1495:HOH:O	1.70	0.91
1:B:122:LYS:HG3	3:B:1495:HOH:O	1.70	0.90
1:B:74:GLU:HB2	3:B:333:HOH:O	1.72	0.90
1:C:69:ARG:HB3	1:C:69:ARG:HH11	1.36	0.87
1:B:256:ARG:HD2	3:B:299:HOH:O	1.75	0.86
1:C:5:VAL:HG23	1:C:9:TYR:HB2	1.59	0.84
1:B:13:ARG:HH11	1:B:13:ARG:CG	1.97	0.78
1:D:5:VAL:HG23	1:D:9:TYR:HB2	1.64	0.78
1:D:68:ILE:O	1:D:68:ILE:HD12	1.84	0.77
1:A:95:PHE:HB3	3:A:1293:HOH:O	1.84	0.76
1:C:45:LYS:C	1:C:47:PRO:HD2	2.05	0.76
1:D:23:ILE:HD11	1:D:38:LYS:HE2	1.68	0.75
1:A:60:GLN:HA	1:A:60:GLN:NE2	1.98	0.74
1:C:271:GLN:NE2	1:C:274:ARG:NH1	2.37	0.73
1:A:140:LYS:HD2	1:A:140:LYS:H	1.54	0.72
1:D:237:ILE:HD13	1:D:252:LEU:HB3	1.70	0.71
1:A:5:VAL:O	1:A:9:TYR:HB2	1.88	0.71
1:C:33:GLU:OE1	1:C:69:ARG:NH2	2.24	0.71
1:B:13:ARG:HH11	1:B:13:ARG:HG3	1.55	0.71
1:C:156:TYR:O	1:C:165:ILE:HG23	1.91	0.71
1:A:39:LEU:CD2	1:A:79:VAL:HG12	2.20	0.71
1:C:271:GLN:NE2	1:C:274:ARG:HH12	1.89	0.70
1:D:47:PRO:HB3	3:D:336:HOH:O	1.89	0.70
1:B:54:LYS:O	1:B:58:MET:HG3	1.91	0.70
1:C:69:ARG:CB	1:C:69:ARG:HH11	2.04	0.70
1:B:23:ILE:CG2	1:B:24:TYR:N	2.55	0.69
1:B:221:LYS:HE3	1:B:225:TYR:OH	1.92	0.69
1:C:44:THR:OG1	1:C:45:LYS:N	2.22	0.69
1:C:46:HIS:N	1:C:47:PRO:HD2	2.07	0.69
1:B:237:ILE:HD12	1:B:253:ASN:OD1	1.91	0.69
1:B:172:ASN:HD22	1:B:222:ARG:HH22	1.40	0.69
1:D:123:ASN:OD1	1:D:157:ARG:NE	2.23	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:238:GLU:HG3	3:A:300:HOH:O	1.92	0.68
1:C:165:ILE:HD12	1:C:189:GLU:OE1	1.93	0.68
1:D:40:GLU:HA	3:D:314:HOH:O	1.95	0.67
1:A:60:GLN:CA	1:A:60:GLN:HE21	1.95	0.67
1:D:188:ILE:HD11	3:D:308:HOH:O	1.95	0.67
1:D:173:LEU:HD22	1:D:184:THR:HG22	1.77	0.66
1:C:70:TRP:CH2	1:C:72:GLY:HA3	2.31	0.65
1:D:181:SER:HB2	1:D:197:GLU:OE1	1.97	0.65
1:A:70:TRP:HZ3	1:A:79:VAL:CG2	2.11	0.64
1:B:236:PRO:HG2	1:B:239:VAL:HG23	1.79	0.64
1:B:259:ARG:NH1	1:B:262:ASP:OD1	2.29	0.64
1:C:271:GLN:HE22	1:C:274:ARG:NH1	1.95	0.64
1:B:226:GLU:O	1:B:230:GLU:HG2	1.98	0.64
1:B:8:ARG:O	1:B:29:ILE:HG22	1.98	0.64
1:C:46:HIS:N	1:C:47:PRO:CD	2.60	0.64
1:B:130:LYS:HE3	1:B:132:ASP:HB2	1.77	0.64
1:A:64:GLY:HA3	1:A:115:ARG:NE	2.13	0.63
1:A:5:VAL:HG23	1:A:9:TYR:HB2	1.80	0.63
1:B:137:GLY:HA3	1:B:141:LYS:O	1.99	0.63
1:A:217:LYS:O	1:A:227:ARG:NH1	2.30	0.63
1:B:13:ARG:HG3	1:B:13:ARG:NH1	2.13	0.63
1:D:11:LEU:HD11	1:D:39:LEU:HD11	1.81	0.63
1:A:254:PHE:CD2	1:A:269:LEU:HD21	2.34	0.62
1:A:39:LEU:HD22	1:A:79:VAL:HG12	1.81	0.62
1:A:53:SER:O	1:A:57:LYS:HG3	2.00	0.62
1:A:226:GLU:O	1:A:230:GLU:HG2	1.99	0.62
1:D:69:ARG:HH11	1:D:69:ARG:CB	2.11	0.61
1:D:167:TYR:O	1:D:167:TYR:HD1	1.83	0.61
1:A:42:VAL:HG23	1:A:78:ASN:ND2	2.15	0.61
1:D:190:GLN:HA	1:D:194:ASP:OD2	2.00	0.61
1:B:119:ILE:CD1	1:B:147:ILE:HD13	2.31	0.61
1:D:167:TYR:CD1	1:D:167:TYR:O	2.53	0.61
1:A:119:ILE:CD1	1:A:147:ILE:HD13	2.31	0.61
1:C:202:VAL:O	1:C:205:TYR:HB3	2.01	0.60
1:B:236:PRO:HG2	1:B:239:VAL:CG2	2.32	0.60
1:B:259:ARG:HG3	1:B:262:ASP:OD2	2.01	0.60
1:C:120:HIS:CG	1:C:192:ARG:HG2	2.36	0.60
1:A:10:ARG:NH1	3:A:719:HOH:O	2.34	0.60
1:B:33:GLU:OE1	1:B:69:ARG:NH2	2.33	0.59
1:A:213:TRP:CE2	1:A:232:LYS:HE2	2.37	0.59
1:B:92:LEU:HD11	1:B:136:MET:HG2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:118:TYR:CE2	3:B:1495:HOH:O	2.52	0.59
1:D:154:LYS:HG2	1:D:155:LYS:O	2.03	0.59
1:B:173:LEU:HD12	1:B:184:THR:HG22	1.85	0.59
1:B:227:ARG:HH11	1:B:227:ARG:HG3	1.68	0.59
1:B:119:ILE:HD11	1:B:147:ILE:HD13	1.85	0.58
1:A:141:LYS:HD2	1:A:144:LEU:HD22	1.84	0.58
1:D:70:TRP:CH2	1:D:72:GLY:HA3	2.38	0.58
1:C:229:SER:O	1:C:233:MET:HG3	2.04	0.58
1:A:271:GLN:OE1	1:A:274:ARG:NH1	2.37	0.58
1:A:223:GLN:HG2	3:A:732:HOH:O	2.02	0.57
1:C:78:ASN:OD1	3:C:759:HOH:O	2.16	0.57
1:C:236:PRO:HG2	1:C:239:VAL:CG2	2.35	0.57
1:C:13:ARG:HB3	1:C:13:ARG:NH1	2.19	0.57
1:A:22:ASP:C	1:A:23:ILE:HD12	2.25	0.57
1:A:91:ASP:O	1:A:95:PHE:CD2	2.58	0.57
1:C:108:LEU:O	1:C:112:MET:HG3	2.05	0.56
1:A:119:ILE:HD12	1:A:147:ILE:HD13	1.86	0.56
1:D:154:LYS:HZ3	1:D:189:GLU:CD	2.09	0.56
1:C:167:TYR:HB3	3:C:337:HOH:O	2.05	0.56
1:C:18:GLY:C	3:C:307:HOH:O	2.43	0.56
1:B:171:LYS:NZ	1:B:189:GLU:OE2	2.38	0.56
1:D:123:ASN:O	1:D:155:LYS:HG2	2.06	0.56
1:A:6:GLY:C	1:A:8:ARG:H	2.06	0.56
1:D:156:TYR:CZ	1:D:192:ARG:HD3	2.40	0.56
1:A:247:GLU:HG3	1:A:272:LEU:CD2	2.36	0.56
1:C:4:ARG:CB	1:C:9:TYR:O	2.54	0.55
1:D:237:ILE:HD13	1:D:252:LEU:CB	2.35	0.55
1:B:89:LEU:HD23	1:B:92:LEU:HD12	1.88	0.55
1:D:4:ARG:CB	1:D:10:ARG:HA	2.37	0.55
1:A:140:LYS:HD2	1:A:140:LYS:N	2.20	0.55
1:A:64:GLY:HA3	1:A:115:ARG:HE	1.72	0.55
1:D:94:ASN:OD1	1:D:98:ARG:NH1	2.39	0.55
1:C:93:PHE:O	1:C:98:ARG:HA	2.07	0.54
1:D:141:LYS:HD2	1:D:144:LEU:HD12	1.89	0.54
1:B:161:THR:O	1:B:162:HIS:HB2	2.07	0.54
1:D:136:MET:SD	1:D:145:VAL:HG22	2.47	0.54
1:D:285:ASP:O	1:D:286:TYR:HB2	2.08	0.54
1:B:23:ILE:HD12	1:B:23:ILE:N	2.23	0.54
1:C:119:ILE:HD11	1:C:147:ILE:HD13	1.90	0.54
1:A:71:CYS:HB3	3:A:354:HOH:O	2.07	0.54
1:B:13:ARG:O	1:B:14:LYS:C	2.46	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:222:ARG:HG2	1:D:222:ARG:O	2.06	0.54
1:C:237:ILE:HD13	1:C:252:LEU:HB3	1.88	0.54
1:A:178:ARG:HD2	1:A:179:TYR:CZ	2.43	0.53
1:A:223:GLN:CG	3:A:732:HOH:O	2.55	0.53
1:C:123:ASN:OD1	1:C:157:ARG:NE	2.39	0.53
1:C:55:ILE:O	1:C:59:MET:HG2	2.09	0.53
1:A:10:ARG:HB2	1:A:29:ILE:HD12	1.91	0.53
1:C:256:ARG:NH2	3:C:953:HOH:O	2.36	0.53
1:C:4:ARG:CB	1:C:10:ARG:HA	2.39	0.52
1:A:24:TYR:N	1:A:24:TYR:CD1	2.77	0.52
1:C:94:ASN:OD1	1:C:98:ARG:NH1	2.41	0.52
1:B:110:ASP:CG	1:B:274:ARG:HH22	2.12	0.52
1:B:56:TYR:CE1	1:B:66:PRO:HG2	2.44	0.52
1:A:141:LYS:O	1:A:144:LEU:HB2	2.10	0.52
1:D:154:LYS:NZ	1:D:189:GLU:CD	2.62	0.52
1:A:214:GLN:HG3	2:A:295:SO4:O4	2.09	0.52
1:B:252:LEU:O	1:B:256:ARG:HG3	2.09	0.52
1:D:98:ARG:NH2	1:D:205:TYR:OH	2.41	0.52
1:B:34:GLU:HG2	3:B:1357:HOH:O	2.09	0.52
1:A:126:HIS:CE1	1:A:128:ASP:HB3	2.44	0.52
1:B:222:ARG:O	1:B:226:GLU:HG2	2.10	0.52
1:C:141:LYS:CD	1:C:144:LEU:HD12	2.30	0.52
1:D:23:ILE:CD1	1:D:38:LYS:HG3	2.40	0.52
1:D:247:GLU:HG2	1:D:276:LEU:HB2	1.92	0.51
1:D:269:LEU:O	1:D:272:LEU:HB2	2.10	0.51
1:B:221:LYS:HE3	1:B:225:TYR:CZ	2.46	0.51
1:B:28:ASP:O	1:B:30:ALA:N	2.44	0.51
1:D:22:ASP:O	1:D:38:LYS:HA	2.11	0.51
1:B:50:HIS:O	1:B:53:SER:HB3	2.11	0.51
1:B:69:ARG:HB2	1:B:81:VAL:O	2.10	0.51
1:D:154:LYS:NZ	1:D:189:GLU:OE1	2.43	0.50
1:A:49:LEU:HD23	1:A:78:ASN:O	2.11	0.50
1:A:59:MET:HB3	1:A:65:ILE:HG21	1.91	0.50
1:B:23:ILE:CG2	1:B:24:TYR:H	1.97	0.50
1:D:169:GLU:OE1	3:D:308:HOH:O	2.19	0.50
1:A:218:ALA:HB3	1:A:224:LYS:HE3	1.93	0.50
1:D:53:SER:OG	1:D:71:CYS:SG	2.68	0.50
1:D:60:GLN:HE21	1:D:60:GLN:HA	1.77	0.50
1:C:11:LEU:HD23	1:C:12:GLY:H	1.76	0.50
1:D:167:TYR:OH	1:D:188:ILE:HD12	2.12	0.50
1:C:271:GLN:HE22	1:C:274:ARG:HH12	1.56	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:110:ASP:OD1	1:B:274:ARG:NH2	2.45	0.49
1:B:254:PHE:CD2	1:B:269:LEU:HD21	2.48	0.49
1:C:156:TYR:CE1	1:C:157:ARG:HD3	2.47	0.49
1:A:23:ILE:C	1:A:24:TYR:CD1	2.86	0.49
1:B:178:ARG:HD2	1:B:179:TYR:CZ	2.47	0.49
1:D:174:THR:O	1:D:174:THR:HG23	2.12	0.49
1:C:5:VAL:O	1:C:9:TYR:HB2	2.12	0.49
1:C:23:ILE:HD12	1:C:23:ILE:N	2.28	0.49
1:A:74:GLU:HB2	3:A:414:HOH:O	2.11	0.49
1:A:70:TRP:CH2	1:A:72:GLY:HA3	2.47	0.49
1:A:218:ALA:CB	1:A:224:LYS:HE3	2.43	0.49
1:D:226:GLU:O	1:D:230:GLU:HG2	2.13	0.49
1:A:22:ASP:O	1:A:38:LYS:HA	2.13	0.49
1:D:216:LEU:HD13	1:D:227:ARG:HB3	1.95	0.48
1:D:5:VAL:CG2	1:D:9:TYR:HB2	2.39	0.48
1:C:173:LEU:HG	1:C:184:THR:HG22	1.94	0.48
1:A:80:MET:HE3	1:A:82:MET:SD	2.53	0.48
1:B:256:ARG:HB3	3:B:299:HOH:O	2.13	0.48
1:C:120:HIS:ND1	1:C:192:ARG:HG2	2.28	0.48
1:B:48:GLN:O	1:B:49:LEU:C	2.50	0.48
1:B:134:PHE:C	1:B:135:LEU:HD12	2.34	0.48
1:B:227:ARG:NH1	1:B:227:ARG:HG3	2.28	0.48
1:B:52:GLU:O	1:B:55:ILE:N	2.40	0.48
1:B:229:SER:OG	1:B:233:MET:CE	2.62	0.48
1:D:204:MET:CE	1:D:241:CYS:HA	2.44	0.48
1:B:246:SER:HB2	3:B:375:HOH:O	2.12	0.48
1:A:168:ARG:NH1	3:A:307:HOH:O	2.46	0.47
1:B:119:ILE:HD11	1:B:147:ILE:HG21	1.94	0.47
1:D:33:GLU:OE1	1:D:69:ARG:NH2	2.47	0.47
1:B:263:LYS:HE2	3:B:310:HOH:O	2.14	0.47
1:D:158:ASP:HA	3:D:1307:HOH:O	2.13	0.47
1:B:92:LEU:HD11	1:B:136:MET:CG	2.44	0.47
1:A:167:TYR:O	1:A:168:ARG:HD3	2.14	0.47
1:C:134:PHE:C	1:C:135:LEU:HD12	2.35	0.47
1:B:56:TYR:HB3	1:B:68:ILE:CD1	2.45	0.47
1:B:60:GLN:HE21	1:B:60:GLN:CA	2.27	0.47
1:B:62:GLY:HA3	1:B:118:TYR:CZ	2.50	0.47
1:D:49:LEU:HA	1:D:49:LEU:HD12	1.58	0.47
1:D:13:ARG:HG3	1:D:13:ARG:HH11	1.80	0.47
1:D:115:ARG:O	1:D:119:ILE:HG13	2.15	0.47
1:C:141:LYS:HD2	1:C:144:LEU:CD1	2.33	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:154:LYS:NZ	1:D:189:GLU:OE2	2.48	0.47
1:B:51:ILE:O	1:B:52:GLU:C	2.52	0.47
1:B:237:ILE:HG13	1:B:256:ARG:NH2	2.30	0.46
1:C:104:THR:O	1:C:108:LEU:HG	2.15	0.46
1:B:222:ARG:CG	1:B:222:ARG:NH1	2.50	0.46
1:D:202:VAL:O	1:D:205:TYR:HB3	2.16	0.46
1:D:274:ARG:O	1:D:277:PHE:HB3	2.15	0.46
1:D:50:HIS:CB	3:D:305:HOH:O	2.63	0.46
1:C:46:HIS:O	1:C:47:PRO:C	2.53	0.46
1:C:274:ARG:NH2	2:C:295:SO4:O3	2.48	0.46
1:A:8:ARG:NH1	1:A:28:ASP:OD1	2.49	0.46
1:C:5:VAL:HG23	1:C:9:TYR:CB	2.38	0.46
1:D:4:ARG:CB	1:D:9:TYR:O	2.63	0.46
1:B:271:GLN:OE1	1:B:271:GLN:HA	2.15	0.46
1:C:109:ALA:HB2	1:C:203:LEU:HD21	1.98	0.46
1:C:126:HIS:O	1:C:127:ARG:HB2	2.15	0.46
1:D:60:GLN:HE21	1:D:60:GLN:CA	2.29	0.46
1:A:70:TRP:CZ3	1:A:79:VAL:CG2	2.95	0.46
3:A:428:HOH:O	1:D:167:TYR:HE2	1.98	0.46
1:B:173:LEU:CD1	1:B:184:THR:HG22	2.45	0.46
1:A:270:ARG:NH2	2:A:297:SO4:O2	2.33	0.46
1:B:213:TRP:CE2	1:B:232:LYS:HE2	2.51	0.46
1:C:15:ILE:HG21	1:C:25:LEU:HB2	1.97	0.46
1:C:44:THR:O	1:C:45:LYS:HB2	2.16	0.45
1:C:123:ASN:HB2	1:C:155:LYS:NZ	2.31	0.45
1:C:158:ASP:CB	1:D:161:THR:HG21	2.47	0.45
1:B:11:LEU:HD11	1:B:39:LEU:HD11	1.98	0.45
1:D:23:ILE:HD11	1:D:38:LYS:CE	2.42	0.45
1:C:255:CYS:HA	1:C:258:LEU:HD12	1.98	0.45
1:D:37:ILE:HG12	1:D:81:VAL:HG22	1.98	0.45
1:B:34:GLU:CG	3:B:1357:HOH:O	2.63	0.45
1:B:115:ARG:HH21	1:B:144:LEU:HD23	1.81	0.45
1:B:110:ASP:OD1	1:B:274:ARG:NH1	2.49	0.45
1:C:120:HIS:CE1	1:C:192:ARG:HG2	2.52	0.44
1:C:12:GLY:HA3	1:C:25:LEU:O	2.17	0.44
1:C:56:TYR:CE1	1:C:66:PRO:HG2	2.52	0.44
1:D:259:ARG:HG3	1:D:262:ASP:OD2	2.18	0.44
1:B:60:GLN:HE21	1:B:60:GLN:N	2.15	0.44
1:B:117:GLU:HB2	1:B:266:TYR:CD1	2.53	0.44
1:C:5:VAL:CG2	1:C:9:TYR:HB2	2.37	0.44
1:C:11:LEU:HD23	1:C:12:GLY:N	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:156:TYR:CZ	1:D:157:ARG:HD3	2.53	0.44
1:A:49:LEU:CD2	1:A:78:ASN:O	2.65	0.44
1:B:56:TYR:CB	1:B:68:ILE:CD1	2.96	0.44
1:B:211:LEU:HD13	1:B:213:TRP:CZ2	2.53	0.44
1:C:56:TYR:O	1:C:60:GLN:NE2	2.51	0.44
1:D:164:HIS:CD2	1:D:261:ASP:HA	2.53	0.44
1:D:105:VAL:HG21	1:D:207:ASN:OD1	2.18	0.44
1:A:8:ARG:NH1	1:A:28:ASP:OD2	2.51	0.43
1:A:286:TYR:CD1	1:A:286:TYR:N	2.83	0.43
1:A:38:LYS:HG2	1:A:49:LEU:HD13	1.99	0.43
1:A:126:HIS:HE1	1:A:128:ASP:HB3	1.83	0.43
1:B:229:SER:OG	1:B:233:MET:HE2	2.18	0.43
1:A:34:GLU:HB3	1:A:84:LEU:HD22	1.98	0.43
1:B:55:ILE:HD11	3:B:1251:HOH:O	2.18	0.43
1:A:140:LYS:CD	1:A:140:LYS:H	2.24	0.43
1:D:201:TYR:OH	1:D:256:ARG:NH1	2.51	0.43
1:A:38:LYS:HE3	1:A:80:MET:HE1	1.99	0.43
1:B:158:ASP:O	1:B:162:HIS:HA	2.19	0.43
1:D:161:THR:OG1	1:D:161:THR:O	2.35	0.43
1:B:111:GLN:O	1:B:115:ARG:HG2	2.17	0.43
1:B:140:LYS:H	1:B:140:LYS:HD2	1.83	0.43
1:B:60:GLN:NE2	1:B:60:GLN:CA	2.81	0.43
1:A:188:ILE:HG22	1:A:189:GLU:N	2.33	0.43
1:A:5:VAL:CG2	1:A:9:TYR:HB2	2.46	0.43
1:A:69:ARG:O	1:A:70:TRP:HB2	2.18	0.43
1:A:96:CYS:O	1:A:97:SER:HB2	2.19	0.43
1:A:60:GLN:CA	1:A:60:GLN:NE2	2.68	0.43
1:D:154:LYS:HE2	1:D:165:ILE:HD13	1.99	0.43
1:C:211:LEU:HD13	1:C:213:TRP:CZ2	2.54	0.43
1:B:168:ARG:HG3	1:B:169:GLU:N	2.34	0.43
1:B:259:ARG:CD	3:B:564:HOH:O	2.67	0.42
1:D:177:ALA:O	1:D:232:LYS:NZ	2.49	0.42
1:A:125:ILE:HG23	1:A:156:TYR:CD2	2.53	0.42
1:A:50:HIS:CD2	1:A:50:HIS:O	2.72	0.42
1:A:129:VAL:HG13	1:A:134:PHE:HE2	1.84	0.42
1:A:70:TRP:HZ3	1:A:79:VAL:HG22	1.84	0.42
1:A:247:GLU:HG2	1:A:276:LEU:HB2	2.01	0.42
1:A:224:LYS:O	1:A:228:ILE:HG13	2.19	0.42
1:A:218:ALA:CB	1:A:224:LYS:HB2	2.50	0.42
1:D:270:ARG:O	1:D:274:ARG:HG3	2.19	0.42
1:A:84:LEU:HG	1:A:138:LEU:HD11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:109:ALA:O	1:A:113:ILE:HG13	2.18	0.42
1:D:29:ILE:O	1:D:29:ILE:CG2	2.68	0.42
1:B:230:GLU:HB3	3:B:352:HOH:O	2.18	0.42
1:B:56:TYR:CG	1:B:68:ILE:CD1	3.02	0.42
1:A:143:ASN:HD22	1:A:286:TYR:HD2	1.68	0.42
1:A:201:TYR:OH	3:A:740:HOH:O	2.21	0.42
1:B:125:ILE:HG23	1:B:156:TYR:CD2	2.54	0.42
1:A:6:GLY:C	1:A:8:ARG:N	2.73	0.42
1:B:12:GLY:O	1:B:13:ARG:HB2	2.19	0.42
1:D:95:PHE:CE2	1:D:293:LEU:HD13	2.55	0.42
1:A:33:GLU:OE1	1:A:69:ARG:NH2	2.52	0.42
1:A:130:LYS:HE2	1:A:133:ASN:HD21	1.85	0.42
1:D:72:GLY:O	1:D:79:VAL:HG12	2.19	0.41
1:D:70:TRP:HZ3	1:D:79:VAL:CG1	2.33	0.41
1:A:178:ARG:HG2	1:A:211:LEU:HD12	2.02	0.41
1:B:65:ILE:HG13	1:B:118:TYR:CE2	2.55	0.41
1:C:69:ARG:CG	1:C:69:ARG:HH11	2.32	0.41
1:D:167:TYR:CZ	1:D:188:ILE:HD12	2.55	0.41
1:A:62:GLY:HA3	1:A:118:TYR:CZ	2.54	0.41
1:B:63:VAL:HG12	1:B:144:LEU:HD21	2.02	0.41
1:D:17:SER:O	1:D:23:ILE:HD13	2.20	0.41
1:C:236:PRO:HG2	1:C:239:VAL:HG23	2.01	0.41
1:B:125:ILE:O	1:B:125:ILE:HG13	2.19	0.41
1:D:224:LYS:HE3	1:D:224:LYS:HB2	1.88	0.41
1:D:38:LYS:HD2	1:D:49:LEU:HD11	2.01	0.41
1:A:5:VAL:HG23	1:A:5:VAL:O	2.20	0.41
1:A:171:LYS:HD2	1:A:189:GLU:OE1	2.21	0.41
1:A:117:GLU:HB2	1:A:266:TYR:CD1	2.56	0.41
1:D:169:GLU:OE1	1:D:188:ILE:CD1	2.69	0.41
1:C:23:ILE:HD11	1:C:38:LYS:HE2	2.02	0.41
1:D:228:ILE:O	1:D:232:LYS:HB2	2.21	0.41
1:A:108:LEU:HD21	1:A:290:TRP:HH2	1.86	0.41
1:C:178:ARG:HD2	1:C:179:TYR:CZ	2.56	0.41
1:D:60:GLN:OE1	1:D:68:ILE:HG13	2.21	0.41
1:D:134:PHE:C	1:D:135:LEU:HD12	2.41	0.41
1:B:56:TYR:HB3	1:B:68:ILE:HD12	2.02	0.40
1:C:42:VAL:HB	1:C:76:ASP:O	2.21	0.40
1:C:66:PRO:HA	1:C:83:GLU:OE2	2.21	0.40
1:A:60:GLN:OE1	1:A:67:THR:HA	2.20	0.40
1:A:270:ARG:HB3	1:A:274:ARG:NH2	2.36	0.40
1:B:71:CYS:HB3	3:B:323:HOH:O	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:23:ILE:HD12	1:D:38:LYS:HG3	2.03	0.40
1:B:171:LYS:HE2	1:B:171:LYS:HB3	1.73	0.40
1:D:141:LYS:CD	1:D:144:LEU:HD12	2.50	0.40
1:D:134:PHE:CE1	1:D:147:ILE:HD12	2.56	0.40
1:C:214:GLN:HG3	2:C:296:SO4:O4	2.20	0.40
1:A:170:ASN:ND2	1:B:221:LYS:HE2	2.36	0.40
1:A:24:TYR:N	1:A:24:TYR:HD1	2.18	0.40
1:C:13:ARG:CB	1:C:13:ARG:HH11	2.34	0.40
1:D:244:TYR:HB3	1:D:245:PRO:CD	2.52	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	275/296 (93%)	259 (94%)	14 (5%)	2 (1%)	26	31
1	B	273/296 (92%)	250 (92%)	17 (6%)	6 (2%)	8	6
1	C	280/296 (95%)	257 (92%)	17 (6%)	6 (2%)	9	7
1	D	278/296 (94%)	253 (91%)	22 (8%)	3 (1%)	17	18
All	All	1106/1184 (93%)	1019 (92%)	70 (6%)	17 (2%)	13	12

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	13	ARG
1	B	29	ILE
1	C	45	LYS
1	B	149	ASP
1	C	21	GLY
1	A	222	ARG

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Mol	Chain	Res	Type
1	B	7	ASN
1	B	49	LEU
1	D	7	ASN
1	A	170	ASN
1	C	149	ASP
1	C	246	SER
1	D	167	TYR
1	B	12	GLY
1	C	47	PRO
1	D	15	ILE
1	C	46	HIS

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	240/259 (93%)	223 (93%)	17 (7%)	18	23
1	B	241/259 (93%)	220 (91%)	21 (9%)	13	15
1	C	234/259 (90%)	218 (93%)	16 (7%)	20	25
1	D	242/259 (93%)	226 (93%)	16 (7%)	21	27
All	All	957/1036 (92%)	887 (93%)	70 (7%)	17	22

All (70) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	ARG
1	A	11	LEU
1	A	24	TYR
1	A	29	ILE
1	A	34	GLU
1	A	41	CYS
1	A	42	VAL
1	A	48	GLN
1	A	53	SER
1	A	60	GLN

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Mol	Chain	Res	Type
1	A	76	ASP
1	A	170	ASN
1	A	172	ASN
1	A	238	GLU
1	A	261	ASP
1	A	272	LEU
1	A	279	ARG
1	B	7	ASN
1	B	10	ARG
1	B	11	LEU
1	B	13	ARG
1	B	29	ILE
1	B	41	CYS
1	B	42	VAL
1	B	48	GLN
1	B	53	SER
1	B	60	GLN
1	B	69	ARG
1	B	74	GLU
1	B	76	ASP
1	B	82	MET
1	B	144	LEU
1	B	170	ASN
1	B	173	LEU
1	B	189	GLU
1	B	222	ARG
1	B	271	GLN
1	B	274	ARG
1	C	7	ASN
1	C	11	LEU
1	C	22	ASP
1	C	29	ILE
1	C	44	THR
1	C	60	GLN
1	C	68	ILE
1	C	69	ARG
1	C	76	ASP
1	C	95	PHE
1	C	99	LYS
1	C	170	ASN
1	C	173	LEU
1	C	242	LYS

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Mol	Chain	Res	Type
1	C	267	SER
1	C	274	ARG
1	D	7	ASN
1	D	8	ARG
1	D	11	LEU
1	D	14	LYS
1	D	25	LEU
1	D	42	VAL
1	D	54	LYS
1	D	60	GLN
1	D	69	ARG
1	D	76	ASP
1	D	161	THR
1	D	173	LEU
1	D	189	GLU
1	D	222	ARG
1	D	224	LYS
1	D	232	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	ASN
1	A	50	HIS
1	A	78	ASN
1	A	170	ASN
1	A	172	ASN
1	A	223	GLN
1	B	7	ASN
1	B	78	ASN
1	B	172	ASN
1	B	190	GLN
1	B	223	GLN
1	B	291	ASN
1	C	7	ASN
1	C	172	ASN
1	C	271	GLN
1	D	78	ASN
1	D	163	GLN
1	D	170	ASN
1	D	172	ASN
1	D	190	GLN

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Mol	Chain	Res	Type
1	D	223	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

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	295	-	4,4,4	1.27	0	6,6,6	0.41	0
2	SO4	A	296	-	4,4,4	1.16	0	6,6,6	0.68	0
2	SO4	A	297	-	4,4,4	1.72	1 (25%)	6,6,6	0.25	0
2	SO4	B	295	-	4,4,4	1.22	1 (25%)	6,6,6	0.50	0
2	SO4	B	296	-	4,4,4	1.19	0	6,6,6	0.81	0
2	SO4	B	297	-	4,4,4	1.17	0	6,6,6	0.84	0
2	SO4	C	295	-	4,4,4	1.00	0	6,6,6	0.33	0
2	SO4	C	296	-	4,4,4	0.75	0	6,6,6	0.95	0
2	SO4	D	295	-	4,4,4	0.95	0	6,6,6	0.41	0
2	SO4	D	296	-	4,4,4	1.29	0	6,6,6	0.41	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SO4	A	295	-	-	0/0/0/0	0/0/0/0
2	SO4	A	296	-	-	0/0/0/0	0/0/0/0
2	SO4	A	297	-	-	0/0/0/0	0/0/0/0
2	SO4	B	295	-	-	0/0/0/0	0/0/0/0
2	SO4	B	296	-	-	0/0/0/0	0/0/0/0
2	SO4	B	297	-	-	0/0/0/0	0/0/0/0
2	SO4	C	295	-	-	0/0/0/0	0/0/0/0
2	SO4	C	296	-	-	0/0/0/0	0/0/0/0
2	SO4	D	295	-	-	0/0/0/0	0/0/0/0
2	SO4	D	296	-	-	0/0/0/0	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	295	SO4	O2-S	2.20	1.54	1.47
2	A	297	SO4	O2-S	2.24	1.54	1.47

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	295	SO4	1	0
2	A	297	SO4	1	0
2	C	295	SO4	1	0
2	C	296	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, 95^{th} 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	281/296 (94%)	0.24	10 (3%)	46	55	34, 49, 79, 87	1 (0%)
1	B	279/296 (94%)	0.29	14 (5%)	32	41	31, 48, 76, 83	1 (0%)
1	C	286/296 (96%)	0.26	16 (5%)	28	36	32, 47, 81, 91	1 (0%)
1	D	284/296 (95%)	0.41	22 (7%)	16	23	33, 50, 84, 95	1 (0%)
All	All	1130/1184 (95%)	0.30	62 (5%)	29	37	31, 49, 80, 95	4 (0%)

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	170	ASN	7.1
1	C	158	ASP	6.9
1	C	217	LYS	5.9
1	A	23	ILE	5.8
1	D	161	THR	5.8
1	B	39	LEU	5.1
1	D	17	SER	5.0
1	C	159	ALA	4.9
1	D	159	ALA	4.7
1	A	76	ASP	4.6
1	D	170	ASN	4.4
1	D	158	ASP	4.1
1	A	217	LYS	3.9
1	C	167	TYR	3.9
1	A	74	GLU	3.7
1	D	293	LEU	3.6
1	C	168	ARG	3.6
1	C	5	VAL	3.6
1	D	217	LYS	3.5
1	D	167	TYR	3.4
1	B	41	CYS	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	37	ILE	3.2
1	A	22	ASP	3.2
1	B	5	VAL	3.2
1	D	176	THR	3.1
1	C	171	LYS	3.0
1	B	13	ARG	3.0
1	C	166	PRO	2.9
1	D	218	ALA	2.9
1	B	42	VAL	2.8
1	C	25	LEU	2.8
1	B	76	ASP	2.8
1	C	216	LEU	2.8
1	B	168	ARG	2.7
1	D	219	ALA	2.7
1	D	162	HIS	2.6
1	C	218	ALA	2.6
1	D	166	PRO	2.6
1	D	160	ARG	2.6
1	B	77	TYR	2.5
1	D	42	VAL	2.5
1	D	58	MET	2.4
1	B	7	ASN	2.4
1	B	95	PHE	2.4
1	B	170	ASN	2.3
1	C	13	ARG	2.3
1	D	5	VAL	2.3
1	C	173	LEU	2.2
1	A	11	LEU	2.2
1	A	77	TYR	2.2
1	D	43	LYS	2.2
1	A	218	ALA	2.2
1	C	21	GLY	2.2
1	B	49	LEU	2.2
1	D	49	LEU	2.2
1	B	174	THR	2.2
1	D	23	ILE	2.1
1	A	7	ASN	2.1
1	B	225	TYR	2.1
1	D	168	ARG	2.0
1	C	11	LEU	2.0
1	D	150	PHE	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} 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	LLDF	B-factors(Å^2)	Q<0.9
2	SO4	C	296	5/5	0.98	0.14	0.41	65,67,67,71	0
2	SO4	A	295	5/5	0.98	0.12	-0.33	62,64,64,65	0
2	SO4	D	295	5/5	0.96	0.14	-0.43	68,70,70,72	0
2	SO4	B	297	5/5	0.97	0.12	-0.67	102,102,103,103	0
2	SO4	A	296	5/5	0.94	0.14	-0.74	77,78,78,79	0
2	SO4	B	295	5/5	0.98	0.12	-0.83	55,56,58,58	0
2	SO4	D	296	5/5	0.99	0.10	-0.96	58,60,60,61	0
2	SO4	A	297	5/5	0.93	0.12	-	104,104,104,105	0
2	SO4	B	296	5/5	0.96	0.11	-	86,87,88,88	0
2	SO4	C	295	5/5	0.98	0.10	-	54,56,57,57	0

6.5 Other polymers (i)

There are no such residues in this entry.