Full wwPDB X-ray Structure Validation Report ⓘ

Oct 30, 2023 – 06:34 PM JST

PDB ID	:	4XSM
Title	:	Crystal structure of D-tagatose 3-epimerase C66S from Pseudomonas cichorii in complex with D-talitol
Authors	:	Yoshida, H.; Yoshihara, A.; Ishii, T.; Izumori, K.; Kamitori, S.
Deposited on	:	2015-01-22
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
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:

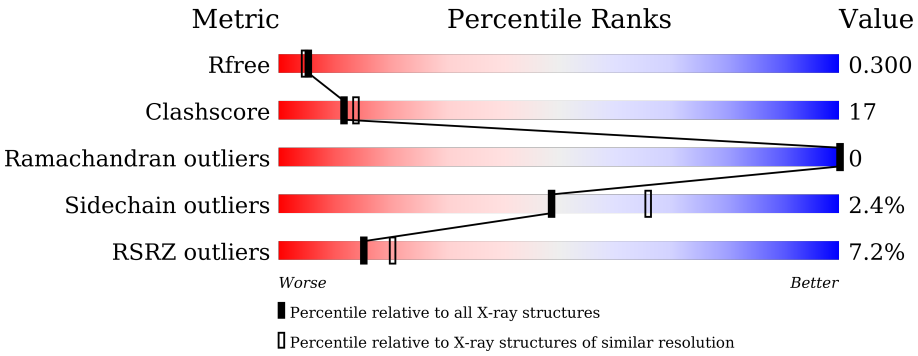
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (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 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 <=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	300	5% 66% 32% ·
1	B	300	4% 70% 25% · ·
1	C	300	6% 63% 35% · ·
1	D	300	13% 59% 37% · ·

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	TLZ	A	402	-	-	X	-

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 9637 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 D-tagatose 3-epimerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	294	Total	C	N	O	S	0	0	0
			2314	1465	399	432	18			
1	B	290	Total	C	N	O	S	0	0	0
			2287	1451	392	426	18			
1	C	297	Total	C	N	O	S	0	0	0
			2344	1483	408	435	18			
1	D	292	Total	C	N	O	S	0	0	0
			2297	1456	394	429	18			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	66	SER	CYS	engineered mutation	UNP O50580
A	291	GLY	-	expression tag	UNP O50580
A	292	SER	-	expression tag	UNP O50580
A	293	ARG	-	expression tag	UNP O50580
A	294	SER	-	expression tag	UNP O50580
A	295	HIS	-	expression tag	UNP O50580
A	296	HIS	-	expression tag	UNP O50580
A	297	HIS	-	expression tag	UNP O50580
A	298	HIS	-	expression tag	UNP O50580
A	299	HIS	-	expression tag	UNP O50580
A	300	HIS	-	expression tag	UNP O50580
B	66	SER	CYS	engineered mutation	UNP O50580
B	291	GLY	-	expression tag	UNP O50580
B	292	SER	-	expression tag	UNP O50580
B	293	ARG	-	expression tag	UNP O50580
B	294	SER	-	expression tag	UNP O50580
B	295	HIS	-	expression tag	UNP O50580
B	296	HIS	-	expression tag	UNP O50580
B	297	HIS	-	expression tag	UNP O50580
B	298	HIS	-	expression tag	UNP O50580
B	299	HIS	-	expression tag	UNP O50580

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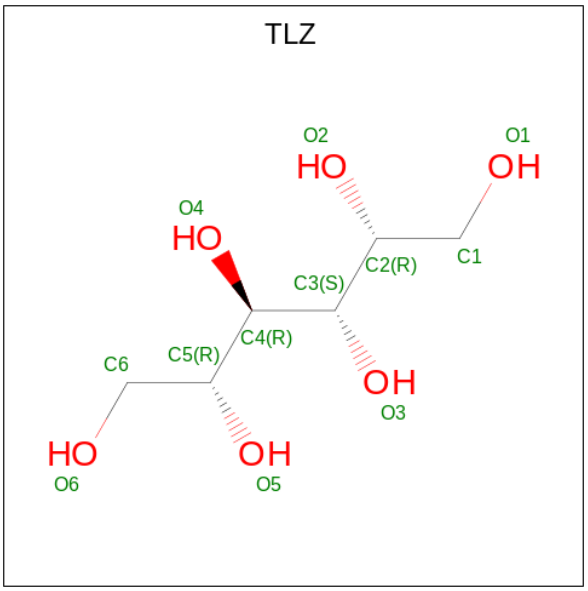
Chain	Residue	Modelled	Actual	Comment	Reference
B	300	HIS	-	expression tag	UNP O50580
C	66	SER	CYS	engineered mutation	UNP O50580
C	291	GLY	-	expression tag	UNP O50580
C	292	SER	-	expression tag	UNP O50580
C	293	ARG	-	expression tag	UNP O50580
C	294	SER	-	expression tag	UNP O50580
C	295	HIS	-	expression tag	UNP O50580
C	296	HIS	-	expression tag	UNP O50580
C	297	HIS	-	expression tag	UNP O50580
C	298	HIS	-	expression tag	UNP O50580
C	299	HIS	-	expression tag	UNP O50580
C	300	HIS	-	expression tag	UNP O50580
D	66	SER	CYS	engineered mutation	UNP O50580
D	291	GLY	-	expression tag	UNP O50580
D	292	SER	-	expression tag	UNP O50580
D	293	ARG	-	expression tag	UNP O50580
D	294	SER	-	expression tag	UNP O50580
D	295	HIS	-	expression tag	UNP O50580
D	296	HIS	-	expression tag	UNP O50580
D	297	HIS	-	expression tag	UNP O50580
D	298	HIS	-	expression tag	UNP O50580
D	299	HIS	-	expression tag	UNP O50580
D	300	HIS	-	expression tag	UNP O50580

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Mn 1 1	0	0
2	B	1	Total Mn 1 1	0	0
2	C	1	Total Mn 1 1	0	0
2	D	1	Total Mn 1 1	0	0

- Molecule 3 is D-altritol (three-letter code: TLZ) (formula: $C_6H_{14}O_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 12 6 6	0	0
3	B	1	Total C O 12 6 6	0	0
3	C	1	Total C O 12 6 6	0	0
3	D	1	Total C O 12 6 6	0	0

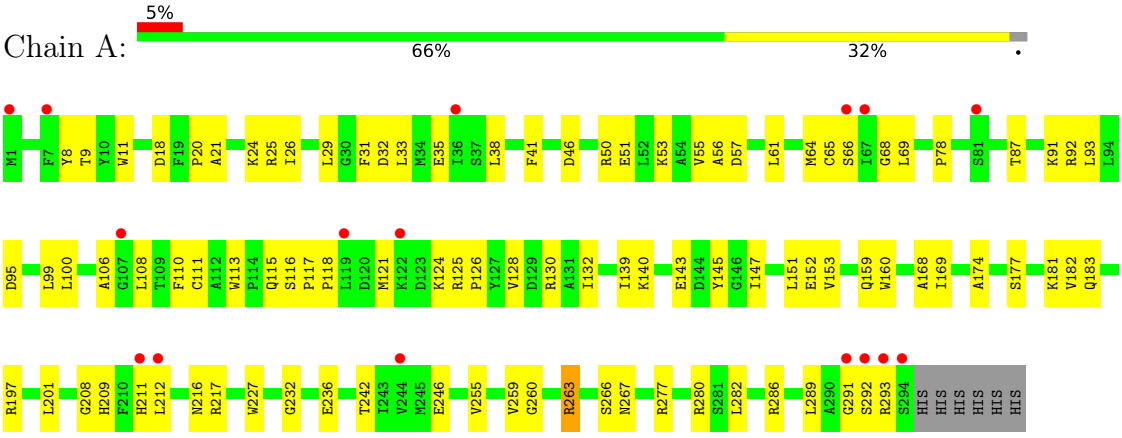
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	104	Total O 104 104	0	0
4	B	86	Total O 86 86	0	0
4	C	84	Total O 84 84	0	0
4	D	69	Total O 69 69	0	0

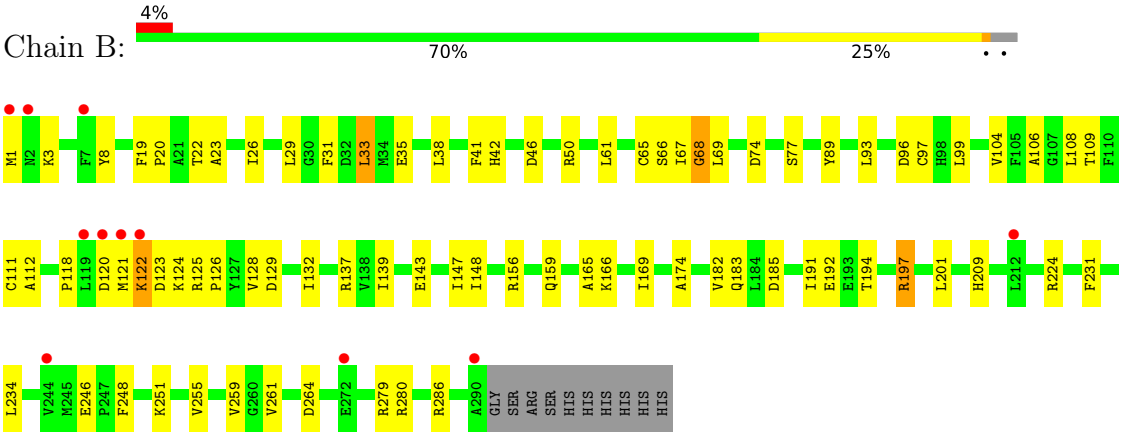
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

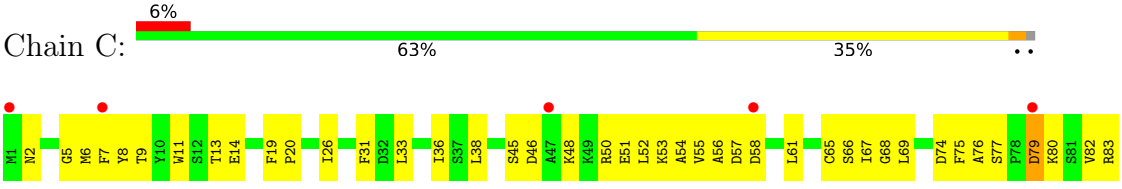
• Molecule 1: D-tagatose 3-epimerase

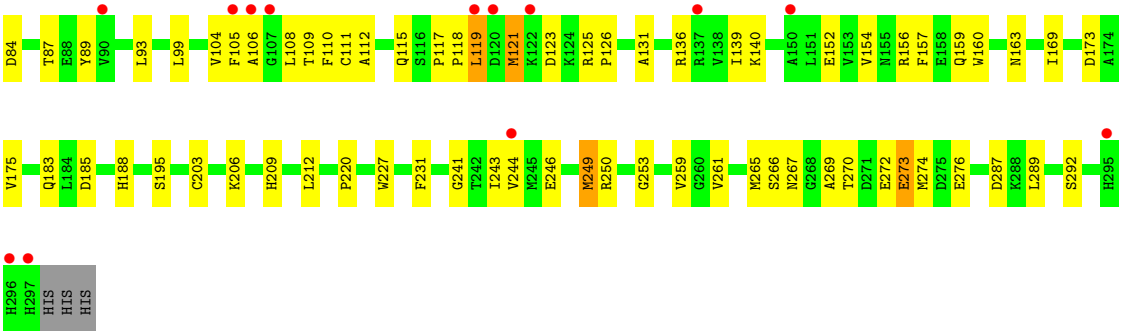


• Molecule 1: D-tagatose 3-epimerase

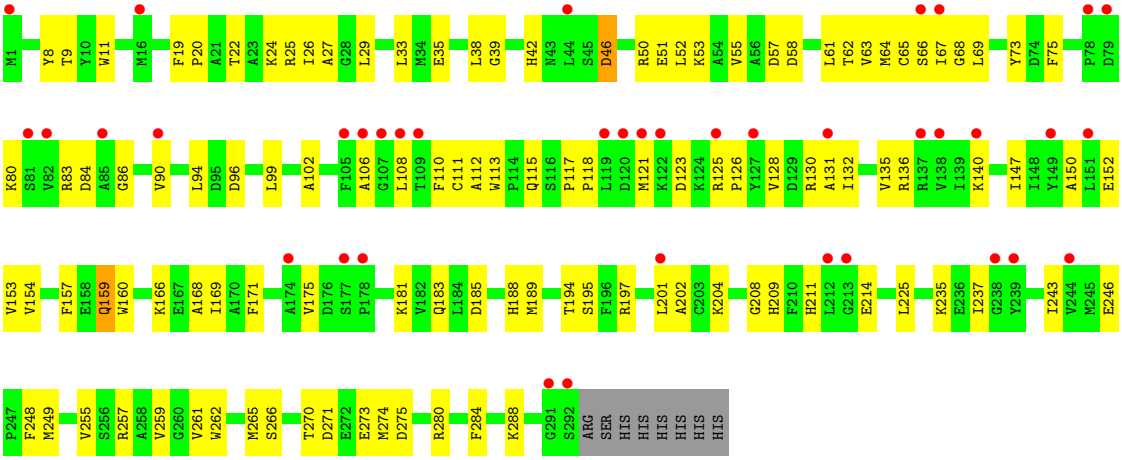


• Molecule 1: D-tagatose 3-epimerase





• Molecule 1: D-tagatose 3-epimerase



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	52.43Å 127.03Å 98.83Å 90.00° 101.33° 90.00°	Depositor
Resolution (Å)	25.68 – 2.30 25.68 – 2.30	Depositor EDS
% Data completeness (in resolution range)	96.6 (25.68-2.30) 96.7 (25.68-2.30)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.32 (at 2.31Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, R_{free}	0.245 , 0.307 0.239 , 0.300	Depositor DCC
R_{free} test set	5534 reflections (10.18%)	wwPDB-VP
Wilson B-factor (Å^2)	30.3	Xtriage
Anisotropy	0.389	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 54.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.52$, $< L^2 > = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	9637	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.58% 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, 0.333 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: MN, TLZ

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	0.41	0/2365	0.67	0/3190
1	B	0.42	0/2338	0.66	1/3155 (0.0%)
1	C	0.39	0/2398	0.62	0/3235
1	D	0.37	0/2348	0.62	0/3168
All	All	0.40	0/9449	0.64	1/12748 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	68	GLY	N-CA-C	-5.46	99.44	113.10

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	2314	0	2271	83	0
1	B	2287	0	2245	63	0
1	C	2344	0	2292	94	0
1	D	2297	0	2253	88	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	12	0	13	8	0
3	B	12	0	13	2	0
3	C	12	0	13	2	0
3	D	12	0	12	1	0
4	A	104	0	0	5	0
4	B	86	0	0	2	0
4	C	84	0	0	8	0
4	D	69	0	0	4	0
All	All	9637	0	9112	322	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 17.

All (322) 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:A:277:ARG:HG2	1:A:280:ARG:NH2	1.92	0.84
1:B:106:ALA:HB1	1:B:183:GLN:OE1	1.78	0.84
1:A:64:MET:HE1	1:A:242:THR:HB	1.62	0.81
1:A:106:ALA:HB1	1:A:183:GLN:OE1	1.81	0.81
1:B:183:GLN:HG3	1:B:209:HIS:HB3	1.60	0.81
1:C:45:SER:H	1:C:48:LYS:NZ	1.78	0.81
1:A:33:LEU:HD21	1:A:64:MET:CE	2.10	0.81
1:C:269:ALA:HB1	1:C:273:GLU:HG2	1.63	0.80
1:C:2:ASN:HD22	1:C:289:LEU:HD22	1.46	0.79
1:D:115:GLN:HE21	1:D:160:TRP:HE1	1.28	0.78
1:D:51:GLU:O	1:D:55:VAL:HG23	1.84	0.78
1:C:156:ARG:HA	1:C:163:ASN:HD21	1.47	0.77
1:C:45:SER:H	1:C:48:LYS:HZ2	1.32	0.77
1:D:22:THR:O	1:D:26:ILE:HG12	1.84	0.76
1:C:106:ALA:HB1	1:C:183:GLN:OE1	1.85	0.76
1:C:259:VAL:HG23	1:C:261:VAL:HG23	1.68	0.75
1:A:108:LEU:HG	1:A:113:TRP:HB2	1.69	0.75
1:D:46:ASP:HB2	4:D:509:HOH:O	1.85	0.75
1:C:51:GLU:O	1:C:55:VAL:HG23	1.85	0.75
1:A:292:SER:O	1:A:293:ARG:HD3	1.88	0.74
1:C:118:PRO:O	1:C:121:MET:HB3	1.87	0.73
1:A:216:ASN:HD21	1:B:194:THR:CG2	2.02	0.73
1:A:169:ILE:HD13	1:A:182:VAL:HG21	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:197:ARG:NH2	1:D:201:LEU:HD11	2.06	0.70
1:A:53:LYS:HD3	1:A:100:LEU:HA	1.74	0.70
1:A:277:ARG:HG2	1:A:280:ARG:HH22	1.55	0.69
1:B:38:LEU:HG	1:B:65:CYS:HB3	1.75	0.69
1:C:119:LEU:HD23	1:C:119:LEU:H	1.55	0.69
1:C:246:GLU:O	1:C:246:GLU:HG2	1.92	0.69
1:C:76:ALA:HB2	1:C:131:ALA:HB2	1.75	0.69
1:A:31:PHE:CE1	1:A:282:LEU:HD13	2.27	0.68
1:C:83:ARG:O	1:C:87:THR:HG23	1.94	0.68
1:C:152:GLU:HG3	1:C:183:GLN:NE2	2.08	0.67
1:B:197:ARG:NH2	1:B:201:LEU:HD11	2.10	0.67
1:D:66:SER:HA	1:D:106:ALA:O	1.95	0.66
1:A:33:LEU:HD21	1:A:64:MET:HE2	1.78	0.66
1:C:154:VAL:HG12	1:C:188:HIS:NE2	2.10	0.65
1:D:280:ARG:HG2	1:D:280:ARG:HH21	1.62	0.65
1:B:122:LYS:HD3	1:B:122:LYS:N	2.12	0.65
1:C:115:GLN:HB3	1:C:159:GLN:NE2	2.11	0.65
1:A:216:ASN:HD21	1:B:194:THR:HG22	1.61	0.64
3:D:402:TLZ:H3	3:D:402:TLZ:O3	1.96	0.64
1:D:19:PHE:HB2	1:D:20:PRO:HD3	1.79	0.64
1:D:153:VAL:CG2	1:D:168:ALA:HB2	2.28	0.64
1:A:217:ARG:HD2	4:A:576:HOH:O	1.97	0.63
1:A:56:ALA:HB1	1:A:61:LEU:O	1.98	0.63
1:C:13:THR:HB	1:C:253:GLY:HA3	1.80	0.63
1:C:287:ASP:O	1:C:292:SER:HB3	1.98	0.63
1:A:92:ARG:O	1:A:95:ASP:HB2	1.98	0.62
1:B:139:ILE:O	1:B:143:GLU:HG3	1.99	0.62
1:D:128:VAL:O	1:D:132:ILE:HG13	1.98	0.62
1:A:108:LEU:HD12	1:A:111:CYS:SG	2.40	0.62
1:B:123:ASP:O	1:B:126:PRO:HD2	1.98	0.62
1:C:212:LEU:HD21	1:C:243:ILE:HD11	1.80	0.62
1:D:11:TRP:CH2	1:D:25:ARG:HG2	2.35	0.62
1:C:117:PRO:HG2	1:D:262:TRP:CZ3	2.35	0.62
1:A:117:PRO:HG3	1:A:160:TRP:CD2	2.35	0.61
1:C:19:PHE:HB3	1:C:52:LEU:HD13	1.82	0.61
1:C:38:LEU:HG	1:C:65:CYS:HB3	1.83	0.61
1:A:145:TYR:HB3	1:A:147:ILE:HG13	1.84	0.60
1:D:140:LYS:H	1:D:140:LYS:HD2	1.65	0.60
1:D:255:VAL:O	1:D:259:VAL:HG22	2.02	0.59
1:D:270:THR:OG1	1:D:273:GLU:HG3	2.02	0.59
1:D:204:LYS:HE2	1:D:237:ILE:HA	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:139:ILE:O	1:A:143:GLU:HG3	2.02	0.59
1:A:217:ARG:HB2	4:A:519:HOH:O	2.01	0.59
1:C:80:LYS:HD3	1:C:84:ASP:OD2	2.04	0.58
1:D:118:PRO:O	1:D:121:MET:HB2	2.03	0.58
1:B:108:LEU:HD12	1:B:111:CYS:SG	2.43	0.58
1:C:5:GLY:HA3	1:C:33:LEU:HD23	1.86	0.58
1:D:185:ASP:O	1:D:189:MET:HG3	2.03	0.58
1:D:204:LYS:HA	1:D:237:ILE:HB	1.86	0.58
1:B:259:VAL:HG23	1:B:261:VAL:HG23	1.86	0.57
1:D:19:PHE:HB3	1:D:52:LEU:HD13	1.86	0.57
1:D:181:LYS:HD3	4:D:565:HOH:O	2.03	0.57
1:A:64:MET:CE	1:A:242:THR:HB	2.33	0.57
1:B:125:ARG:HB3	1:B:126:PRO:HD3	1.87	0.57
1:C:250:ARG:HA	4:C:517:HOH:O	2.04	0.57
1:B:231:PHE:HA	1:B:234:LEU:HD12	1.86	0.57
1:C:2:ASN:HD22	1:C:289:LEU:CD2	2.14	0.56
1:A:66:SER:HA	1:A:106:ALA:O	2.06	0.56
1:A:99:LEU:HD23	1:A:99:LEU:C	2.26	0.56
1:C:14:GLU:HB3	4:C:582:HOH:O	2.06	0.56
1:D:284:PHE:CZ	1:D:288:LYS:HE3	2.41	0.56
1:D:140:LYS:H	1:D:140:LYS:CD	2.19	0.55
1:C:19:PHE:HB2	1:C:20:PRO:HD3	1.88	0.55
1:C:13:THR:O	1:C:253:GLY:HA3	2.07	0.55
1:A:115:GLN:HG2	1:A:116:SER:N	2.19	0.55
1:C:46:ASP:O	1:C:50:ARG:HG3	2.07	0.55
1:A:118:PRO:HD2	1:A:121:MET:HB2	1.89	0.55
1:A:125:ARG:HB3	4:A:504:HOH:O	2.05	0.55
1:C:11:TRP:HE3	4:C:515:HOH:O	1.90	0.55
1:C:272:GLU:O	1:C:276:GLU:HG2	2.07	0.55
1:C:118:PRO:HG2	1:C:121:MET:HB2	1.88	0.55
1:A:216:ASN:HD21	1:B:194:THR:HG23	1.72	0.55
1:D:246:GLU:O	1:D:246:GLU:HG2	2.07	0.54
1:D:20:PRO:O	1:D:24:LYS:HG3	2.08	0.54
1:A:8:TYR:CE1	1:A:9:THR:HG23	2.43	0.54
1:B:69:LEU:HB2	1:B:111:CYS:O	2.07	0.54
1:A:35:GLU:HG3	1:A:64:MET:HG3	1.90	0.54
1:B:125:ARG:NH2	1:B:129:ASP:OD1	2.38	0.54
1:C:259:VAL:CG2	1:C:261:VAL:HG23	2.36	0.54
1:C:66:SER:HA	1:C:106:ALA:O	2.08	0.53
1:D:136:ARG:O	1:D:140:LYS:HE2	2.07	0.53
1:C:112:ALA:HB3	1:C:115:GLN:OE1	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:119:LEU:HA	1:D:257:ARG:NH2	2.23	0.53
1:D:194:THR:HB	4:D:551:HOH:O	2.08	0.53
1:A:211:HIS:CE1	3:A:402:TLZ:O4	2.62	0.53
1:C:125:ARG:NE	4:C:501:HOH:O	2.41	0.53
1:A:263:ARG:NH2	1:B:192:GLU:OE1	2.42	0.53
1:A:110:PHE:CD1	1:A:151:LEU:HD22	2.44	0.52
1:A:216:ASN:O	1:A:217:ARG:HB2	2.09	0.52
1:A:217:ARG:HH12	3:A:402:TLZ:H2	1.74	0.52
1:D:67:ILE:HG13	1:D:68:GLY:N	2.23	0.52
1:B:251:LYS:HD3	1:B:264:ASP:N	2.24	0.52
1:C:115:GLN:HE21	1:C:160:TRP:HE1	1.56	0.52
1:C:241:GLY:HA3	4:C:524:HOH:O	2.09	0.52
1:D:90:VAL:O	1:D:94:LEU:HG	2.09	0.52
1:A:11:TRP:CH2	1:A:25:ARG:HG2	2.44	0.52
1:A:64:MET:HE1	1:A:209:HIS:CE1	2.45	0.52
1:B:67:ILE:HG22	1:B:109:THR:HG22	1.91	0.52
1:D:126:PRO:O	1:D:130:ARG:HG3	2.10	0.52
1:D:150:ALA:HA	1:D:181:LYS:O	2.09	0.52
1:A:25:ARG:O	1:A:29:LEU:HG	2.10	0.52
1:B:251:LYS:HE2	1:B:264:ASP:HB2	1.91	0.52
1:C:117:PRO:HG3	1:C:160:TRP:CG	2.45	0.52
1:A:68:GLY:HA2	1:A:108:LEU:HB2	1.91	0.51
1:B:3:LYS:HB3	1:B:33:LEU:HD22	1.92	0.51
1:D:80:LYS:HB2	1:D:83:ARG:NH1	2.25	0.51
1:A:33:LEU:HD21	1:A:64:MET:HE3	1.91	0.51
1:C:67:ILE:HG22	1:C:109:THR:HG22	1.92	0.51
1:D:280:ARG:HG2	1:D:280:ARG:NH2	2.24	0.51
1:A:117:PRO:HG3	1:A:160:TRP:CG	2.46	0.51
1:D:64:MET:HA	1:D:102:ALA:HB1	1.93	0.51
1:B:125:ARG:NE	1:B:129:ASP:OD1	2.43	0.51
1:B:280:ARG:CB	1:B:280:ARG:HH21	2.23	0.51
1:D:75:PHE:HB2	1:D:110:PHE:O	2.11	0.51
1:D:38:LEU:HG	1:D:65:CYS:HB3	1.93	0.51
1:A:99:LEU:HD23	1:A:99:LEU:O	2.11	0.50
1:B:42:HIS:ND1	1:B:96:ASP:OD2	2.42	0.50
1:D:69:LEU:O	1:D:112:ALA:HA	2.12	0.50
1:B:197:ARG:CZ	1:B:201:LEU:HD11	2.41	0.50
1:C:123:ASP:O	1:C:126:PRO:HD2	2.10	0.50
1:D:271:ASP:O	1:D:274:MET:HB2	2.12	0.50
1:A:64:MET:HE1	1:A:242:THR:CB	2.37	0.50
1:A:286:ARG:HG2	1:A:286:ARG:HH11	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:104:VAL:HG12	1:C:105:PHE:N	2.26	0.50
1:C:117:PRO:HG2	1:D:262:TRP:CE3	2.46	0.50
1:D:55:VAL:O	1:D:58:ASP:HB3	2.11	0.50
1:A:181:LYS:HB2	1:A:208:GLY:HA3	1.93	0.50
1:B:125:ARG:HB3	4:B:502:HOH:O	2.12	0.50
1:C:270:THR:O	1:C:274:MET:HG2	2.12	0.50
1:D:181:LYS:HB2	1:D:208:GLY:HA3	1.93	0.50
1:C:136:ARG:NH1	1:C:175:VAL:O	2.45	0.49
1:D:249:MET:HB3	1:D:266:SER:HB3	1.93	0.49
1:C:89:TYR:CE2	1:C:93:LEU:HD11	2.47	0.49
1:D:140:LYS:HD2	1:D:140:LYS:N	2.27	0.49
1:A:232:GLY:O	1:A:236:GLU:HG3	2.13	0.49
1:C:140:LYS:HG2	4:C:541:HOH:O	2.12	0.49
1:A:24:LYS:HB2	4:A:557:HOH:O	2.12	0.49
1:B:66:SER:HA	1:B:106:ALA:O	2.13	0.49
1:B:118:PRO:HG2	1:B:121:MET:HB2	1.94	0.49
1:C:115:GLN:NE2	1:C:160:TRP:HE1	2.10	0.49
1:C:269:ALA:HA	1:C:273:GLU:OE1	2.13	0.49
1:A:140:LYS:HA	1:A:143:GLU:CD	2.33	0.49
1:D:118:PRO:HD2	1:D:121:MET:CG	2.43	0.49
1:C:227:TRP:O	1:C:231:PHE:HD1	1.96	0.48
1:A:53:LYS:NZ	1:A:57:ASP:OD1	2.45	0.48
1:A:139:ILE:HG12	1:A:177:SER:CB	2.43	0.48
1:D:154:VAL:CG2	1:D:159:GLN:HB2	2.43	0.48
1:A:69:LEU:HB2	1:A:111:CYS:O	2.13	0.48
1:D:27:ALA:HB2	1:D:61:LEU:HD22	1.94	0.48
1:A:212:LEU:HD22	1:A:227:TRP:HZ3	1.77	0.48
1:B:22:THR:O	1:B:26:ILE:HG12	2.13	0.48
1:C:77:SER:O	1:C:83:ARG:HD3	2.14	0.48
1:B:108:LEU:N	1:B:108:LEU:HD22	2.29	0.48
1:C:79:ASP:HB3	1:C:82:VAL:HG23	1.94	0.48
1:A:78:PRO:HA	1:A:130:ARG:NE	2.28	0.48
1:D:249:MET:HA	1:D:265:MET:HB2	1.95	0.47
1:A:182:VAL:HG12	1:A:183:GLN:N	2.30	0.47
1:D:102:ALA:O	1:D:147:ILE:CD1	2.63	0.47
1:D:29:LEU:HD21	1:D:275:ASP:HB3	1.96	0.47
1:C:246:GLU:OE2	3:C:402:TLZ:O4	2.32	0.47
1:D:80:LYS:HG2	1:D:84:ASP:OD2	2.14	0.47
1:D:117:PRO:HB3	1:D:121:MET:HG3	1.97	0.47
1:B:67:ILE:HG13	1:B:68:GLY:N	2.30	0.47
1:D:108:LEU:N	1:D:108:LEU:HD22	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:266:SER:O	1:C:267:ASN:HB2	2.14	0.47
1:A:246:GLU:OE2	3:A:402:TLZ:O4	2.24	0.47
1:C:69:LEU:HB2	1:C:111:CYS:O	2.14	0.47
1:D:108:LEU:HG	1:D:113:TRP:HB2	1.96	0.47
1:A:38:LEU:HD21	1:A:65:CYS:SG	2.55	0.46
3:A:402:TLZ:C6	3:A:402:TLZ:O3	2.62	0.46
1:C:152:GLU:HG3	1:C:183:GLN:CD	2.35	0.46
1:B:74:ASP:HB3	1:B:77:SER:HB2	1.97	0.46
1:D:25:ARG:NH2	1:D:271:ASP:HB3	2.31	0.46
1:D:153:VAL:HG22	1:D:168:ALA:HB2	1.97	0.46
1:D:197:ARG:NH2	1:D:201:LEU:CD1	2.76	0.46
1:C:53:LYS:HZ3	1:C:57:ASP:CG	2.18	0.46
1:C:67:ILE:HG13	1:C:68:GLY:N	2.30	0.46
1:D:69:LEU:HB2	1:D:111:CYS:O	2.14	0.46
1:C:156:ARG:CA	1:C:163:ASN:HD21	2.22	0.46
1:D:152:GLU:HB2	1:D:183:GLN:OE1	2.16	0.46
1:B:104:VAL:HG22	1:B:148:ILE:HD12	1.98	0.46
1:B:120:ASP:O	1:B:122:LYS:HD3	2.16	0.46
1:C:154:VAL:HG12	1:C:188:HIS:CD2	2.50	0.46
1:C:270:THR:HG23	4:C:507:HOH:O	2.14	0.46
1:D:284:PHE:O	1:D:288:LYS:HG2	2.16	0.46
1:A:197:ARG:NE	1:A:201:LEU:HD11	2.31	0.45
1:B:89:TYR:CE2	1:B:93:LEU:HD11	2.51	0.45
1:C:36:ILE:O	1:C:36:ILE:HG13	2.17	0.45
1:C:38:LEU:HD21	1:C:65:CYS:SG	2.56	0.45
1:B:255:VAL:O	1:B:259:VAL:HG22	2.16	0.45
1:C:169:ILE:HD11	1:C:203:CYS:SG	2.56	0.45
1:D:136:ARG:NH1	1:D:175:VAL:O	2.49	0.45
1:C:5:GLY:C	1:C:244:VAL:HG13	2.36	0.45
1:A:38:LEU:HD12	1:A:93:LEU:HB3	1.99	0.45
1:C:5:GLY:CA	1:C:33:LEU:HD23	2.46	0.45
1:B:137:ARG:HG3	1:B:137:ARG:HH11	1.81	0.45
1:C:56:ALA:HB1	1:C:61:LEU:O	2.17	0.45
1:D:46:ASP:O	1:D:50:ARG:HG3	2.17	0.45
1:D:99:LEU:C	1:D:99:LEU:HD23	2.37	0.45
1:A:18:ASP:OD2	1:A:21:ALA:HB2	2.16	0.45
1:B:50:ARG:NH1	1:B:50:ARG:HG2	2.31	0.45
1:C:50:ARG:NH1	1:C:50:ARG:HG2	2.32	0.45
1:C:45:SER:N	1:C:48:LYS:HZ2	2.09	0.44
3:A:402:TLZ:O3	3:A:402:TLZ:H3	2.17	0.44
1:D:117:PRO:HG3	1:D:160:TRP:CG	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:8:TYR:CE1	1:D:9:THR:HG23	2.53	0.44
4:A:531:HOH:O	1:B:224:ARG:HD3	2.17	0.44
1:B:166:LYS:HD3	4:B:555:HOH:O	2.18	0.44
1:A:217:ARG:HH12	3:A:402:TLZ:C6	2.30	0.44
1:A:260:GLY:O	1:B:156:ARG:HD3	2.18	0.44
1:B:41:PHE:CD1	1:B:41:PHE:C	2.91	0.44
1:A:125:ARG:HB3	1:A:126:PRO:HD3	1.99	0.44
1:B:35:GLU:OE2	1:B:66:SER:HB3	2.17	0.44
1:B:124:LYS:O	1:B:128:VAL:HG23	2.17	0.44
1:B:169:ILE:HD13	1:B:182:VAL:HG21	2.00	0.44
1:C:54:ALA:O	1:C:58:ASP:OD1	2.36	0.44
1:C:209:HIS:HE1	1:C:244:VAL:HG23	1.83	0.44
1:A:153:VAL:HG22	1:A:168:ALA:HB2	2.00	0.43
1:C:13:THR:HB	1:C:253:GLY:CA	2.48	0.43
1:C:75:PHE:HB2	1:C:110:PHE:O	2.18	0.43
1:D:11:TRP:CZ2	1:D:25:ARG:HG2	2.51	0.43
1:D:214:GLU:OE1	1:D:225:LEU:HG	2.17	0.43
1:D:246:GLU:HG2	1:D:248:PHE:CE2	2.53	0.43
1:B:26:ILE:HG22	1:B:31:PHE:HB2	1.99	0.43
1:D:132:ILE:O	1:D:136:ARG:HG3	2.17	0.43
1:B:125:ARG:N	1:B:126:PRO:CD	2.82	0.43
1:C:77:SER:O	1:C:83:ARG:NH2	2.46	0.43
1:A:41:PHE:CE2	1:A:100:LEU:HD11	2.53	0.43
1:C:157:PHE:HB3	1:D:157:PHE:HB3	2.01	0.43
1:A:51:GLU:O	1:A:55:VAL:HG23	2.19	0.43
1:A:212:LEU:HD22	1:A:227:TRP:CZ3	2.54	0.43
1:B:280:ARG:NH2	1:B:280:ARG:HB2	2.34	0.43
1:D:38:LEU:O	1:D:39:GLY:C	2.57	0.43
1:A:20:PRO:HB3	1:A:55:VAL:HG21	2.01	0.43
1:A:246:GLU:OE1	3:A:402:TLZ:H4	2.19	0.43
1:D:131:ALA:O	1:D:135:VAL:HG23	2.18	0.43
1:C:6:MET:HG3	1:C:7:PHE:N	2.34	0.42
1:B:29:LEU:HD22	1:B:279:ARG:HG3	2.02	0.42
1:C:249:MET:HA	1:C:265:MET:HB2	2.00	0.42
1:A:140:LYS:O	1:A:143:GLU:HB2	2.19	0.42
1:A:289:LEU:C	1:A:291:GLY:H	2.22	0.42
1:C:108:LEU:HD13	1:C:108:LEU:HA	1.90	0.42
1:C:188:HIS:HB2	4:C:520:HOH:O	2.19	0.42
1:A:26:ILE:HG22	1:A:31:PHE:HB2	2.00	0.42
1:C:185:ASP:OD1	1:C:185:ASP:C	2.58	0.42
1:A:246:GLU:O	1:A:246:GLU:HG2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:118:PRO:HD2	1:D:121:MET:HG2	2.02	0.42
1:C:79:ASP:HB3	1:C:82:VAL:CG2	2.50	0.42
1:D:73:TYR:HB3	1:D:86:GLY:HA2	2.02	0.42
1:A:152:GLU:OE1	3:A:402:TLZ:H8	2.20	0.42
1:D:201:LEU:HA	1:D:237:ILE:HG21	2.02	0.42
1:B:112:ALA:O	1:B:159:GLN:NE2	2.37	0.41
1:B:185:ASP:C	1:B:185:ASP:OD1	2.57	0.41
1:B:246:GLU:OE1	3:B:402:TLZ:H4	2.19	0.41
1:C:6:MET:HB3	1:C:26:ILE:HD12	2.02	0.41
1:B:19:PHE:HB2	1:B:20:PRO:HD3	2.02	0.41
1:B:132:ILE:HD13	1:B:174:ALA:CB	2.50	0.41
1:B:165:ALA:O	1:B:169:ILE:HG12	2.20	0.41
1:D:169:ILE:HD13	1:D:202:ALA:O	2.20	0.41
1:D:181:LYS:HA	4:D:565:HOH:O	2.20	0.41
1:A:266:SER:O	1:A:267:ASN:HB3	2.21	0.41
1:C:156:ARG:CA	1:C:163:ASN:ND2	2.83	0.41
1:D:126:PRO:O	1:D:130:ARG:NH1	2.53	0.41
1:D:183:GLN:HA	1:D:209:HIS:O	2.20	0.41
1:A:132:ILE:HD13	1:A:174:ALA:CB	2.49	0.41
1:C:74:ASP:HB3	1:C:77:SER:HB2	2.01	0.41
1:D:62:THR:HG22	1:D:63:VAL:N	2.35	0.41
1:B:50:ARG:HG2	1:B:50:ARG:HH11	1.86	0.41
1:B:224:ARG:HG3	1:B:224:ARG:HH11	1.85	0.41
1:C:99:LEU:HD23	1:C:99:LEU:C	2.40	0.41
1:A:160:TRP:CD1	1:A:160:TRP:N	2.88	0.41
1:B:191:ILE:O	1:B:191:ILE:HG22	2.19	0.41
1:B:23:ALA:HB1	1:B:61:LEU:CD2	2.51	0.41
1:B:246:GLU:OE2	3:B:402:TLZ:O4	2.33	0.41
1:D:35:GLU:OE1	1:D:211:HIS:NE2	2.51	0.41
1:A:46:ASP:O	1:A:50:ARG:HG3	2.21	0.41
1:C:139:ILE:HD12	1:C:139:ILE:HA	1.91	0.41
1:C:173:ASP:OD1	1:C:206:LYS:NZ	2.44	0.41
1:D:42:HIS:ND1	1:D:96:ASP:OD2	2.33	0.41
1:D:123:ASP:OD1	1:D:125:ARG:HB2	2.21	0.41
1:D:168:ALA:O	1:D:171:PHE:HB3	2.20	0.41
1:C:8:TYR:CE1	1:C:9:THR:HG23	2.56	0.41
1:C:156:ARG:HA	1:C:163:ASN:ND2	2.24	0.41
1:D:243:ILE:HG23	1:D:243:ILE:O	2.20	0.41
1:A:145:TYR:HB3	1:A:147:ILE:CD1	2.51	0.40
1:A:255:VAL:O	1:A:259:VAL:HG22	2.21	0.40
1:D:53:LYS:HE3	1:D:57:ASP:OD2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:87:THR:O	1:A:91:LYS:HG3	2.21	0.40
1:A:117:PRO:HA	1:A:118:PRO:HD3	1.92	0.40
1:C:5:GLY:HA2	1:C:31:PHE:HB3	2.02	0.40
1:C:152:GLU:OE1	3:C:402:TLZ:H8	2.21	0.40
1:A:124:LYS:O	1:A:128:VAL:HG23	2.22	0.40
1:B:19:PHE:CZ	1:B:41:PHE:HB2	2.56	0.40
1:B:246:GLU:HG2	1:B:248:PHE:CE2	2.56	0.40
1:C:220:PRO:HB3	1:C:227:TRP:CH2	2.57	0.40
1:A:197:ARG:O	1:A:201:LEU:HG	2.22	0.40
1:D:154:VAL:HA	1:D:188:HIS:CG	2.56	0.40
1:D:259:VAL:HG23	1:D:261:VAL:HG23	2.04	0.40
1:B:97:CYS:HB3	1:B:147:ILE:HD13	2.03	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	292/300 (97%)	276 (94%)	16 (6%)	0	100	100
1	B	288/300 (96%)	267 (93%)	21 (7%)	0	100	100
1	C	295/300 (98%)	281 (95%)	14 (5%)	0	100	100
1	D	290/300 (97%)	278 (96%)	12 (4%)	0	100	100
All	All	1165/1200 (97%)	1102 (95%)	63 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	243/249 (98%)	240 (99%)	3 (1%)	71	84
1	B	240/249 (96%)	232 (97%)	8 (3%)	38	53
1	C	246/249 (99%)	240 (98%)	6 (2%)	49	66
1	D	241/249 (97%)	235 (98%)	6 (2%)	47	65
All	All	970/996 (97%)	947 (98%)	23 (2%)	49	66

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	ASP
1	A	159	GLN
1	A	263	ARG
1	B	1	MET
1	B	8	TYR
1	B	33	LEU
1	B	46	ASP
1	B	99	LEU
1	B	122	LYS
1	B	197	ARG
1	B	286	ARG
1	C	79	ASP
1	C	119	LEU
1	C	121	MET
1	C	195	SER
1	C	249	MET
1	C	273	GLU
1	D	33	LEU
1	D	46	ASP
1	D	159	GLN
1	D	166	LYS
1	D	195	SER
1	D	235	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	216	ASN
1	A	267	ASN
1	A	283	GLN
1	C	2	ASN
1	C	163	ASN
1	D	115	GLN
1	D	190	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	TLZ	C	402	2	11,11,11	0.30	0	14,14,14	0.66	0
3	TLZ	B	402	2	11,11,11	0.38	0	14,14,14	0.77	0
3	TLZ	A	402	2	11,11,11	0.38	0	14,14,14	0.72	0
3	TLZ	D	402	2	11,11,11	0.48	0	14,14,14	0.96	1 (7%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	TLZ	C	402	2	-	11/16/16/16	-
3	TLZ	B	402	2	-	13/16/16/16	-
3	TLZ	A	402	2	-	12/16/16/16	-
3	TLZ	D	402	2	-	6/16/16/16	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	D	402	TLZ	C5-C4-C3	3.10	117.32	112.47

There are no chirality outliers.

All (42) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	402	TLZ	O5-C5-C6-O6
3	A	402	TLZ	C4-C5-C6-O6
3	A	402	TLZ	O3-C3-C4-C5
3	A	402	TLZ	O3-C3-C4-O4
3	A	402	TLZ	O2-C2-C3-O3
3	B	402	TLZ	O5-C5-C6-O6
3	B	402	TLZ	C4-C5-C6-O6
3	B	402	TLZ	O3-C3-C4-C5
3	B	402	TLZ	O1-C1-C2-C3
3	B	402	TLZ	O1-C1-C2-O2
3	C	402	TLZ	O2-C2-C3-O3
3	D	402	TLZ	O3-C3-C4-C5
3	D	402	TLZ	C2-C3-C4-C5
3	D	402	TLZ	O3-C3-C4-O4
3	D	402	TLZ	C2-C3-C4-O4
3	A	402	TLZ	C2-C3-C4-O4
3	B	402	TLZ	O3-C3-C4-O4
3	C	402	TLZ	O3-C3-C4-O4
3	A	402	TLZ	C1-C2-C3-O3
3	A	402	TLZ	C1-C2-C3-C4
3	C	402	TLZ	O3-C3-C4-C5
3	A	402	TLZ	C2-C3-C4-C5
3	B	402	TLZ	C2-C3-C4-C5
3	A	402	TLZ	O2-C2-C3-C4

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Mol	Chain	Res	Type	Atoms
3	C	402	TLZ	C1-C2-C3-O3
3	C	402	TLZ	O2-C2-C3-C4
3	B	402	TLZ	O4-C4-C5-O5
3	B	402	TLZ	C2-C3-C4-O4
3	C	402	TLZ	C2-C3-C4-C5
3	B	402	TLZ	O4-C4-C5-C6
3	C	402	TLZ	C1-C2-C3-C4
3	C	402	TLZ	O4-C4-C5-C6
3	B	402	TLZ	C3-C4-C5-C6
3	C	402	TLZ	C3-C4-C5-C6
3	D	402	TLZ	C3-C4-C5-C6
3	C	402	TLZ	C2-C3-C4-O4
3	C	402	TLZ	O4-C4-C5-O5
3	D	402	TLZ	O5-C5-C6-O6
3	A	402	TLZ	O1-C1-C2-O2
3	B	402	TLZ	C3-C4-C5-O5
3	A	402	TLZ	O1-C1-C2-C3
3	B	402	TLZ	O2-C2-C3-O3

There are no ring outliers.

4 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	402	TLZ	2	0
3	B	402	TLZ	2	0
3	A	402	TLZ	8	0
3	D	402	TLZ	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	294/300 (98%)	0.32	16 (5%)	25	32	22, 32, 43, 82	0
1	B	290/300 (96%)	0.25	11 (3%)	40	47	21, 31, 44, 71	0
1	C	297/300 (99%)	0.38	18 (6%)	21	27	24, 35, 47, 80	0
1	D	292/300 (97%)	0.79	39 (13%)	3	4	28, 41, 58, 79	0
All	All	1173/1200 (97%)	0.43	84 (7%)	15	20	21, 34, 52, 82	0

All (84) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	292	SER	8.7
1	D	1	MET	8.5
1	A	292	SER	6.1
1	B	1	MET	6.0
1	C	296	HIS	5.9
1	A	291	GLY	5.9
1	D	122	LYS	5.3
1	C	297	HIS	5.0
1	A	294	SER	4.8
1	C	122	LYS	4.7
1	D	106	ALA	4.3
1	A	1	MET	4.3
1	C	1	MET	3.9
1	D	16	MET	3.7
1	D	120	ASP	3.6
1	A	293	ARG	3.5
1	C	295	HIS	3.4
1	D	291	GLY	3.4
1	A	244	VAL	3.3
1	D	137	ARG	3.3
1	D	119	LEU	3.2

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Mol	Chain	Res	Type	RSRZ
1	D	78	PRO	3.2
1	D	109	THR	3.1
1	D	82	VAL	3.1
1	D	125	ARG	3.0
1	D	67	ILE	3.0
1	C	119	LEU	3.0
1	C	120	ASP	2.9
1	C	106	ALA	2.9
1	D	244	VAL	2.8
1	D	85	ALA	2.8
1	D	121	MET	2.8
1	B	119	LEU	2.8
1	D	107	GLY	2.7
1	B	244	VAL	2.7
1	D	174	ALA	2.7
1	D	66	SER	2.6
1	B	290	ALA	2.6
1	A	212	LEU	2.6
1	D	108	LEU	2.6
1	D	44	LEU	2.5
1	C	79	ASP	2.5
1	B	121	MET	2.5
1	D	151	LEU	2.5
1	D	79	ASP	2.5
1	D	239	TYR	2.5
1	D	131	ALA	2.4
1	C	150	ALA	2.4
1	D	105	PHE	2.4
1	D	201	LEU	2.4
1	C	47	ALA	2.4
1	D	178	PRO	2.4
1	C	244	VAL	2.4
1	D	177	SER	2.4
1	B	2	ASN	2.4
1	A	211	HIS	2.4
1	B	272	GLU	2.4
1	A	119	LEU	2.3
1	D	212	LEU	2.3
1	D	140	LYS	2.3
1	D	138	VAL	2.3
1	B	7	PHE	2.3
1	B	122	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	36	ILE	2.3
1	C	58	ASP	2.2
1	C	105	PHE	2.2
1	D	127	TYR	2.2
1	A	7	PHE	2.2
1	A	66	SER	2.2
1	A	107	GLY	2.2
1	C	107	GLY	2.2
1	C	7	PHE	2.2
1	B	212	LEU	2.1
1	D	213	GLY	2.1
1	D	90	VAL	2.1
1	C	137	ARG	2.1
1	A	67	ILE	2.1
1	B	120	ASP	2.1
1	C	90	VAL	2.1
1	A	122	LYS	2.0
1	D	81	SER	2.0
1	D	238	GLY	2.0
1	D	149	TYR	2.0
1	A	81	SER	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 monosaccharides 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, 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	B-factors(Å^2)	Q<0.9
3	TLZ	B	402	12/12	0.77	0.34	53,58,60,61	0
3	TLZ	D	402	12/12	0.78	0.32	59,62,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	TLZ	A	402	12/12	0.81	0.39	45,54,55,58	0
3	TLZ	C	402	12/12	0.88	0.26	50,55,57,57	0
2	MN	D	401	1/1	0.96	0.08	46,46,46,46	0
2	MN	B	401	1/1	0.98	0.13	33,33,33,33	0
2	MN	C	401	1/1	0.99	0.12	35,35,35,35	0
2	MN	A	401	1/1	0.99	0.13	32,32,32,32	0

6.5 Other polymers

There are no such residues in this entry.