



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:47 PM GMT

PDB ID : 1V5B
Title : The Structure Of The Mutant, S225A and E251L, Of 3-Isopropylmalate Dehydrogenase From Bacillus Coagulans
Authors : Fujita, K.; Minami, H.; Suzuki, K.; Tsunoda, M.; Sekiguchi, T.; Mizui, R.; Tsuzaki, S.; Nakamura, S.; Takenaka, A.
Deposited on : 2003-11-22
Resolution : 2.95 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) 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

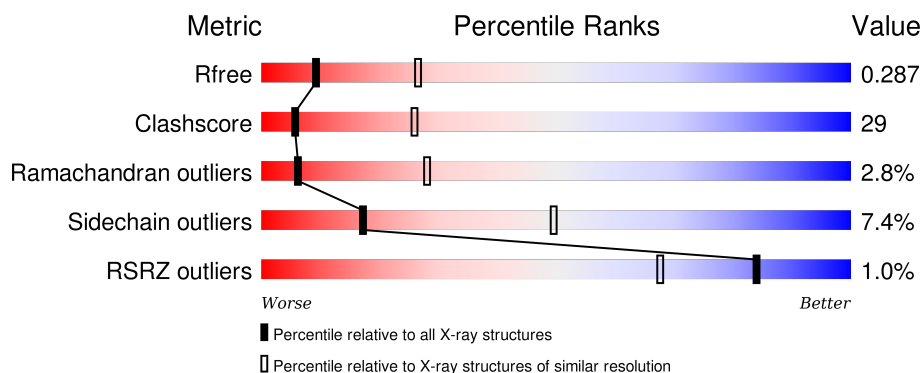
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.95 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	2184 (3.00-2.92)
Clashscore	102246	2552 (3.00-2.92)
Ramachandran outliers	100387	2468 (3.00-2.92)
Sidechain outliers	100360	2471 (3.00-2.92)
RSRZ outliers	91569	2201 (3.00-2.92)

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 $\leq 5\%$. 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	366	<div> <div>45%</div> <div>46%</div> <div>6%</div> </div>
1	B	366	<div> <div>3%</div> <div>51%</div> <div>42%</div> <div>5%</div> </div>
1	C	366	<div> <div>42%</div> <div>49%</div> <div>7%</div> </div>
1	D	366	<div> <div>50%</div> <div>42%</div> <div>5%</div> </div>
1	E	366	<div> <div>2%</div> <div>48%</div> <div>44%</div> <div>5%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	366	
1	G	366	
1	H	366	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	H	1002	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 21885 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 3-isopropylmalate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	356	Total	C	N	O	S	0	0	0
			2696	1695	467	521	13			
1	B	357	Total	C	N	O	S	0	0	0
			2710	1702	470	525	13			
1	C	356	Total	C	N	O	S	0	0	0
			2709	1702	471	523	13			
1	D	357	Total	C	N	O	S	0	0	0
			2711	1704	469	525	13			
1	E	356	Total	C	N	O	S	0	0	0
			2694	1696	462	523	13			
1	F	357	Total	C	N	O	S	0	0	0
			2705	1699	468	525	13			
1	G	357	Total	C	N	O	S	0	0	0
			2715	1706	472	524	13			
1	H	357	Total	C	N	O	S	0	0	0
			2710	1702	472	523	13			

There are 16 discrepancies between the modelled and reference sequences:

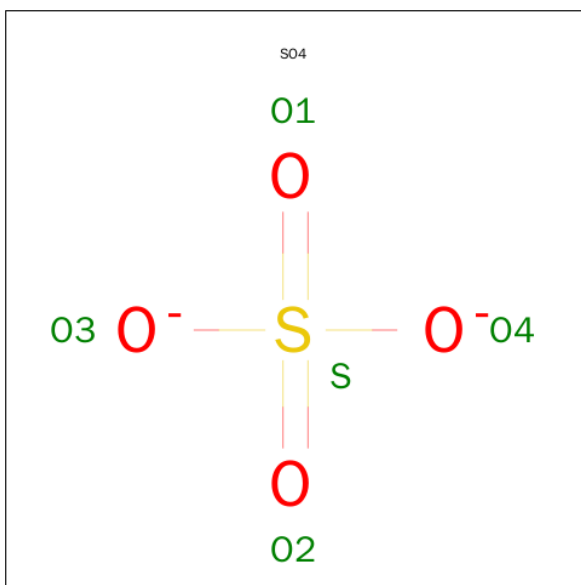
Chain	Residue	Modelled	Actual	Comment	Reference
A	225	ALA	SER	ENGINEERED	UNP P12010
A	251	LEU	GLU	ENGINEERED	UNP P12010
B	225	ALA	SER	ENGINEERED	UNP P12010
B	251	LEU	GLU	ENGINEERED	UNP P12010
C	225	ALA	SER	ENGINEERED	UNP P12010
C	251	LEU	GLU	ENGINEERED	UNP P12010
D	225	ALA	SER	ENGINEERED	UNP P12010
D	251	LEU	GLU	ENGINEERED	UNP P12010
E	225	ALA	SER	ENGINEERED	UNP P12010
E	251	LEU	GLU	ENGINEERED	UNP P12010
F	225	ALA	SER	ENGINEERED	UNP P12010
F	251	LEU	GLU	ENGINEERED	UNP P12010
G	225	ALA	SER	ENGINEERED	UNP P12010

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Chain	Residue	Modelled	Actual	Comment	Reference
G	251	LEU	GLU	ENGINEERED	UNP P12010
H	225	ALA	SER	ENGINEERED	UNP P12010
H	251	LEU	GLU	ENGINEERED	UNP P12010

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	23	Total	O	0	0
			23	23		
3	B	23	Total	O	0	0
			23	23		
3	C	21	Total	O	0	0
			21	21		

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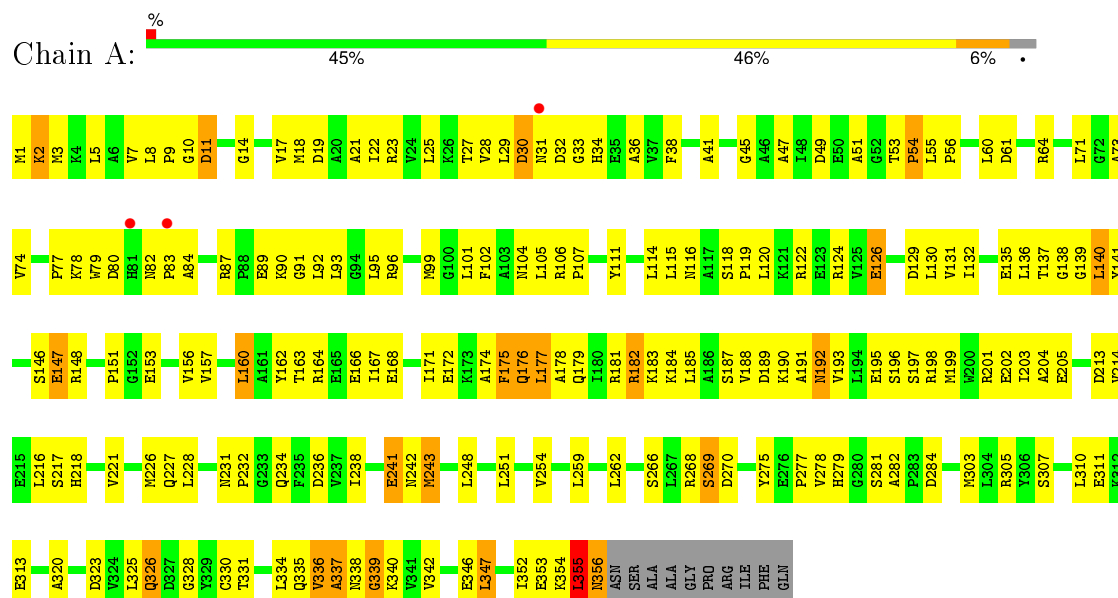
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	27	Total 27	O 27	0	0
3	E	28	Total 28	O 28	0	0
3	F	33	Total 33	O 33	0	0
3	G	28	Total 28	O 28	0	0
3	H	27	Total 27	O 27	0	0

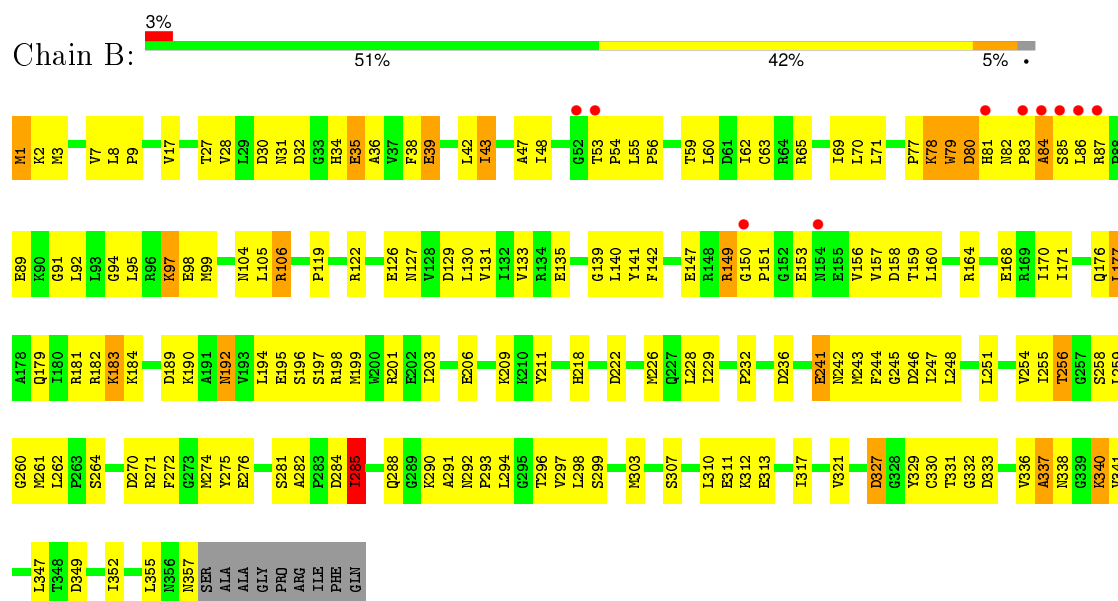
3 Residue-property plots

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.

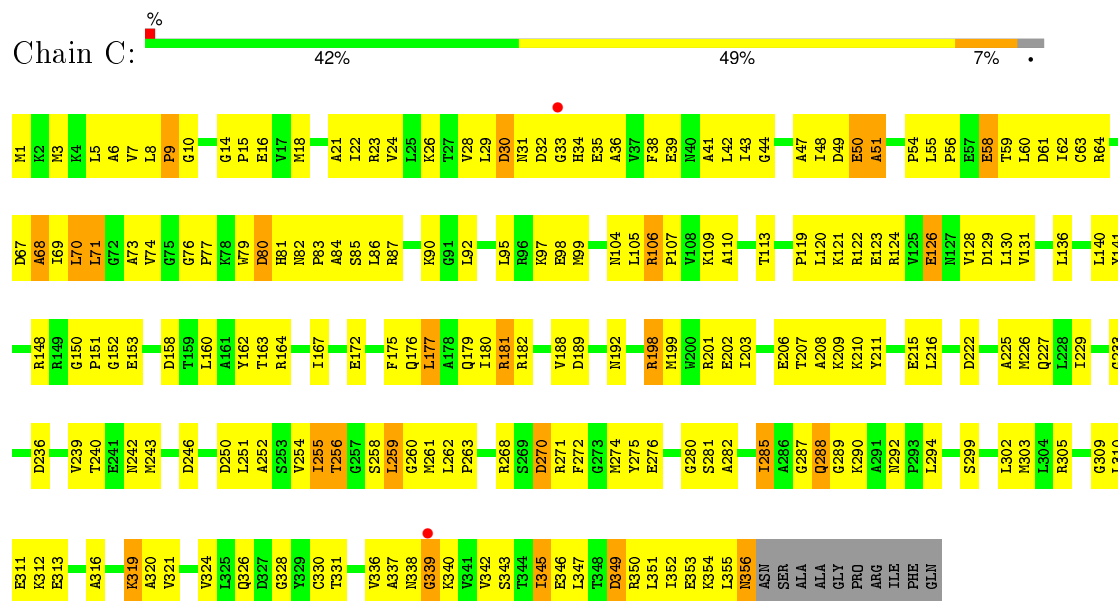
• Molecule 1: 3-isopropylmalate dehydrogenase



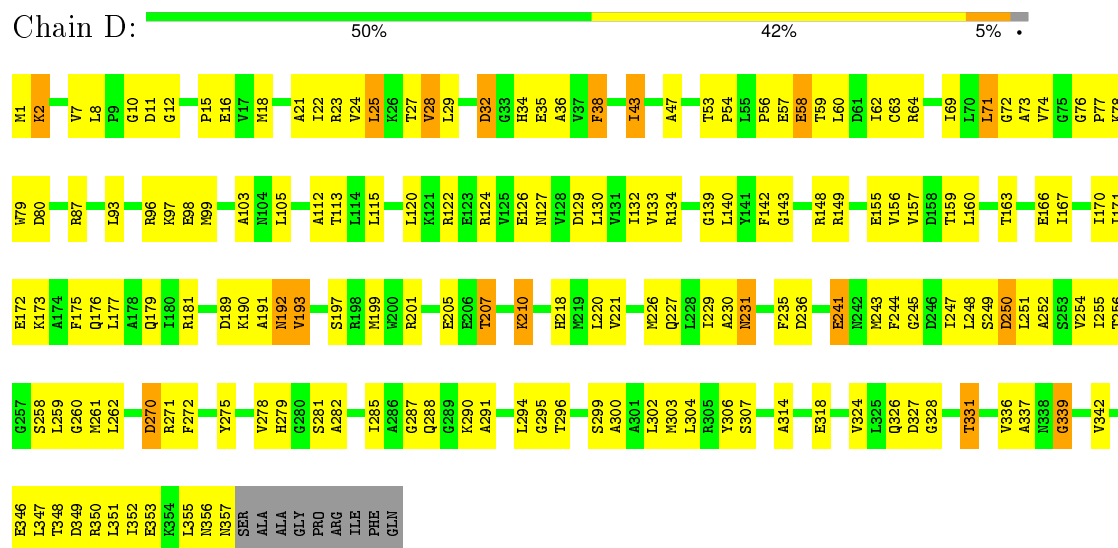
• Molecule 1: 3-isopropylmalate dehydrogenase



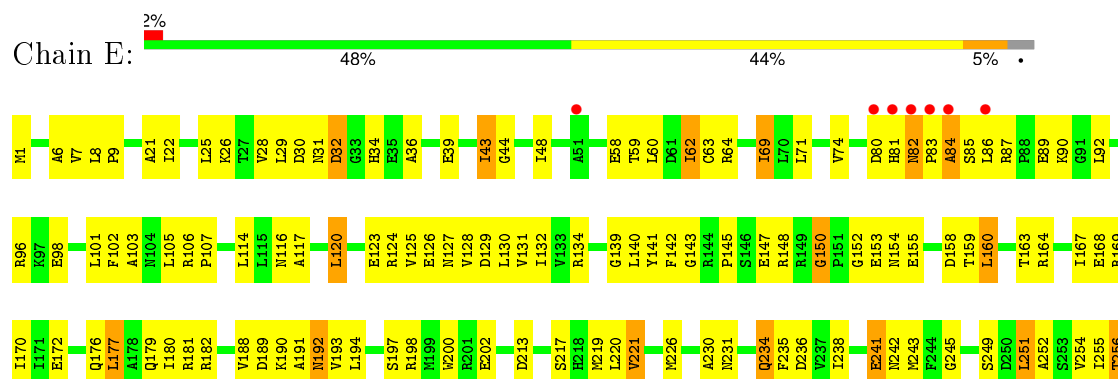
- Molecule 1: 3-isopropylmalate dehydrogenase

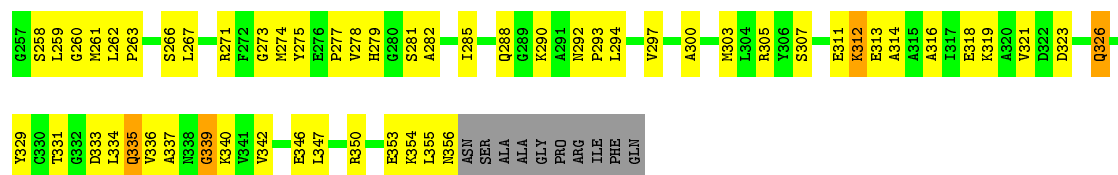


- Molecule 1: 3-isopropylmalate dehydrogenase

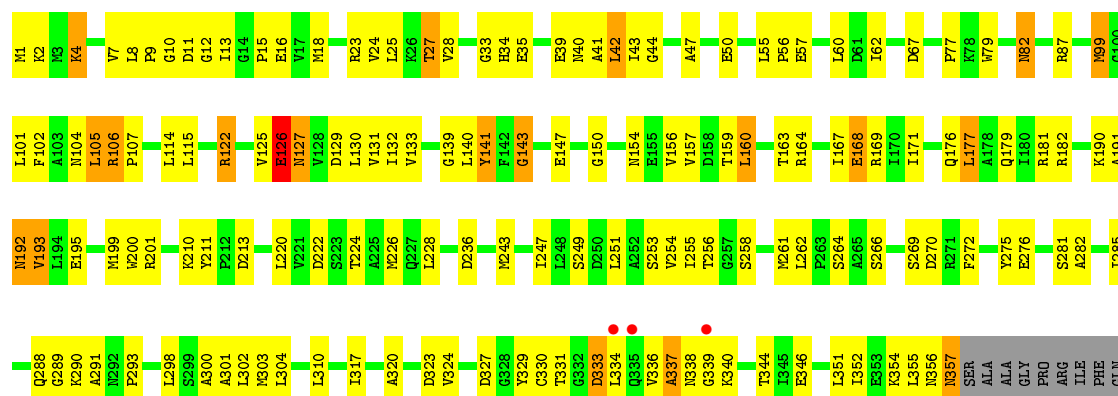


- Molecule 1: 3-isopropylmalate dehydrogenase

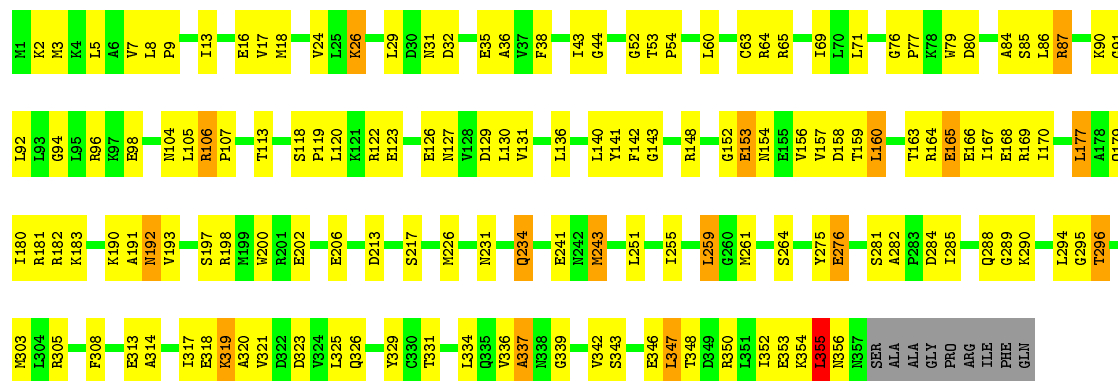




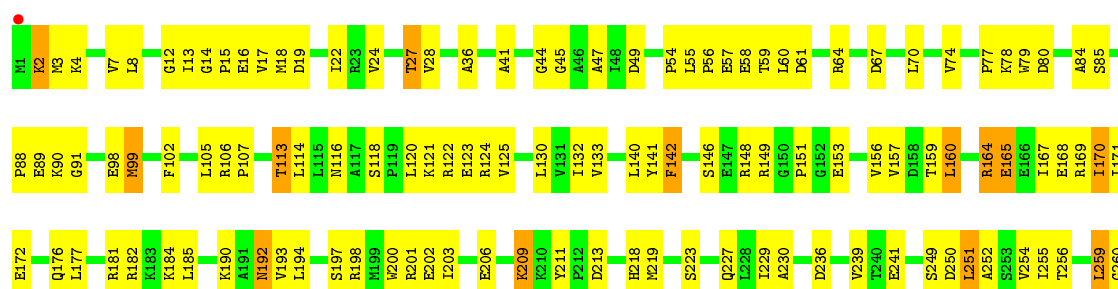
• Molecule 1: 3-isopropylmalate dehydrogenase

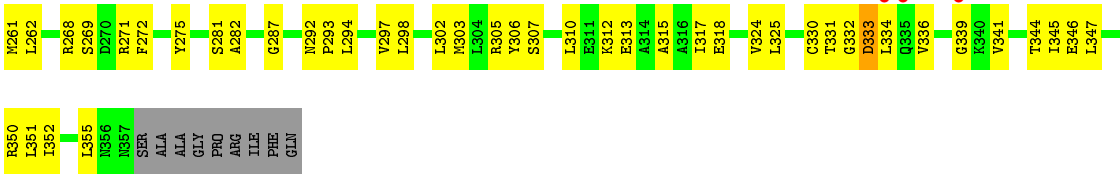


• Molecule 1: 3-isopropylmalate dehydrogenase



• Molecule 1: 3-isopropylmalate dehydrogenase





R350	L351	I352
I355	N356	N357
SER	ALA	ALA
ALA	GLY	GLY
PRO	ARG	ARG
ILE	PHE	PHE
GLN	GLN	GLN

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	134.20 Å 241.30 Å 114.10 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.45 – 2.95 44.45 – 2.95	Depositor EDS
% Data completeness (in resolution range)	(Not available) (44.45-2.95) 94.5 (44.45-2.95)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.42 (at 2.96 Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.214 , 0.290 0.215 , 0.287	Depositor DCC
R_{free} test set	7508 reflections (10.10%)	DCC
Wilson B-factor (Å ²)	44.4	Xtriage
Anisotropy	0.246	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 58.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 74349 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	21885	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.99% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.38	0/2735	0.68	0/3701
1	B	0.38	0/2749	0.66	0/3720
1	C	0.38	0/2748	0.70	0/3716
1	D	0.40	0/2750	0.67	0/3720
1	E	0.39	0/2733	0.69	0/3698
1	F	0.38	0/2744	0.69	0/3714
1	G	0.41	0/2754	0.69	0/3724
1	H	0.40	0/2749	0.68	0/3719
All	All	0.39	0/21962	0.68	0/29712

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	2696	0	2737	198	0
1	B	2710	0	2744	182	0
1	C	2709	0	2761	219	0
1	D	2711	0	2753	160	0
1	E	2694	0	2734	175	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	2705	0	2738	138	0
1	G	2715	0	2765	118	0
1	H	2710	0	2754	140	0
2	A	5	0	0	0	0
2	C	5	0	0	0	0
2	H	15	0	0	2	0
3	A	23	0	0	2	0
3	B	23	0	0	0	0
3	C	21	0	0	0	0
3	D	27	0	0	0	0
3	E	28	0	0	0	0
3	F	33	0	0	2	0
3	G	28	0	0	0	0
3	H	27	0	0	2	0
All	All	21885	0	21986	1269	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 29.

All (1269) 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:F:330:CYS:HB2	1:F:334:LEU:HD13	1.38	1.05
1:D:1:MET:HB2	1:D:2:LYS:HZ3	1.21	1.04
1:D:2:LYS:H	1:D:2:LYS:HE2	1.21	1.03
1:C:28:VAL:HG22	1:C:355:LEU:HD21	1.41	1.00
1:C:342:VAL:HB	1:C:346:GLU:HG2	1.42	0.99
1:H:345:ILE:H	1:H:345:ILE:HD12	1.27	0.97
1:D:2:LYS:H	1:D:2:LYS:CE	1.77	0.96
1:F:104:ASN:HD21	1:F:106:ARG:HH12	1.13	0.96
1:E:150:GLY:HA2	1:E:153:GLU:H	1.30	0.95
1:B:195:GLU:HA	1:B:198:ARG:HD2	1.48	0.94
1:A:82:ASN:HB2	1:A:83:PRO:HD2	1.50	0.94
1:E:7:VAL:HG12	1:E:9:PRO:HD3	1.51	0.93
1:D:190:LYS:HE3	1:D:192:ASN:HD21	1.34	0.93
1:E:192:ASN:HD22	1:E:192:ASN:H	1.13	0.92
1:E:285:ILE:HD12	1:E:290:LYS:HD2	1.50	0.92
1:A:96:ARG:HH21	1:A:136:LEU:HB3	1.34	0.91
1:B:179:GLN:HE21	1:B:183:LYS:NZ	1.67	0.91
1:F:27:THR:HG21	1:F:352:ILE:HG23	1.53	0.91
1:C:84:ALA:HA	1:C:87:ARG:HD3	1.51	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:258:SER:O	1:B:261:MET:HB3	1.75	0.87
1:H:352:ILE:HA	1:H:355:LEU:HD12	1.56	0.86
1:F:115:LEU:HD11	1:F:126:GLU:HB3	1.56	0.86
1:C:251:LEU:O	1:C:254:VAL:HG22	1.76	0.86
1:B:55:LEU:HD11	1:B:60:LEU:HD21	1.58	0.86
1:A:139:GLY:HA2	1:A:160:LEU:HD13	1.58	0.85
1:E:192:ASN:HD22	1:E:192:ASN:N	1.73	0.85
1:C:342:VAL:HB	1:C:346:GLU:CG	2.07	0.85
1:C:210:LYS:HD3	1:C:210:LYS:O	1.76	0.84
1:B:179:GLN:HE21	1:B:183:LYS:HZ2	1.19	0.83
1:B:71:LEU:HD21	1:B:92:LEU:HD11	1.59	0.83
1:B:331:THR:HG23	1:B:347:LEU:HD22	1.58	0.83
1:H:259:LEU:HD12	1:H:260:GLY:N	1.94	0.83
1:G:192:ASN:ND2	1:G:193:VAL:HG23	1.93	0.82
1:E:59:THR:O	1:E:62:ILE:HG23	1.78	0.82
1:F:106:ARG:HB2	1:F:106:ARG:HH11	1.44	0.82
1:B:327:ASP:HA	1:C:337:ALA:HB1	1.60	0.82
1:E:323:ASP:HB3	1:E:354:LYS:HE2	1.62	0.81
1:G:120:LEU:O	1:H:121:LYS:HE3	1.80	0.81
1:A:104:ASN:HD21	1:A:106:ARG:HD3	1.46	0.81
1:D:2:LYS:HE2	1:D:2:LYS:N	1.96	0.81
1:A:226:MET:HB2	1:B:254:VAL:HG11	1.63	0.80
1:G:140:LEU:HD13	1:G:160:LEU:HB2	1.62	0.80
1:H:140:LEU:HD12	1:H:160:LEU:HD22	1.62	0.80
1:B:77:PRO:O	1:B:80:ASP:HB2	1.82	0.80
1:E:48:ILE:HD11	1:E:86:LEU:O	1.81	0.80
1:E:43:ILE:HD13	1:E:44:GLY:N	1.97	0.79
1:B:317:ILE:O	1:B:321:VAL:HG23	1.82	0.79
1:C:356:ASN:C	1:C:356:ASN:HD22	1.86	0.78
1:H:345:ILE:HD12	1:H:345:ILE:N	1.99	0.78
1:E:90:LYS:HE3	1:E:90:LYS:HA	1.66	0.78
1:C:47:ALA:O	1:C:51:ALA:HB3	1.84	0.78
1:E:312:LYS:HE2	1:E:312:LYS:HA	1.66	0.77
1:C:58:GLU:O	1:C:62:ILE:HG12	1.85	0.77
1:F:167:ILE:O	1:F:171:ILE:HG12	1.83	0.77
1:C:163:THR:O	1:C:167:ILE:HG12	1.84	0.77
1:B:147:GLU:HG3	1:B:149:ARG:HD2	1.66	0.77
1:G:17:VAL:HB	1:G:296:THR:HG21	1.65	0.77
1:B:104:ASN:HD21	1:B:106:ARG:HH11	1.29	0.76
1:B:329:TYR:CE1	1:B:340:LYS:HD2	2.20	0.76
1:G:8:LEU:HB2	1:G:71:LEU:HD12	1.65	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:155:GLU:HG2	1:F:163:THR:HG22	1.68	0.76
1:G:85:SER:HA	1:G:90:LYS:HG2	1.67	0.76
1:C:43:ILE:HG13	1:C:44:GLY:H	1.51	0.76
1:B:27:THR:HG21	1:B:352:ILE:HG23	1.67	0.76
1:C:3:MET:HE1	1:C:5:LEU:HD11	1.68	0.76
1:A:310:LEU:HB3	1:A:313:GLU:HB2	1.68	0.75
1:B:82:ASN:HD22	1:B:86:LEU:HD22	1.52	0.75
1:G:77:PRO:HA	1:G:80:ASP:OD2	1.87	0.75
1:C:343:SER:OG	1:C:345:ILE:HG22	1.87	0.74
1:B:259:LEU:HD12	1:B:260:GLY:H	1.52	0.74
1:B:56:PRO:HG2	1:B:59:THR:OG1	1.86	0.74
1:C:39:GLU:OE2	1:C:62:ILE:HG23	1.87	0.74
1:A:122:ARG:HB3	1:A:126:GLU:OE1	1.88	0.74
1:H:47:ALA:HB1	1:H:56:PRO:HD3	1.70	0.74
1:E:259:LEU:HD12	1:E:260:GLY:H	1.51	0.74
1:E:143:GLY:HA3	1:E:159:THR:O	1.86	0.74
1:D:25:LEU:HD12	1:D:29:LEU:HG	1.70	0.73
1:H:192:ASN:ND2	1:H:193:VAL:HG23	2.04	0.73
1:A:199:MET:O	1:A:203:ILE:HG12	1.89	0.73
1:C:222:ASP:HB3	1:D:247:ILE:HG22	1.67	0.73
1:F:125:VAL:HG21	1:F:255:ILE:O	1.88	0.73
1:H:331:THR:HG23	1:H:347:LEU:HD22	1.69	0.73
1:H:312:LYS:HB3	1:H:313:GLU:OE2	1.88	0.73
1:E:43:ILE:HD13	1:E:44:GLY:H	1.50	0.73
1:A:87:ARG:NH1	1:A:87:ARG:HB3	2.04	0.73
1:C:162:TYR:HB3	1:C:167:ILE:HD11	1.71	0.73
1:C:77:PRO:HA	1:C:80:ASP:OD2	1.88	0.73
1:C:177:LEU:HD22	1:C:181:ARG:HD2	1.71	0.73
1:A:192:ASN:HD22	1:A:193:VAL:N	1.87	0.73
1:H:345:ILE:H	1:H:345:ILE:CD1	1.99	0.72
1:H:294:LEU:HD12	1:H:334:LEU:HD12	1.71	0.72
1:H:28:VAL:HG21	1:H:317:ILE:HD11	1.72	0.72
1:C:104:ASN:HD21	1:C:106:ARG:NH1	1.87	0.72
1:B:190:LYS:HE3	1:B:192:ASN:HD21	1.54	0.72
1:E:336:VAL:HG21	1:E:339:GLY:HA3	1.70	0.72
1:H:58:GLU:HA	1:H:61:ASP:OD2	1.88	0.72
1:A:178:ALA:O	1:A:183:LYS:HA	1.90	0.71
1:E:140:LEU:HD23	1:E:243:MET:CE	2.21	0.71
1:D:336:VAL:HG12	1:D:337:ALA:H	1.53	0.71
1:C:76:GLY:HA3	1:C:79:TRP:HZ3	1.55	0.71
1:A:2:LYS:N	1:A:2:LYS:HD3	2.06	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:43:ILE:HG13	1:C:44:GLY:N	2.06	0.71
1:D:261:MET:HE3	1:D:294:LEU:HB3	1.73	0.70
1:F:4:LYS:N	1:F:4:LYS:HD3	2.06	0.70
1:C:210:LYS:HD2	1:C:211:TYR:CE1	2.26	0.70
1:H:55:LEU:HD21	1:H:60:LEU:HD21	1.72	0.70
1:E:182:ARG:NH2	1:E:236:ASP:HA	2.06	0.70
1:F:192:ASN:ND2	1:F:193:VAL:HG23	2.07	0.70
1:F:7:VAL:HG12	1:F:9:PRO:HD3	1.74	0.70
1:D:192:ASN:ND2	1:D:193:VAL:HG23	2.07	0.69
1:C:3:MET:CE	1:C:5:LEU:HD11	2.21	0.69
1:F:7:VAL:HB	1:F:40:ASN:HB3	1.73	0.69
1:B:206:GLU:O	1:B:209:LYS:HG2	1.92	0.69
1:F:126:GLU:O	1:F:127:ASN:HB2	1.91	0.69
1:G:13:ILE:O	1:G:17:VAL:HG22	1.92	0.69
1:E:312:LYS:CE	1:E:312:LYS:HA	2.22	0.69
1:A:84:ALA:HA	1:A:87:ARG:CD	2.23	0.69
1:D:63:CYS:HB3	1:D:99:MET:CE	2.23	0.69
1:G:119:PRO:HA	1:H:124:ARG:HE	1.58	0.69
1:A:96:ARG:NH2	1:A:136:LEU:HD22	2.08	0.69
1:E:164:ARG:O	1:E:168:GLU:HG3	1.92	0.69
1:A:122:ARG:O	1:A:126:GLU:HG3	1.91	0.69
1:D:241:GLU:OE1	1:D:243:MET:HB3	1.92	0.69
1:C:23:ARG:HH21	1:C:352:ILE:HD12	1.58	0.69
1:F:293:PRO:HD3	1:F:344:THR:HG23	1.76	0.68
1:F:130:LEU:HD13	1:F:132:ILE:HD13	1.72	0.68
1:H:324:VAL:HG21	1:H:351:LEU:HD23	1.75	0.68
1:C:199:MET:CE	1:D:148:ARG:HD3	2.23	0.68
1:C:28:VAL:O	1:C:31:ASN:HB2	1.93	0.68
1:E:192:ASN:ND2	1:E:192:ASN:H	1.87	0.68
1:G:164:ARG:O	1:G:168:GLU:HG3	1.93	0.68
1:D:143:GLY:HA3	1:D:159:THR:O	1.94	0.68
1:C:1:MET:N	1:C:34:HIS:CD2	2.62	0.68
1:C:324:VAL:HG22	1:C:354:LYS:HD3	1.77	0.67
1:D:256:THR:C	1:D:258:SER:H	1.97	0.67
1:A:190:LYS:HE3	1:A:192:ASN:HD21	1.58	0.67
1:B:179:GLN:NE2	1:B:183:LYS:HZ2	1.91	0.67
1:D:1:MET:HA	1:D:34:HIS:ND1	2.09	0.67
1:D:47:ALA:HB1	1:D:56:PRO:HD3	1.75	0.67
1:H:18:MET:O	1:H:18:MET:HE3	1.93	0.67
1:A:93:LEU:O	1:A:96:ARG:HB3	1.94	0.67
1:F:356:ASN:O	1:F:357:ASN:HB2	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:28:VAL:HG21	1:H:317:ILE:CD1	2.24	0.67
1:C:150:GLY:HA2	1:C:153:GLU:H	1.59	0.67
1:C:6:ALA:HB3	1:C:69:ILE:HD13	1.75	0.67
1:C:177:LEU:CD2	1:C:181:ARG:HD2	2.25	0.67
1:F:43:ILE:HG12	1:F:44:GLY:H	1.59	0.67
1:G:107:PRO:HB3	1:G:131:VAL:HG22	1.76	0.67
1:B:259:LEU:C	1:B:261:MET:N	2.48	0.66
1:C:229:ILE:CD1	1:D:229:ILE:HD11	2.25	0.66
1:H:259:LEU:HD12	1:H:260:GLY:H	1.58	0.66
1:D:28:VAL:CG2	1:D:355:LEU:HD13	2.25	0.66
1:F:115:LEU:CD1	1:F:126:GLU:HB3	2.26	0.66
1:E:189:ASP:O	1:E:220:LEU:HA	1.95	0.66
1:A:174:ALA:HB1	1:A:185:LEU:HD11	1.77	0.66
1:D:126:GLU:O	1:D:127:ASN:HB2	1.95	0.66
1:A:87:ARG:HH11	1:A:87:ARG:HB3	1.58	0.66
1:E:83:PRO:C	1:E:85:SER:H	1.98	0.66
1:A:138:GLY:HA3	1:A:162:TYR:CE1	2.31	0.66
1:D:149:ARG:HD2	1:D:155:GLU:OE2	1.94	0.66
1:A:107:PRO:HB3	1:A:131:VAL:HG22	1.77	0.66
1:F:330:CYS:SG	1:F:336:VAL:HG21	2.36	0.66
1:C:129:ASP:O	1:C:182:ARG:NH2	2.30	0.65
1:A:29:LEU:HD13	1:A:36:ALA:HB2	1.78	0.65
1:C:198:ARG:O	1:C:202:GLU:HG3	1.96	0.65
1:B:192:ASN:HD22	1:B:192:ASN:N	1.95	0.65
1:A:132:ILE:HD12	1:A:238:ILE:HD11	1.78	0.65
1:C:24:VAL:O	1:C:28:VAL:HG23	1.97	0.65
1:B:27:THR:CG2	1:B:352:ILE:HG23	2.26	0.65
1:E:82:ASN:HB3	1:E:83:PRO:HD2	1.77	0.65
1:H:114:LEU:HD21	1:H:334:LEU:HB3	1.79	0.65
1:C:55:LEU:HD11	1:C:60:LEU:CD2	2.26	0.65
1:A:116:ASN:HB3	1:A:335:GLN:NE2	2.10	0.65
1:B:71:LEU:HD21	1:B:92:LEU:CD1	2.25	0.65
1:A:189:ASP:HB2	1:A:197:SER:HB3	1.78	0.65
1:D:227:GLN:OE1	1:D:227:GLN:HA	1.95	0.65
1:H:294:LEU:HD12	1:H:334:LEU:CD1	2.27	0.65
1:E:336:VAL:CG2	1:E:339:GLY:HA3	2.26	0.65
1:E:126:GLU:O	1:E:127:ASN:HB2	1.95	0.65
1:C:55:LEU:HD21	1:C:60:LEU:HD21	1.77	0.65
1:A:105:LEU:O	1:A:106:ARG:HG3	1.97	0.64
1:A:60:LEU:O	1:A:64:ARG:HG3	1.96	0.64
1:H:293:PRO:O	1:H:297:VAL:HG23	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:106:ARG:NH1	1:F:106:ARG:HB2	2.09	0.64
1:G:126:GLU:O	1:G:127:ASN:HB2	1.97	0.64
1:E:83:PRO:O	1:E:85:SER:N	2.31	0.64
1:E:316:ALA:HA	1:E:319:LYS:HZ3	1.62	0.64
1:C:31:ASN:HD21	1:C:312:LYS:NZ	1.94	0.64
1:C:342:VAL:CB	1:C:346:GLU:HG2	2.24	0.64
1:A:140:LEU:HD22	1:A:140:LEU:H	1.61	0.64
1:C:181:ARG:NH1	1:C:236:ASP:OD1	2.30	0.64
1:F:288:GLN:HB3	1:F:290:LYS:HD3	1.79	0.64
1:E:198:ARG:O	1:E:202:GLU:HG3	1.97	0.64
1:A:268:ARG:HG3	1:A:269:SER:N	2.12	0.64
1:H:89:GLU:CD	1:H:89:GLU:H	2.01	0.64
1:C:210:LYS:HD3	1:C:210:LYS:C	2.17	0.64
1:E:141:TYR:CD1	1:F:193:VAL:HG11	2.32	0.64
1:F:102:PHE:CE2	1:F:169:ARG:HD2	2.33	0.64
1:E:69:ILE:HG22	1:E:273:GLY:O	1.97	0.64
1:E:329:TYR:CE1	1:E:340:LYS:HE3	2.33	0.64
1:E:256:THR:HG22	1:E:258:SER:H	1.62	0.64
1:B:259:LEU:C	1:B:261:MET:H	2.01	0.64
1:E:231:ASN:O	1:E:234:GLN:HG2	1.98	0.64
1:D:63:CYS:HB3	1:D:99:MET:HE2	1.78	0.64
1:A:231:ASN:ND2	1:A:234:GLN:HB3	2.13	0.64
1:E:150:GLY:HA2	1:E:153:GLU:N	2.08	0.64
1:B:2:LYS:HD2	1:B:35:GLU:HB3	1.79	0.64
1:E:316:ALA:HA	1:E:319:LYS:NZ	2.13	0.64
1:C:285:ILE:O	1:C:285:ILE:HD13	1.98	0.63
1:C:74:VAL:HG21	1:C:92:LEU:HD13	1.80	0.63
1:H:164:ARG:O	1:H:168:GLU:HG3	1.97	0.63
1:B:259:LEU:CD1	1:B:260:GLY:H	2.10	0.63
1:H:4:LYS:O	1:H:67:ASP:HB2	1.98	0.63
1:A:323:ASP:HB3	1:A:354:LYS:HE2	1.81	0.63
1:G:319:LYS:CE	1:G:319:LYS:HA	2.28	0.63
1:H:206:GLU:O	1:H:209:LYS:HG3	1.98	0.63
1:A:336:VAL:CG2	1:A:339:GLY:HA3	2.29	0.63
1:C:188:VAL:HB	1:C:240:THR:HB	1.81	0.63
1:E:292:ASN:HD21	1:E:334:LEU:HD11	1.64	0.63
1:C:305:ARG:NH2	1:C:311:GLU:HB2	2.14	0.63
1:C:82:ASN:HB2	1:C:83:PRO:HD2	1.81	0.63
1:F:139:GLY:HA2	1:F:160:LEU:CD1	2.29	0.63
1:E:172:GLU:O	1:E:176:GLN:HG3	1.99	0.63
1:C:345:ILE:HD13	1:C:345:ILE:O	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:258:SER:O	1:C:261:MET:HG2	1.99	0.63
1:C:182:ARG:HH22	1:C:236:ASP:HA	1.64	0.62
1:G:154:ASN:HA	1:H:164:ARG:HB2	1.80	0.62
1:F:25:LEU:HD13	1:F:300:ALA:HB1	1.81	0.62
1:A:87:ARG:HH11	1:A:87:ARG:CB	2.12	0.62
1:B:2:LYS:NZ	1:B:2:LYS:HB3	2.14	0.62
1:A:132:ILE:HD12	1:A:238:ILE:CD1	2.29	0.62
1:A:141:TYR:HB2	1:A:242:ASN:HD21	1.64	0.62
1:D:93:LEU:O	1:D:93:LEU:HD23	1.98	0.62
1:B:104:ASN:HD21	1:B:106:ARG:NH1	1.96	0.62
1:H:310:LEU:HB3	1:H:313:GLU:OE1	1.99	0.62
1:A:162:TYR:CG	1:A:167:ILE:HD11	2.34	0.62
1:H:57:GLU:CD	1:H:57:GLU:H	2.03	0.62
1:F:2:LYS:HA	1:F:35:GLU:O	1.99	0.62
1:F:330:CYS:CB	1:F:336:VAL:HG21	2.29	0.62
1:A:141:TYR:CE1	1:A:243:MET:SD	2.93	0.61
1:B:245:GLY:C	1:B:247:ILE:H	2.03	0.61
1:C:328:GLY:HA3	1:C:340:LYS:HE2	1.82	0.61
1:H:3:MET:O	1:H:36:ALA:HA	2.00	0.61
1:C:3:MET:HE2	1:C:5:LEU:HD21	1.81	0.61
1:C:182:ARG:NH2	1:C:236:ASP:HA	2.14	0.61
1:E:140:LEU:HD23	1:E:243:MET:HE2	1.82	0.61
1:E:141:TYR:HB2	1:E:242:ASN:HD21	1.65	0.61
1:D:77:PRO:HA	1:D:80:ASP:OD1	2.00	0.61
1:H:185:LEU:HD11	1:H:239:VAL:HG12	1.82	0.61
1:G:231:ASN:ND2	1:G:234:GLN:HG2	2.15	0.61
1:G:261:MET:HA	1:G:295:GLY:CA	2.31	0.61
1:E:262:LEU:O	1:E:278:VAL:HG23	2.00	0.61
1:D:247:ILE:HD12	1:D:248:LEU:N	2.14	0.61
1:F:43:ILE:HG12	1:F:44:GLY:N	2.15	0.61
1:F:210:LYS:HD3	1:F:211:TYR:CE1	2.34	0.61
1:D:336:VAL:HG12	1:D:337:ALA:N	2.15	0.61
1:H:133:VAL:HG12	1:H:170:ILE:HD11	1.83	0.61
1:B:310:LEU:HD22	1:B:313:GLU:OE2	2.01	0.61
1:C:148:ARG:NH1	1:D:199:MET:HG3	2.15	0.61
1:B:259:LEU:HD12	1:B:260:GLY:N	2.14	0.61
1:D:10:GLY:HA3	1:D:73:ALA:O	2.00	0.61
1:H:7:VAL:C	1:H:8:LEU:HD12	2.21	0.61
1:A:80:ASP:HA	1:A:87:ARG:NH2	2.16	0.61
1:D:71:LEU:HD13	1:D:72:GLY:N	2.15	0.61
1:C:275:TYR:CZ	1:C:303:MET:HA	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:55:LEU:HD11	1:A:60:LEU:HD21	1.83	0.60
1:E:255:ILE:HD12	1:E:256:THR:N	2.16	0.60
1:A:78:LYS:HE2	1:A:79:TRP:NE1	2.16	0.60
1:A:176:GLN:O	1:A:179:GLN:HB3	2.00	0.60
1:C:271:ARG:HG3	1:C:271:ARG:HH21	1.66	0.60
1:C:305:ARG:HH22	1:C:311:GLU:HB2	1.66	0.60
1:C:67:ASP:O	1:C:68:ALA:HB2	2.01	0.60
1:E:69:ILE:C	1:E:69:ILE:HD13	2.22	0.60
1:G:179:GLN:HE21	1:G:213:ASP:CG	2.03	0.60
1:E:254:VAL:HG11	1:F:226:MET:HB3	1.83	0.60
1:A:83:PRO:O	1:A:87:ARG:HG3	2.01	0.60
1:E:148:ARG:HD3	1:F:199:MET:CE	2.30	0.60
1:H:18:MET:SD	1:H:70:LEU:HD22	2.41	0.60
1:C:229:ILE:HD13	1:D:229:ILE:HD11	1.82	0.60
1:A:191:ALA:CB	1:A:201:ARG:HE	2.15	0.60
1:B:130:LEU:HD12	1:B:130:LEU:C	2.22	0.60
1:E:182:ARG:HH21	1:E:236:ASP:HA	1.65	0.60
1:A:231:ASN:HD21	1:A:234:GLN:HB3	1.67	0.60
1:A:141:TYR:HB2	1:A:242:ASN:ND2	2.17	0.60
1:C:206:GLU:O	1:C:207:THR:HB	2.00	0.60
1:B:340:LYS:NZ	1:C:338:ASN:ND2	2.50	0.60
1:C:259:LEU:HD12	1:C:260:GLY:N	2.16	0.60
1:E:84:ALA:HA	1:E:87:ARG:HG2	1.83	0.60
1:D:8:LEU:HD23	1:D:43:ILE:HG13	1.83	0.60
1:C:355:LEU:O	1:C:356:ASN:HB3	2.01	0.60
1:A:163:THR:OG1	1:A:166:GLU:HG3	2.02	0.60
1:C:29:LEU:C	1:C:31:ASN:H	2.05	0.59
1:H:292:ASN:OD1	1:H:294:LEU:HG	2.01	0.59
1:D:205:GLU:OE1	1:D:205:GLU:HA	2.02	0.59
1:F:164:ARG:O	1:F:168:GLU:HB2	2.02	0.59
1:A:228:LEU:O	1:A:232:PRO:HB3	2.01	0.59
1:A:124:ARG:HE	1:B:119:PRO:HA	1.66	0.59
1:E:285:ILE:O	1:E:285:ILE:CG2	2.50	0.59
1:E:89:GLU:H	1:E:89:GLU:CD	2.05	0.59
1:C:113:THR:HG21	1:C:326:GLN:HA	1.83	0.59
1:D:120:LEU:HD11	1:D:255:ILE:HB	1.84	0.59
1:G:164:ARG:HG2	1:G:168:GLU:OE2	2.02	0.59
1:G:353:GLU:O	1:G:356:ASN:ND2	2.36	0.59
1:A:254:VAL:HG11	1:B:226:MET:HB3	1.83	0.59
1:F:330:CYS:HB3	1:F:336:VAL:HG21	1.83	0.59
1:F:122:ARG:O	1:F:126:GLU:HG2	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:104:ASN:HD21	1:C:106:ARG:HH11	1.48	0.59
1:B:192:ASN:HD22	1:B:192:ASN:H	1.50	0.59
1:A:338:ASN:HA	3:A:1023:HOH:O	2.02	0.59
1:C:28:VAL:CG2	1:C:355:LEU:HD21	2.27	0.59
1:H:56:PRO:HG2	1:H:59:THR:OG1	2.02	0.59
1:H:54:PRO:HB2	1:H:91:GLY:HA3	1.83	0.59
1:C:141:TYR:CD2	1:C:242:ASN:ND2	2.71	0.59
1:A:192:ASN:ND2	1:A:193:VAL:HG23	2.17	0.58
1:D:314:ALA:O	1:D:318:GLU:HG3	2.03	0.58
1:C:336:VAL:CG2	1:C:339:GLY:HA2	2.33	0.58
1:C:18:MET:HE1	1:C:70:LEU:HD22	1.85	0.58
1:E:147:GLU:HA	1:F:195:GLU:HG2	1.85	0.58
1:B:285:ILE:O	1:B:285:ILE:HG12	2.02	0.58
1:B:330:CYS:HB3	1:B:336:VAL:HG21	1.85	0.58
1:H:182:ARG:NH2	1:H:236:ASP:HA	2.18	0.58
1:D:2:LYS:HA	1:D:35:GLU:HB3	1.85	0.58
1:G:325:LEU:HD21	1:G:334:LEU:HD13	1.84	0.58
1:B:7:VAL:HG12	1:B:9:PRO:HD3	1.85	0.58
1:G:60:LEU:O	1:G:64:ARG:HG3	2.04	0.58
1:F:13:ILE:HD12	1:F:291:ALA:HB1	1.84	0.58
1:C:104:ASN:HB2	1:C:136:LEU:HD11	1.83	0.58
1:C:43:ILE:CG1	1:C:44:GLY:H	2.16	0.58
1:A:55:LEU:HD11	1:A:60:LEU:CD2	2.33	0.58
1:E:293:PRO:O	1:E:297:VAL:HG23	2.04	0.58
1:G:7:VAL:HG12	1:G:9:PRO:HD3	1.85	0.58
1:A:146:SER:HA	1:A:157:VAL:O	2.02	0.58
1:E:275:TYR:CZ	1:E:303:MET:HA	2.38	0.58
1:F:143:GLY:HA3	1:F:159:THR:O	2.04	0.58
1:D:16:GLU:OE2	1:D:287:GLY:N	2.36	0.58
1:E:124:ARG:HH21	1:E:230:ALA:HA	1.69	0.57
1:D:163:THR:OG1	1:D:166:GLU:HG3	2.04	0.57
1:E:271:ARG:HG3	1:E:271:ARG:HH11	1.69	0.57
1:C:330:CYS:O	1:C:342:VAL:HG22	2.04	0.57
1:E:285:ILE:CD1	1:E:290:LYS:HD2	2.31	0.57
1:F:115:LEU:HD11	1:F:126:GLU:CB	2.32	0.57
1:C:107:PRO:HB3	1:C:131:VAL:HG22	1.85	0.57
1:D:258:SER:O	1:D:261:MET:HG2	2.04	0.57
1:G:119:PRO:HA	1:H:124:ARG:NE	2.19	0.57
1:A:326:GLN:HA	1:A:326:GLN:OE1	2.03	0.57
1:E:266:SER:C	1:E:267:LEU:HD23	2.25	0.57
1:C:5:LEU:HD12	1:C:38:PHE:CE1	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:199:MET:HE2	1:D:148:ARG:HD3	1.86	0.57
1:B:275:TYR:OH	1:B:307:SER:HB2	2.03	0.57
1:D:18:MET:O	1:D:22:ILE:HG12	2.03	0.57
1:A:77:PRO:HD2	3:A:1021:HOH:O	2.03	0.57
1:G:84:ALA:HA	1:G:87:ARG:NH1	2.19	0.57
1:C:3:MET:CE	1:C:5:LEU:HD21	2.34	0.57
1:F:104:ASN:HD21	1:F:106:ARG:NH1	1.94	0.57
1:E:44:GLY:HA3	1:E:74:VAL:HG12	1.86	0.57
1:E:192:ASN:ND2	1:E:192:ASN:N	2.46	0.57
1:E:29:LEU:HD13	1:E:36:ALA:HB2	1.86	0.57
1:C:95:LEU:O	1:C:99:MET:HG2	2.05	0.57
1:D:192:ASN:HD22	1:D:192:ASN:H	1.51	0.57
1:H:124:ARG:NH1	1:H:230:ALA:O	2.38	0.57
1:E:164:ARG:HD2	1:F:154:ASN:OD1	2.05	0.57
1:C:225:ALA:HB1	1:D:251:LEU:HD13	1.87	0.57
1:E:132:ILE:HD12	1:E:249:SER:HA	1.86	0.57
1:A:89:GLU:OE1	1:A:89:GLU:N	2.31	0.57
1:B:126:GLU:HG2	1:B:127:ASN:OD1	2.05	0.57
1:E:83:PRO:C	1:E:85:SER:N	2.58	0.57
1:B:28:VAL:CG1	1:B:355:LEU:HD13	2.35	0.57
1:D:261:MET:HE3	1:D:294:LEU:CB	2.35	0.57
1:G:319:LYS:HA	1:G:319:LYS:HE2	1.86	0.57
1:D:21:ALA:HB2	1:D:296:THR:HG22	1.86	0.57
1:D:324:VAL:HG21	1:D:351:LEU:HD23	1.86	0.57
1:F:18:MET:O	1:F:18:MET:HE3	2.05	0.57
1:D:167:ILE:O	1:D:170:ILE:HG22	2.05	0.57
1:B:55:LEU:HD11	1:B:60:LEU:CD2	2.33	0.56
1:C:67:ASP:O	1:C:68:ALA:CB	2.52	0.56
1:A:163:THR:HG23	1:A:166:GLU:OE1	2.04	0.56
1:F:105:LEU:HD13	1:F:133:VAL:HG22	1.86	0.56
1:G:3:MET:HE3	1:G:5:LEU:HD21	1.85	0.56
1:A:96:ARG:NH1	1:A:96:ARG:HG2	2.20	0.56
1:C:84:ALA:HA	1:C:87:ARG:CD	2.31	0.56
1:E:69:ILE:CG2	1:E:274:MET:HA	2.36	0.56
1:D:2:LYS:CE	1:D:2:LYS:N	2.60	0.56
1:E:132:ILE:HD11	1:E:252:ALA:HB2	1.86	0.56
1:D:79:TRP:O	1:D:87:ARG:HG2	2.05	0.56
1:G:177:LEU:HD22	1:G:181:ARG:HG3	1.88	0.56
1:C:158:ASP:HB2	1:D:160:LEU:HB3	1.87	0.56
1:A:135:GLU:CD	1:A:137:THR:H	2.08	0.56
1:C:41:ALA:HB1	1:C:59:THR:HG23	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:176:GLN:O	1:C:179:GLN:HB2	2.06	0.56
1:D:99:MET:HE3	1:D:272:PHE:HZ	1.71	0.56
1:G:105:LEU:HD23	1:G:107:PRO:HD3	1.88	0.56
1:A:141:TYR:CB	1:A:242:ASN:HD21	2.19	0.56
1:A:191:ALA:HB2	1:A:201:ARG:HE	1.71	0.56
1:A:124:ARG:NE	1:B:119:PRO:HA	2.20	0.56
1:E:6:ALA:CB	1:E:62:ILE:HD11	2.36	0.56
1:B:2:LYS:HB3	1:B:2:LYS:HZ2	1.71	0.56
1:D:247:ILE:C	1:D:247:ILE:HD12	2.25	0.56
1:E:69:ILE:HG23	1:E:274:MET:HA	1.87	0.56
1:A:275:TYR:CZ	1:A:303:MET:HA	2.40	0.56
1:F:177:LEU:O	1:F:181:ARG:HG3	2.06	0.56
1:G:123:GLU:H	1:G:123:GLU:CD	2.09	0.56
1:E:177:LEU:HD22	1:E:181:ARG:HD2	1.87	0.55
1:C:285:ILE:CG1	1:C:290:LYS:HE3	2.36	0.55
1:B:122:ARG:HB2	1:B:122:ARG:NH1	2.21	0.55
1:C:76:GLY:HA3	1:C:79:TRP:CZ3	2.41	0.55
1:C:336:VAL:HG22	1:C:339:GLY:HA2	1.89	0.55
1:D:342:VAL:HB	1:D:346:GLU:HB3	1.89	0.55
1:C:192:ASN:H	1:C:192:ASN:ND2	2.03	0.55
1:E:271:ARG:NH1	1:E:271:ARG:HG3	2.21	0.55
1:C:256:THR:C	1:C:258:SER:H	2.07	0.55
1:A:140:LEU:HD13	1:A:160:LEU:HB2	1.88	0.55
1:E:96:ARG:HG3	1:E:101:LEU:HD12	1.88	0.55
1:E:241:GLU:OE1	1:E:243:MET:HB3	2.06	0.55
1:B:150:GLY:CA	1:B:153:GLU:H	2.19	0.55
1:F:298:LEU:O	1:F:301:ALA:HB3	2.07	0.55
1:G:18:MET:HA	1:G:18:MET:CE	2.37	0.55
1:E:58:GLU:O	1:E:62:ILE:HG22	2.07	0.55
1:G:158:ASP:HB2	1:H:160:LEU:HB3	1.88	0.55
1:B:2:LYS:CD	1:B:35:GLU:HB3	2.35	0.55
1:C:151:PRO:O	1:C:153:GLU:N	2.39	0.55
1:E:105:LEU:HD12	1:E:105:LEU:N	2.21	0.55
1:E:84:ALA:HA	1:E:87:ARG:CG	2.37	0.55
1:H:18:MET:O	1:H:22:ILE:HG13	2.07	0.55
1:E:167:ILE:HG23	1:E:200:TRP:CE3	2.42	0.55
1:F:27:THR:HG21	1:F:352:ILE:CG2	2.31	0.55
1:E:80:ASP:C	1:E:87:ARG:HH12	2.09	0.55
1:E:259:LEU:C	1:E:261:MET:H	2.09	0.55
1:A:1:MET:HB2	1:A:2:LYS:HZ2	1.72	0.55
1:G:3:MET:HE2	1:G:5:LEU:HD11	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:41:ALA:HB2	1:F:62:ILE:HD12	1.88	0.55
1:H:167:ILE:HG23	1:H:200:TRP:CE3	2.42	0.55
1:C:141:TYR:HB2	1:C:242:ASN:ND2	2.21	0.55
1:A:310:LEU:HD12	1:A:313:GLU:OE2	2.06	0.55
1:A:1:MET:HB2	1:A:2:LYS:NZ	2.22	0.55
1:D:207:THR:HA	1:D:210:LYS:HG3	1.89	0.55
1:C:23:ARG:NH2	1:C:352:ILE:HD12	2.22	0.55
1:A:353:GLU:O	1:A:356:ASN:ND2	2.40	0.55
1:F:77:PRO:HD2	3:F:381:HOH:O	2.07	0.55
1:D:259:LEU:HA	1:D:262:LEU:HG	1.87	0.54
1:G:259:LEU:C	1:G:259:LEU:HD12	2.27	0.54
1:B:244:PHE:O	1:B:248:LEU:HG	2.07	0.54
1:B:259:LEU:O	1:B:261:MET:N	2.40	0.54
1:G:163:THR:OG1	1:G:166:GLU:HG3	2.08	0.54
1:E:292:ASN:ND2	1:E:334:LEU:HD11	2.22	0.54
1:D:105:LEU:CD2	1:D:133:VAL:HG22	2.37	0.54
1:F:191:ALA:HB3	1:F:201:ARG:NH2	2.23	0.54
1:A:96:ARG:HG2	1:A:96:ARG:HH11	1.72	0.54
1:H:113:THR:OG1	1:H:336:VAL:HG13	2.06	0.54
1:A:325:LEU:HD21	1:A:334:LEU:HD13	1.89	0.54
1:B:285:ILE:HD11	1:B:290:LYS:HB2	1.88	0.54
1:B:84:ALA:HA	1:B:87:ARG:HD2	1.88	0.54
1:H:339:GLY:HA3	3:H:1023:HOH:O	2.08	0.54
1:E:288:GLN:HB3	1:E:290:LYS:HE3	1.89	0.54
1:H:24:VAL:O	1:H:28:VAL:HG23	2.07	0.54
1:G:8:LEU:CB	1:G:71:LEU:HD12	2.35	0.54
1:C:55:LEU:HD11	1:C:60:LEU:HD23	1.88	0.54
1:D:281:SER:O	1:D:282:ALA:C	2.45	0.54
1:C:122:ARG:O	1:C:126:GLU:HB2	2.07	0.54
1:A:148:ARG:NH2	1:B:199:MET:HA	2.22	0.54
1:F:10:GLY:O	1:F:15:PRO:HD3	2.07	0.54
1:B:39:GLU:CD	1:B:62:ILE:HG23	2.28	0.54
1:E:6:ALA:HB2	1:E:62:ILE:HD11	1.90	0.54
1:F:132:ILE:HG21	1:F:249:SER:OG	2.08	0.54
1:D:170:ILE:HG23	1:D:171:ILE:N	2.23	0.54
1:A:124:ARG:HD3	1:B:119:PRO:HB3	1.90	0.54
1:A:5:LEU:HD12	1:A:38:PHE:CE1	2.43	0.54
1:F:28:VAL:HG21	1:F:317:ILE:HD11	1.88	0.54
1:E:134:ARG:HG3	1:E:245:GLY:HA3	1.89	0.54
1:A:84:ALA:HA	1:A:87:ARG:HD3	1.89	0.54
1:E:129:ASP:OD1	1:E:181:ARG:NH2	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:241:GLU:HG2	1:D:244:PHE:CD2	2.43	0.54
1:A:141:TYR:HE1	1:A:243:MET:SD	2.31	0.54
1:F:28:VAL:HG21	1:F:317:ILE:CD1	2.38	0.54
1:C:356:ASN:C	1:C:356:ASN:ND2	2.58	0.54
1:H:192:ASN:N	1:H:192:ASN:HD22	2.05	0.54
1:D:38:PHE:N	1:D:38:PHE:CD1	2.76	0.54
1:H:302:LEU:HD22	1:H:306:TYR:HE2	1.72	0.54
1:D:2:LYS:CB	1:D:35:GLU:HB3	2.38	0.53
1:B:259:LEU:CG	1:B:260:GLY:H	2.21	0.53
1:F:130:LEU:HD13	1:F:132:ILE:CD1	2.37	0.53
1:D:177:LEU:HD22	1:D:306:TYR:CE1	2.42	0.53
1:A:54:PRO:O	1:A:91:GLY:HA3	2.08	0.53
1:D:25:LEU:HD23	1:D:300:ALA:HB1	1.90	0.53
1:D:122:ARG:O	1:D:126:GLU:HB2	2.07	0.53
1:G:167:ILE:HD12	1:G:200:TRP:CE3	2.42	0.53
1:E:62:ILE:HG13	1:E:63:CYS:N	2.23	0.53
1:E:82:ASN:HB3	1:E:86:LEU:HB2	1.89	0.53
1:B:296:THR:O	1:B:299:SER:HB3	2.07	0.53
1:C:69:ILE:HB	1:C:274:MET:HG3	1.90	0.53
1:A:342:VAL:HB	1:A:346:GLU:HG2	1.91	0.53
1:D:58:GLU:OE1	1:D:58:GLU:N	2.42	0.53
1:E:48:ILE:CD1	1:E:86:LEU:O	2.53	0.53
1:G:129:ASP:O	1:G:182:ARG:NH2	2.42	0.53
1:H:14:GLY:N	1:H:15:PRO:HD2	2.24	0.53
1:B:292:ASN:OD1	1:B:294:LEU:HB2	2.09	0.53
1:C:31:ASN:ND2	1:C:312:LYS:NZ	2.57	0.53
1:H:27:THR:HG21	1:H:352:ILE:HG23	1.91	0.53
1:E:87:ARG:HB3	1:E:89:GLU:OE1	2.09	0.53
1:H:47:ALA:CB	1:H:56:PRO:HD3	2.37	0.53
1:E:189:ASP:HB2	1:E:197:SER:OG	2.09	0.53
1:G:261:MET:SD	1:G:334:LEU:HD21	2.49	0.53
1:G:152:GLY:O	1:G:153:GLU:C	2.47	0.53
1:F:129:ASP:O	1:F:182:ARG:NH2	2.42	0.53
1:D:303:MET:O	1:D:307:SER:HB2	2.09	0.53
1:E:117:ALA:HB2	1:E:335:GLN:HB2	1.91	0.53
1:F:125:VAL:HG11	1:F:256:THR:HA	1.90	0.53
1:H:160:LEU:HD12	1:H:160:LEU:C	2.29	0.53
1:C:39:GLU:CD	1:C:62:ILE:HG23	2.29	0.53
1:H:293:PRO:HD3	1:H:344:THR:HG23	1.91	0.53
1:A:337:ALA:C	1:A:339:GLY:N	2.63	0.53
1:G:141:TYR:HE1	1:G:243:MET:SD	2.32	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:328:GLY:O	1:D:339:GLY:HA2	2.07	0.53
1:B:312:LYS:HB3	1:B:313:GLU:OE1	2.09	0.53
1:B:275:TYR:CD1	1:B:275:TYR:N	2.77	0.53
1:D:295:GLY:O	1:D:299:SER:HB2	2.09	0.53
1:A:7:VAL:HG12	1:A:9:PRO:HD3	1.90	0.53
1:B:28:VAL:HG13	1:B:355:LEU:HD13	1.90	0.52
1:H:105:LEU:HD22	1:H:133:VAL:HG22	1.91	0.52
1:G:5:LEU:HD12	1:G:38:PHE:CE1	2.44	0.52
1:C:175:PHE:HZ	1:C:216:LEU:HD22	1.74	0.52
1:F:114:LEU:HD21	1:F:334:LEU:HD23	1.89	0.52
1:E:285:ILE:O	1:E:285:ILE:HG22	2.09	0.52
1:A:11:ASP:OD2	1:A:45:GLY:N	2.42	0.52
1:E:266:SER:O	1:E:267:LEU:HD23	2.09	0.52
1:B:105:LEU:HD22	1:B:133:VAL:HG22	1.91	0.52
1:B:255:ILE:HD12	1:B:256:THR:N	2.25	0.52
1:F:82:ASN:O	1:F:87:ARG:HD2	2.09	0.52
1:C:47:ALA:HB1	1:C:56:PRO:CG	2.40	0.52
1:H:125:VAL:HG21	1:H:256:THR:HA	1.90	0.52
1:A:45:GLY:HA3	1:A:79:TRP:CZ3	2.44	0.52
1:E:275:TYR:CE2	1:E:303:MET:HA	2.43	0.52
1:B:293:PRO:O	1:B:297:VAL:HG23	2.10	0.52
1:C:255:ILE:O	1:C:256:THR:HG23	2.09	0.52
1:D:155:GLU:HG2	1:D:156:VAL:N	2.22	0.52
1:G:94:GLY:O	1:G:98:GLU:HB2	2.10	0.52
1:A:177:LEU:O	1:A:181:ARG:HG3	2.09	0.52
1:D:59:THR:HA	1:D:62:ILE:HD12	1.92	0.52
1:C:74:VAL:HG11	1:C:92:LEU:HD11	1.91	0.52
1:G:179:GLN:NE2	1:G:213:ASP:OD2	2.38	0.52
1:B:8:LEU:HD23	1:B:43:ILE:HG13	1.91	0.52
1:G:264:SER:HB3	1:G:276:GLU:O	2.09	0.52
1:A:216:LEU:HD12	1:A:217:SER:N	2.25	0.52
1:G:285:ILE:CG2	1:G:290:LYS:HD2	2.40	0.52
1:B:156:VAL:HG22	1:B:157:VAL:N	2.25	0.52
1:A:192:ASN:C	1:A:192:ASN:HD22	2.12	0.52
1:F:4:LYS:HG2	1:F:67:ASP:OD2	2.10	0.52
1:F:7:VAL:HB	1:F:40:ASN:CB	2.38	0.52
1:F:4:LYS:HE2	1:F:67:ASP:OD2	2.10	0.52
1:C:34:HIS:HE1	1:C:313:GLU:OE2	1.93	0.52
1:D:285:ILE:HD12	1:D:290:LYS:HB2	1.90	0.52
1:G:346:GLU:HA	1:G:346:GLU:OE1	2.10	0.52
1:H:60:LEU:O	1:H:64:ARG:HG3	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:8:LEU:HB2	1:C:71:LEU:HD12	1.91	0.52
1:F:42:LEU:H	1:F:42:LEU:HD12	1.74	0.52
1:G:24:VAL:CG1	1:G:317:ILE:HD12	2.40	0.52
1:B:192:ASN:H	1:B:192:ASN:ND2	2.08	0.51
1:E:141:TYR:HB2	1:E:242:ASN:ND2	2.24	0.51
1:E:191:ALA:HA	1:E:197:SER:HB3	1.92	0.51
1:C:55:LEU:HD11	1:C:60:LEU:HD21	1.91	0.51
1:A:18:MET:O	1:A:22:ILE:HG12	2.10	0.51
1:A:262:LEU:HB2	1:A:278:VAL:HB	1.92	0.51
1:H:60:LEU:HD13	1:H:98:GLU:HG2	1.91	0.51
1:A:61:ASP:HA	1:A:64:ARG:HD2	1.91	0.51
1:A:275:TYR:CE2	1:A:303:MET:HA	2.45	0.51
1:F:285:ILE:CG2	1:F:285:ILE:O	2.58	0.51
1:G:113:THR:HG21	1:G:326:GLN:HA	1.92	0.51
1:H:261:MET:SD	1:H:334:LEU:HD11	2.51	0.51
1:C:206:GLU:C	1:C:208:ALA:H	2.14	0.51
1:C:18:MET:CE	1:C:70:LEU:HD22	2.41	0.51
1:F:324:VAL:HG21	1:F:351:LEU:HD23	1.91	0.51
1:F:107:PRO:HG2	1:F:302:LEU:HD21	1.92	0.51
1:H:114:LEU:HD13	1:H:334:LEU:HD22	1.92	0.51
1:E:251:LEU:O	1:E:254:VAL:HG22	2.10	0.51
1:B:94:GLY:O	1:B:97:LYS:HG2	2.10	0.51
1:C:31:ASN:HD21	1:C:312:LYS:HZ2	1.57	0.51
1:H:254:VAL:HG23	1:H:255:ILE:N	2.24	0.51
1:F:106:ARG:CB	1:F:106:ARG:HH11	2.18	0.51
1:C:7:VAL:C	1:C:8:LEU:HD12	2.30	0.51
1:F:57:GLU:CD	1:F:60:LEU:HD12	2.31	0.51
1:B:95:LEU:HA	1:B:98:GLU:HB2	1.93	0.51
1:D:190:LYS:HD2	1:D:220:LEU:HD22	1.93	0.51
1:G:126:GLU:O	1:G:127:ASN:CB	2.59	0.51
1:G:355:LEU:O	1:G:356:ASN:OD1	2.29	0.51
1:F:101:LEU:HD13	1:F:266:SER:HB2	1.92	0.51
1:A:305:ARG:HG3	1:A:305:ARG:HH11	1.75	0.51
1:D:2:LYS:H	1:D:2:LYS:CD	2.25	0.50
1:C:320:ALA:O	1:C:324:VAL:HG23	2.11	0.50
1:A:336:VAL:HG23	1:A:339:GLY:HA3	1.92	0.50
1:C:259:LEU:HA	1:C:262:LEU:HG	1.94	0.50
1:B:95:LEU:O	1:B:99:MET:HG2	2.10	0.50
1:E:188:VAL:CG1	1:E:221:VAL:HA	2.41	0.50
1:B:255:ILE:HD12	1:B:256:THR:HG23	1.92	0.50
1:A:18:MET:HE3	1:A:21:ALA:HB3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:124:ARG:HH11	1:D:124:ARG:HG2	1.75	0.50
1:B:84:ALA:HA	1:B:87:ARG:CD	2.41	0.50
1:F:47:ALA:HB1	1:F:56:PRO:HD3	1.93	0.50
1:G:226:MET:SD	1:H:250:ASP:HB3	2.50	0.50
1:C:9:PRO:HG2	1:C:10:GLY:H	1.76	0.50
1:B:189:ASP:OD1	1:B:201:ARG:NH2	2.44	0.50
1:C:206:GLU:O	1:C:207:THR:CB	2.60	0.50
1:B:275:TYR:CZ	1:B:303:MET:HA	2.47	0.50
1:D:296:THR:O	1:D:299:SER:HB3	2.11	0.50
1:D:57:GLU:HG2	1:D:60:LEU:HD12	1.93	0.50
1:D:350:ARG:O	1:D:353:GLU:HB3	2.12	0.50
1:H:77:PRO:HA	1:H:80:ASP:OD1	2.12	0.50
1:A:228:LEU:HD12	1:A:251:LEU:HD12	1.91	0.50
1:C:120:LEU:HD23	1:D:120:LEU:HD23	1.92	0.50
1:B:39:GLU:OE1	1:B:62:ILE:HG12	2.11	0.50
1:H:122:ARG:HD2	2:H:1002:SO4:O3	2.12	0.50
1:F:114:LEU:HD11	1:F:334:LEU:HD23	1.94	0.50
1:C:229:ILE:HD11	1:D:229:ILE:HD11	1.93	0.50
1:B:245:GLY:C	1:B:247:ILE:N	2.65	0.50
1:D:23:ARG:HE	1:D:348:THR:HG21	1.77	0.50
1:C:192:ASN:HD22	1:C:192:ASN:H	1.59	0.50
1:G:337:ALA:C	1:G:339:GLY:H	2.14	0.50
1:B:17:VAL:CG1	1:B:291:ALA:HB1	2.41	0.50
1:G:96:ARG:HD2	1:G:136:LEU:HD13	1.94	0.50
1:E:350:ARG:O	1:E:353:GLU:HB3	2.12	0.50
1:H:41:ALA:HB1	1:H:59:THR:HG23	1.93	0.50
1:D:252:ALA:O	1:D:255:ILE:HG12	2.11	0.50
1:C:347:LEU:O	1:C:351:LEU:HB2	2.12	0.50
1:A:177:LEU:HD22	1:A:181:ARG:HD2	1.94	0.50
1:H:64:ARG:HG2	1:H:99:MET:CE	2.42	0.50
1:B:150:GLY:HA3	1:B:153:GLU:H	1.77	0.50
1:D:132:ILE:HG21	1:D:249:SER:OG	2.11	0.50
1:D:98:GLU:HA	1:D:98:GLU:OE1	2.12	0.50
1:C:39:GLU:OE2	1:C:62:ILE:HD12	2.11	0.50
1:D:63:CYS:HB3	1:D:99:MET:HE1	1.94	0.50
1:E:294:LEU:HD13	1:E:321:VAL:HG13	1.93	0.50
1:D:192:ASN:N	1:D:192:ASN:HD22	2.10	0.49
1:H:113:THR:HG21	1:H:325:LEU:HB3	1.94	0.49
1:E:141:TYR:OH	1:F:190:LYS:HE2	2.12	0.49
1:F:8:LEU:N	1:F:8:LEU:HD12	2.27	0.49
1:H:130:LEU:C	1:H:130:LEU:HD12	2.32	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:331:THR:O	1:C:331:THR:HG22	2.12	0.49
1:C:349:ASP:C	1:C:351:LEU:H	2.15	0.49
1:C:43:ILE:CG1	1:C:44:GLY:N	2.72	0.49
1:C:271:ARG:HG3	1:C:271:ARG:NH2	2.26	0.49
1:G:43:ILE:HG12	1:G:44:GLY:N	2.27	0.49
1:B:255:ILE:HD12	1:B:255:ILE:C	2.33	0.49
1:G:331:THR:HG23	1:G:347:LEU:HG	1.94	0.49
1:C:227:GLN:HA	1:C:227:GLN:NE2	2.28	0.49
1:B:42:LEU:HD12	1:B:42:LEU:N	2.27	0.49
1:F:291:ALA:O	1:F:293:PRO:HD3	2.12	0.49
1:A:330:CYS:HB2	1:A:334:LEU:HB2	1.94	0.49
1:G:60:LEU:HD22	1:G:98:GLU:HG2	1.93	0.49
1:C:119:PRO:HA	1:D:124:ARG:NE	2.27	0.49
1:E:331:THR:HB	1:E:333:ASP:OD1	2.13	0.49
1:G:180:ILE:HD12	1:G:180:ILE:C	2.33	0.49
1:H:24:VAL:HG13	1:H:355:LEU:HD11	1.94	0.49
1:F:122:ARG:O	1:F:126:GLU:CG	2.61	0.49
1:A:190:LYS:H	1:A:197:SER:CB	2.25	0.49
1:H:177:LEU:O	1:H:181:ARG:HG3	2.11	0.49
1:F:337:ALA:O	1:F:339:GLY:N	2.45	0.49
1:A:29:LEU:HD22	1:A:34:HIS:HB2	1.95	0.49
1:B:122:ARG:CB	1:B:122:ARG:HH11	2.25	0.49
1:H:268:ARG:HE	1:H:272:PHE:HB3	1.78	0.49
1:C:141:TYR:CD1	1:D:193:VAL:HG11	2.47	0.49
1:C:252:ALA:O	1:C:255:ILE:HG12	2.13	0.49
1:A:115:LEU:HD12	1:A:122:ARG:CZ	2.42	0.49
1:A:184:LYS:HB2	1:A:236:ASP:HB3	1.95	0.49
1:A:1:MET:N	1:A:34:HIS:CD2	2.80	0.49
1:G:294:LEU:HD12	1:G:334:LEU:HD11	1.93	0.49
1:A:172:GLU:O	1:A:176:GLN:HG2	2.13	0.49
1:B:340:LYS:HZ2	1:C:338:ASN:ND2	2.09	0.49
1:B:53:THR:CG2	1:B:56:PRO:HA	2.43	0.49
1:B:190:LYS:CE	1:B:192:ASN:HD21	2.23	0.49
1:C:285:ILE:HG13	1:C:290:LYS:HE3	1.93	0.49
1:G:317:ILE:O	1:G:321:VAL:HG23	2.13	0.49
1:E:148:ARG:HD3	1:F:199:MET:HE2	1.94	0.49
1:E:181:ARG:NH1	1:E:236:ASP:OD1	2.46	0.49
1:F:323:ASP:O	1:F:327:ASP:OD1	2.31	0.49
1:A:28:VAL:O	1:A:31:ASN:HB2	2.12	0.49
1:G:92:LEU:HD12	1:G:92:LEU:O	2.13	0.49
1:E:140:LEU:HD11	1:E:158:ASP:HB3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:254:VAL:HG13	1:B:226:MET:HE3	1.95	0.49
1:E:277:PRO:HB2	1:E:279:HIS:CD2	2.47	0.49
1:B:3:MET:O	1:B:36:ALA:HA	2.13	0.49
1:A:139:GLY:HA2	1:A:160:LEU:CD1	2.36	0.48
1:B:264:SER:HB3	1:B:276:GLU:O	2.13	0.48
1:D:29:LEU:HD13	1:D:36:ALA:HB2	1.95	0.48
1:A:181:ARG:NH1	1:A:236:ASP:OD1	2.46	0.48
1:H:170:ILE:CG2	1:H:171:ILE:N	2.76	0.48
1:D:331:THR:HG23	1:D:347:LEU:HD22	1.95	0.48
1:H:219:MET:HE1	1:H:227:GLN:HG3	1.94	0.48
1:H:13:ILE:O	1:H:17:VAL:HG22	2.13	0.48
1:H:198:ARG:O	1:H:202:GLU:HG3	2.13	0.48
1:F:104:ASN:ND2	1:F:106:ARG:HH12	1.95	0.48
1:D:25:LEU:HD11	1:D:304:LEU:HD21	1.95	0.48
1:H:332:GLY:O	1:H:333:ASP:C	2.51	0.48
1:B:149:ARG:NH1	1:B:149:ARG:HG2	2.28	0.48
1:H:118:SER:OG	1:H:255:ILE:O	2.23	0.48
1:H:223:SER:O	1:H:227:GLN:HG2	2.14	0.48
1:C:164:ARG:NH1	1:C:203:ILE:HD11	2.28	0.48
1:D:27:THR:OG1	1:D:352:ILE:HG23	2.13	0.48
1:C:63:CYS:SG	1:C:69:ILE:HD11	2.53	0.48
1:C:10:GLY:HA3	1:C:73:ALA:O	2.13	0.48
1:C:311:GLU:HG2	1:C:312:LYS:H	1.78	0.48
1:E:80:ASP:C	1:E:87:ARG:NH1	2.67	0.48
1:A:336:VAL:HG21	1:A:339:GLY:HA3	1.95	0.48
1:A:71:LEU:HD21	1:A:92:LEU:HD21	1.95	0.48
1:A:84:ALA:HA	1:A:87:ARG:HD2	1.93	0.48
1:B:176:GLN:O	1:B:179:GLN:HB3	2.13	0.48
1:E:90:LYS:HA	1:E:90:LYS:CE	2.41	0.48
1:H:313:GLU:N	1:H:313:GLU:OE2	2.47	0.48
1:A:337:ALA:C	1:A:339:GLY:H	2.16	0.48
1:B:83:PRO:O	1:B:85:SER:N	2.47	0.48
1:C:122:ARG:O	1:C:124:ARG:N	2.46	0.48
1:G:281:SER:O	1:G:282:ALA:C	2.52	0.48
1:G:275:TYR:CZ	1:G:303:MET:HA	2.48	0.48
1:B:251:LEU:O	1:B:254:VAL:HG22	2.13	0.48
1:E:235:PHE:CG	1:E:238:ILE:HD11	2.49	0.48
1:F:7:VAL:C	1:F:8:LEU:HD12	2.34	0.48
1:D:99:MET:CE	1:D:272:PHE:HZ	2.25	0.48
1:G:167:ILE:O	1:G:170:ILE:HG22	2.14	0.48
1:G:342:VAL:HB	1:G:346:GLU:HB3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:350:ARG:O	1:C:354:LYS:HG3	2.14	0.48
1:A:2:LYS:HD3	1:A:2:LYS:H	1.76	0.48
1:E:255:ILE:C	1:E:255:ILE:HD12	2.34	0.48
1:E:145:PRO:HB2	1:E:147:GLU:OE1	2.13	0.48
1:F:304:LEU:HD22	1:F:310:LEU:HD12	1.95	0.48
1:F:331:THR:C	1:F:333:ASP:H	2.17	0.48
1:H:315:ALA:HA	1:H:318:GLU:OE1	2.14	0.48
1:E:312:LYS:CA	1:E:312:LYS:HE2	2.41	0.48
1:C:199:MET:HE3	1:D:148:ARG:HD3	1.96	0.48
1:B:259:LEU:HD13	1:B:262:LEU:HD12	1.96	0.47
1:B:71:LEU:CD2	1:B:92:LEU:HD11	2.39	0.47
1:E:120:LEU:HD21	1:E:255:ILE:HG22	1.96	0.47
1:H:164:ARG:HH11	1:H:164:ARG:HG2	1.79	0.47
1:A:241:GLU:OE1	1:A:243:MET:HB3	2.14	0.47
1:D:172:GLU:O	1:D:175:PHE:HB2	2.14	0.47
1:G:143:GLY:HA3	1:G:159:THR:O	2.14	0.47
1:E:226:MET:HE2	1:F:254:VAL:HG13	1.94	0.47
1:E:125:VAL:O	1:E:128:VAL:HG23	2.13	0.47
1:D:189:ASP:HB2	1:D:197:SER:HB3	1.95	0.47
1:E:21:ALA:O	1:E:25:LEU:HB2	2.14	0.47
1:B:201:ARG:HG3	1:B:218:HIS:CE1	2.48	0.47
1:D:176:GLN:O	1:D:179:GLN:HB3	2.14	0.47
1:C:285:ILE:HG12	1:C:290:LYS:HE3	1.96	0.47
1:A:330:CYS:SG	1:A:336:VAL:CG2	3.02	0.47
1:F:131:VAL:HG23	1:F:181:ARG:NH1	2.29	0.47
1:G:18:MET:O	1:G:18:MET:HE2	2.13	0.47
1:G:191:ALA:N	1:G:197:SER:HB3	2.30	0.47
1:D:356:ASN:O	1:D:357:ASN:OD1	2.31	0.47
1:C:256:THR:C	1:C:258:SER:N	2.67	0.47
1:C:1:MET:H3	1:C:34:HIS:CD2	2.30	0.47
1:C:259:LEU:HA	1:C:262:LEU:CD1	2.44	0.47
1:F:130:LEU:C	1:F:130:LEU:HD12	2.35	0.47
1:D:201:ARG:HG3	1:D:218:HIS:CE1	2.48	0.47
1:C:29:LEU:C	1:C:31:ASN:N	2.68	0.47
1:B:28:VAL:HG11	1:B:317:ILE:CD1	2.43	0.47
1:H:114:LEU:CD1	1:H:334:LEU:HD22	2.43	0.47
1:B:192:ASN:ND2	1:B:192:ASN:N	2.61	0.47
1:H:12:GLY:O	1:H:15:PRO:HD2	2.15	0.47
1:D:1:MET:O	1:D:35:GLU:N	2.41	0.47
1:C:345:ILE:O	1:C:349:ASP:OD1	2.33	0.47
1:C:3:MET:O	1:C:36:ALA:HA	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:190:LYS:HE3	1:H:192:ASN:HD21	1.79	0.47
1:C:229:ILE:HD11	1:D:251:LEU:HD11	1.96	0.47
1:F:140:LEU:HD23	1:F:243:MET:HE2	1.96	0.47
1:C:120:LEU:CD2	1:D:120:LEU:HD23	2.44	0.47
1:H:125:VAL:HG21	1:H:255:ILE:O	2.14	0.47
1:D:349:ASP:O	1:D:350:ARG:C	2.53	0.47
1:A:331:THR:HG23	1:A:347:LEU:HD12	1.96	0.47
1:A:188:VAL:CG1	1:A:221:VAL:HA	2.45	0.47
1:C:349:ASP:C	1:C:351:LEU:N	2.67	0.47
1:C:47:ALA:HB1	1:C:56:PRO:CD	2.45	0.47
1:D:11:ASP:O	1:D:281:SER:HB2	2.15	0.47
1:A:7:VAL:C	1:A:8:LEU:HD12	2.36	0.47
1:E:30:ASP:C	1:E:32:ASP:H	2.18	0.47
1:E:1:MET:N	1:E:34:HIS:CD2	2.83	0.47
1:H:85:SER:HA	1:H:90:LYS:HD3	1.96	0.47
1:B:177:LEU:HD12	1:B:181:ARG:HD2	1.97	0.47
1:C:130:LEU:HD12	1:C:130:LEU:C	2.36	0.47
1:H:102:PHE:CE2	1:H:169:ARG:HD2	2.50	0.47
1:C:160:LEU:O	1:D:157:VAL:HA	2.15	0.47
1:A:82:ASN:HB2	1:A:83:PRO:CD	2.34	0.46
1:A:28:VAL:C	1:A:30:ASP:H	2.18	0.46
1:D:76:GLY:C	1:D:78:LYS:H	2.18	0.46
1:H:334:LEU:O	1:H:336:VAL:HG23	2.15	0.46
1:A:2:LYS:CD	1:A:2:LYS:H	2.29	0.46
1:B:54:PRO:HB2	1:B:91:GLY:HA3	1.97	0.46
1:A:3:MET:HE2	1:A:5:LEU:HD11	1.96	0.46
1:F:320:ALA:O	1:F:324:VAL:HG23	2.14	0.46
1:H:106:ARG:HB3	1:H:132:ILE:HB	1.96	0.46
1:A:187:SER:HB3	1:A:218:HIS:CE1	2.50	0.46
1:H:346:GLU:O	1:H:350:ARG:HG2	2.16	0.46
1:H:275:TYR:CZ	1:H:303:MET:HA	2.51	0.46
1:G:305:ARG:HH22	1:G:318:GLU:CD	2.17	0.46
1:C:351:LEU:O	1:C:355:LEU:HB2	2.16	0.46
1:F:167:ILE:HD12	1:F:200:TRP:CE3	2.50	0.46
1:B:330:CYS:O	1:B:341:VAL:HA	2.16	0.46
1:D:348:THR:O	1:D:351:LEU:HB2	2.15	0.46
1:G:26:LYS:HE2	1:G:38:PHE:CE2	2.50	0.46
1:G:3:MET:O	1:G:36:ALA:HA	2.15	0.46
1:A:303:MET:O	1:A:307:SER:HB2	2.15	0.46
1:D:124:ARG:NH1	1:D:124:ARG:HG2	2.31	0.46
1:A:28:VAL:O	1:A:31:ASN:CB	2.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:129:ASP:O	1:A:182:ARG:NH2	2.41	0.46
1:D:2:LYS:CA	1:D:35:GLU:HB3	2.46	0.46
1:C:320:ALA:HB2	1:C:355:LEU:HD13	1.98	0.46
1:B:303:MET:O	1:B:307:SER:HB3	2.15	0.46
1:G:54:PRO:HB2	1:G:91:GLY:HA3	1.96	0.46
1:E:148:ARG:HA	1:E:155:GLU:O	2.15	0.46
1:A:181:ARG:C	1:A:183:LYS:H	2.19	0.46
1:A:32:ASP:HB3	1:A:34:HIS:CE1	2.51	0.46
1:E:194:LEU:HB2	1:E:197:SER:HB2	1.98	0.46
1:C:189:ASP:OD1	1:C:201:ARG:NH2	2.48	0.46
1:E:81:HIS:CA	1:E:87:ARG:HH12	2.29	0.46
1:A:189:ASP:HB2	1:A:197:SER:CB	2.44	0.46
1:B:337:ALA:HB1	1:C:326:GLN:O	2.15	0.46
1:B:255:ILE:CD1	1:B:256:THR:HG23	2.46	0.46
1:A:175:PHE:CZ	1:A:216:LEU:HD22	2.51	0.46
1:F:176:GLN:O	1:F:179:GLN:HB2	2.15	0.46
1:D:221:VAL:HG21	1:D:244:PHE:CD1	2.51	0.46
1:A:231:ASN:O	1:A:234:GLN:HG2	2.15	0.46
1:F:139:GLY:HA2	1:F:160:LEU:HD12	1.97	0.46
1:B:140:LEU:HD12	1:B:159:THR:C	2.36	0.46
1:E:8:LEU:HB3	1:E:71:LEU:HD12	1.96	0.46
1:G:348:THR:HG22	1:G:352:ILE:HD13	1.97	0.46
1:D:2:LYS:O	1:D:2:LYS:HE2	2.15	0.46
1:F:191:ALA:HB3	1:F:201:ARG:HH21	1.79	0.46
1:F:339:GLY:O	1:F:340:LYS:HD2	2.15	0.46
1:H:333:ASP:HB2	3:H:1018:HOH:O	2.16	0.46
1:F:258:SER:OG	1:F:262:LEU:HD21	2.16	0.46
1:B:164:ARG:O	1:B:168:GLU:HG3	2.15	0.46
1:A:195:GLU:HA	1:A:198:ARG:HD2	1.98	0.46
1:G:104:ASN:HD21	1:G:106:ARG:HD3	1.81	0.46
1:B:63:CYS:HB3	1:B:69:ILE:HD11	1.98	0.46
1:D:12:GLY:O	1:D:15:PRO:HD2	2.16	0.46
1:D:256:THR:C	1:D:258:SER:N	2.64	0.46
1:H:4:LYS:HG3	1:H:67:ASP:OD1	2.16	0.46
1:A:3:MET:HE3	1:A:5:LEU:HD21	1.97	0.46
1:B:95:LEU:HD11	1:B:274:MET:SD	2.56	0.46
1:C:42:LEU:HD21	1:C:50:GLU:OE2	2.16	0.46
1:G:313:GLU:OE1	1:G:313:GLU:N	2.46	0.46
1:A:176:GLN:H	1:A:176:GLN:HG2	1.51	0.46
1:A:175:PHE:HZ	1:A:216:LEU:HD22	1.80	0.46
1:B:95:LEU:HD12	1:B:95:LEU:C	2.36	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:311:GLU:O	1:B:312:LYS:C	2.53	0.45
1:A:55:LEU:HG	1:A:55:LEU:O	2.16	0.45
1:C:288:GLN:CB	1:C:290:LYS:HE2	2.46	0.45
1:B:34:HIS:NE2	1:B:313:GLU:OE2	2.47	0.45
1:G:320:ALA:HB2	1:G:355:LEU:HD13	1.97	0.45
1:E:275:TYR:N	1:E:275:TYR:CD1	2.84	0.45
1:E:8:LEU:O	1:E:71:LEU:HD12	2.16	0.45
1:E:154:ASN:HD22	1:E:154:ASN:N	2.15	0.45
1:F:352:ILE:HA	1:F:355:LEU:HD12	1.98	0.45
1:B:1:MET:HA	1:B:34:HIS:HA	1.97	0.45
1:B:106:ARG:O	1:B:131:VAL:HA	2.17	0.45
1:E:259:LEU:HD12	1:E:260:GLY:N	2.27	0.45
1:H:64:ARG:HG2	1:H:99:MET:HE3	1.97	0.45
1:D:69:ILE:HD11	1:D:272:PHE:CZ	2.51	0.45
1:D:73:ALA:HB1	1:D:281:SER:HB3	1.96	0.45
1:G:314:ALA:O	1:G:318:GLU:HG3	2.16	0.45
1:C:226:MET:HE3	1:D:250:ASP:O	2.16	0.45
1:C:299:SER:O	1:C:302:LEU:HB2	2.16	0.45
1:F:329:TYR:O	1:F:330:CYS:HB3	2.16	0.45
1:C:63:CYS:SG	1:C:69:ILE:CD1	3.04	0.45
1:F:43:ILE:CG1	1:F:44:GLY:H	2.27	0.45
1:B:281:SER:O	1:B:282:ALA:C	2.54	0.45
1:D:103:ALA:HB2	1:D:170:ILE:CD1	2.46	0.45
1:D:1:MET:O	1:D:34:HIS:HA	2.16	0.45
1:A:124:ARG:HH11	1:A:124:ARG:HG2	1.81	0.45
1:A:124:ARG:CD	1:B:119:PRO:HB3	2.46	0.45
1:H:165:GLU:O	1:H:169:ARG:HG2	2.17	0.45
1:C:292:ASN:OD1	1:C:294:LEU:HB2	2.16	0.45
1:G:2:LYS:HG3	1:G:35:GLU:HB2	1.98	0.45
1:E:103:ALA:HB2	1:E:170:ILE:CD1	2.46	0.45
1:C:210:LYS:HD2	1:C:211:TYR:CZ	2.50	0.45
1:F:177:LEU:HD22	1:F:181:ARG:HD2	1.99	0.45
1:C:227:GLN:HA	1:C:227:GLN:HE21	1.81	0.45
1:H:172:GLU:O	1:H:176:GLN:HG3	2.16	0.45
1:A:227:GLN:HA	1:A:227:GLN:NE2	2.31	0.45
1:F:125:VAL:O	1:F:127:ASN:N	2.50	0.45
1:B:1:MET:HB3	1:B:2:LYS:H	1.57	0.45
1:D:302:LEU:HD22	1:D:306:TYR:HE2	1.81	0.45
1:F:285:ILE:HD13	1:F:285:ILE:HA	1.83	0.45
1:H:146:SER:HA	1:H:157:VAL:O	2.17	0.45
1:G:190:LYS:HE3	1:G:192:ASN:HD21	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:313:GLU:O	1:B:317:ILE:HG12	2.15	0.45
1:G:163:THR:O	1:G:164:ARG:C	2.55	0.45
1:B:84:ALA:O	1:B:87:ARG:HG3	2.17	0.45
1:F:285:ILE:HG22	1:F:285:ILE:O	2.16	0.45
1:C:119:PRO:HA	1:D:124:ARG:HE	1.81	0.45
1:B:189:ASP:HB2	1:B:197:SER:HB3	1.99	0.45
1:A:196:SER:CB	1:B:158:ASP:OD2	2.65	0.45
1:D:130:LEU:HD12	1:D:130:LEU:C	2.37	0.45
1:A:47:ALA:HB1	1:A:56:PRO:HD3	1.99	0.45
1:C:287:GLY:O	1:C:289:GLY:N	2.49	0.45
1:E:259:LEU:C	1:E:261:MET:N	2.70	0.45
1:A:107:PRO:HA	1:A:130:LEU:O	2.17	0.45
1:F:99:MET:HG3	1:F:272:PHE:CE1	2.52	0.45
1:E:305:ARG:NH1	1:E:311:GLU:OE2	2.49	0.45
1:E:28:VAL:CG1	1:E:313:GLU:HB3	2.47	0.45
1:G:76:GLY:HA3	1:G:79:TRP:CZ3	2.52	0.45
1:A:177:LEU:CD2	1:A:181:ARG:HD2	2.46	0.45
1:D:258:SER:O	1:D:259:LEU:C	2.56	0.45
1:B:288:GLN:HB2	1:B:290:LYS:HG2	1.99	0.45
1:H:13:ILE:HG12	1:H:281:SER:O	2.17	0.45
1:D:24:VAL:HA	1:D:352:ILE:CD1	2.47	0.45
1:F:281:SER:O	1:F:282:ALA:C	2.56	0.45
1:F:39:GLU:O	1:F:39:GLU:HG2	2.17	0.45
1:D:181:ARG:HD3	1:D:236:ASP:OD1	2.17	0.45
1:C:342:VAL:HB	1:C:346:GLU:CB	2.47	0.44
1:E:140:LEU:HD23	1:E:243:MET:HE1	1.95	0.44
1:D:7:VAL:C	1:D:8:LEU:HD12	2.38	0.44
1:E:124:ARG:HH21	1:E:230:ALA:CA	2.30	0.44
1:B:150:GLY:HA2	1:B:153:GLU:H	1.82	0.44
1:D:175:PHE:CE2	1:D:207:THR:HB	2.52	0.44
1:B:189:ASP:CG	1:B:201:ARG:HH21	2.20	0.44
1:D:112:ALA:HA	1:D:115:LEU:HG	1.98	0.44
1:A:277:PRO:HB2	1:A:279:HIS:CD2	2.52	0.44
1:A:111:TYR:HB2	1:A:114:LEU:HD12	1.99	0.44
1:A:248:LEU:HA	1:A:248:LEU:HD23	1.81	0.44
1:B:86:LEU:HD23	1:B:86:LEU:C	2.37	0.44
1:C:47:ALA:HB1	1:C:56:PRO:HD3	1.99	0.44
1:E:182:ARG:NH2	1:E:235:PHE:O	2.49	0.44
1:F:43:ILE:CG1	1:F:44:GLY:N	2.80	0.44
1:A:49:ASP:OD2	1:A:78:LYS:NZ	2.45	0.44
1:A:147:GLU:HG2	1:A:148:ARG:O	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:229:ILE:HD13	1:B:255:ILE:CG2	2.47	0.44
1:C:110:ALA:HB2	1:C:128:VAL:HG12	1.98	0.44
1:H:148:ARG:NH1	1:H:153:GLU:OE1	2.42	0.44
1:B:179:GLN:OE1	1:B:211:TYR:HD2	2.00	0.44
1:B:261:MET:HE2	1:B:298:LEU:HD11	1.99	0.44
1:C:254:VAL:HG23	1:C:255:ILE:N	2.32	0.44
1:G:160:LEU:HD12	1:G:160:LEU:C	2.37	0.44
1:E:259:LEU:HG	1:E:260:GLY:N	2.33	0.44
1:C:60:LEU:O	1:C:64:ARG:HG2	2.18	0.44
1:A:228:LEU:CD1	1:A:251:LEU:HD12	2.47	0.44
1:E:303:MET:O	1:E:307:SER:HB2	2.17	0.44
1:C:122:ARG:C	1:C:124:ARG:N	2.70	0.44
1:H:350:ARG:HA	1:H:350:ARG:NE	2.32	0.44
1:F:275:TYR:CZ	1:F:303:MET:HA	2.53	0.44
1:C:316:ALA:O	1:C:319:LYS:HG3	2.17	0.44
1:F:334:LEU:HB2	1:F:336:VAL:CG2	2.48	0.44
1:D:2:LYS:N	1:D:2:LYS:CD	2.81	0.44
1:B:179:GLN:HE21	1:B:183:LYS:HZ1	1.61	0.44
1:E:177:LEU:O	1:E:180:ILE:HG12	2.17	0.44
1:A:53:THR:C	1:A:55:LEU:H	2.20	0.44
1:B:229:ILE:HD13	1:B:255:ILE:HG22	1.99	0.44
1:B:241:GLU:OE2	1:B:243:MET:HB3	2.17	0.44
1:G:202:GLU:O	1:G:206:GLU:HG3	2.18	0.44
1:B:142:PHE:CD1	1:B:142:PHE:N	2.85	0.44
1:B:79:TRP:C	1:B:81:HIS:H	2.21	0.44
1:F:192:ASN:H	1:F:192:ASN:HD22	1.65	0.44
1:D:56:PRO:HG2	1:D:59:THR:HB	2.00	0.44
1:F:140:LEU:HA	1:F:160:LEU:HA	1.98	0.44
1:H:105:LEU:C	1:H:107:PRO:HD3	2.37	0.44
1:C:99:MET:HE2	1:C:272:PHE:CE2	2.53	0.44
1:B:140:LEU:HA	1:B:159:THR:O	2.17	0.44
1:A:118:SER:HA	1:A:119:PRO:HD3	1.83	0.44
1:D:1:MET:CB	1:D:2:LYS:HZ3	2.10	0.44
1:H:140:LEU:HA	1:H:159:THR:O	2.18	0.44
1:A:163:THR:N	1:A:166:GLU:OE1	2.49	0.44
1:F:156:VAL:HG22	1:F:157:VAL:N	2.32	0.44
1:F:23:ARG:NH2	1:F:352:ILE:HD12	2.33	0.44
1:G:192:ASN:C	1:G:192:ASN:ND2	2.71	0.44
1:A:168:GLU:HG3	1:A:203:ILE:HG23	2.00	0.44
1:A:238:ILE:HG13	1:A:238:ILE:O	2.16	0.44
1:C:164:ARG:HH12	1:C:203:ILE:CD1	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:71:LEU:HD21	1:E:92:LEU:HD13	2.00	0.44
1:C:226:MET:HB3	1:D:254:VAL:HG11	2.00	0.44
1:E:107:PRO:HA	1:E:130:LEU:O	2.18	0.44
1:E:107:PRO:HG2	1:E:263:PRO:HG2	2.00	0.44
1:C:324:VAL:CG2	1:C:354:LYS:HD3	2.46	0.44
1:A:330:CYS:SG	1:A:336:VAL:HG21	2.57	0.44
1:A:8:LEU:CD1	1:A:41:ALA:HB3	2.48	0.44
1:B:272:PHE:CD1	1:B:272:PHE:C	2.90	0.44
1:A:328:GLY:O	1:A:340:LYS:N	2.47	0.44
1:E:179:GLN:O	1:E:179:GLN:HG3	2.17	0.44
1:A:2:LYS:HZ3	1:A:2:LYS:H	1.65	0.44
1:F:4:LYS:N	1:F:4:LYS:CD	2.74	0.44
1:D:139:GLY:C	1:D:160:LEU:HD12	2.38	0.44
1:A:47:ALA:O	1:A:51:ALA:HB3	2.18	0.44
1:G:52:GLY:O	1:G:53:THR:HG23	2.18	0.44
1:E:139:GLY:HA2	1:E:160:LEU:HD13	2.00	0.44
1:E:102:PHE:CE2	1:E:169:ARG:HD2	2.53	0.44
1:D:69:ILE:HD12	1:D:69:ILE:N	2.33	0.43
1:G:18:MET:HA	1:G:18:MET:HE3	1.98	0.43
1:B:177:LEU:O	1:B:181:ARG:HG3	2.17	0.43
1:A:202:GLU:O	1:A:203:ILE:C	2.56	0.43
1:A:190:LYS:HD2	1:A:190:LYS:HA	1.66	0.43
1:F:7:VAL:O	1:F:40:ASN:HB2	2.18	0.43
1:A:49:ASP:OD1	1:A:79:TRP:NE1	2.50	0.43
1:B:99:MET:HE2	1:B:272:PHE:CZ	2.54	0.43
1:G:226:MET:CG	1:H:250:ASP:HB3	2.48	0.43
1:H:13:ILE:HD13	1:H:282:ALA:HB3	1.99	0.43
1:G:16:GLU:OE1	1:G:289:GLY:HA2	2.18	0.43
1:C:14:GLY:N	1:C:15:PRO:HD2	2.33	0.43
1:B:340:LYS:NZ	1:C:338:ASN:HD22	2.15	0.43
1:G:191:ALA:HA	1:G:197:SER:HB3	2.01	0.43
1:F:264:SER:HB3	1:F:276:GLU:O	2.18	0.43
1:D:113:THR:HG21	1:D:326:GLN:HA	1.99	0.43
1:C:349:ASP:O	1:C:351:LEU:N	2.52	0.43
1:E:81:HIS:N	1:E:87:ARG:HH12	2.16	0.43
1:C:285:ILE:O	1:C:285:ILE:CD1	2.64	0.43
1:B:122:ARG:O	1:B:126:GLU:HB2	2.18	0.43
1:B:71:LEU:HB3	1:B:276:GLU:HB3	2.00	0.43
1:G:261:MET:HA	1:G:295:GLY:HA3	2.01	0.43
1:B:8:LEU:HD23	1:B:43:ILE:CG1	2.48	0.43
1:B:275:TYR:CE2	1:B:303:MET:HA	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:355:LEU:O	1:A:356:ASN:CB	2.65	0.43
1:F:12:GLY:O	1:F:15:PRO:HD2	2.18	0.43
1:B:38:PHE:O	1:B:39:GLU:HB2	2.18	0.43
1:G:167:ILE:HD12	1:G:200:TRP:HE3	1.84	0.43
1:D:173:LYS:HD2	1:D:176:GLN:NE2	2.34	0.43
1:B:47:ALA:HB1	1:B:56:PRO:HD3	1.99	0.43
1:E:163:THR:O	1:E:164:ARG:C	2.57	0.43
1:E:114:LEU:HD23	1:E:335:GLN:O	2.19	0.43
1:G:191:ALA:CA	1:G:197:SER:HB3	2.49	0.43
1:D:53:THR:OG1	1:D:54:PRO:HD2	2.18	0.43
1:F:1:MET:HG3	3:F:394:HOH:O	2.18	0.43
1:F:114:LEU:HD21	1:F:334:LEU:CD2	2.49	0.43
1:C:324:VAL:HG21	1:C:351:LEU:HG	2.01	0.43
1:C:162:TYR:O	1:D:156:VAL:HG12	2.18	0.43
1:A:1:MET:H2	1:A:34:HIS:CD2	2.35	0.43
1:H:201:ARG:NH2	1:H:218:HIS:HB3	2.34	0.43
1:H:114:LEU:HD11	1:H:334:LEU:HD13	1.99	0.43
1:H:164:ARG:HH11	1:H:164:ARG:CG	2.32	0.43
1:C:121:LYS:O	1:C:124:ARG:HB2	2.19	0.43
1:A:196:SER:HB3	1:B:158:ASP:OD2	2.18	0.43
1:G:165:GLU:O	1:G:169:ARG:HG2	2.19	0.43
1:C:31:ASN:ND2	1:C:312:LYS:HZ2	2.16	0.43
1:B:340:LYS:HZ1	1:C:338:ASN:HD22	1.66	0.43
1:A:202:GLU:O	1:A:205:GLU:N	2.51	0.43
1:B:122:ARG:HB2	1:B:122:ARG:HH11	1.84	0.43
1:B:83:PRO:O	1:B:84:ALA:C	2.57	0.43
1:B:199:MET:O	1:B:203:ILE:HG13	2.18	0.43
1:G:148:ARG:NH2	1:H:202:GLU:OE2	2.36	0.43
1:B:135:GLU:O	1:B:242:ASN:HA	2.18	0.43
1:D:275:TYR:CD1	1:D:275:TYR:N	2.87	0.43
1:C:311:GLU:HG2	1:C:312:LYS:N	2.34	0.43
1:E:354:LYS:C	1:E:356:ASN:H	2.22	0.43
1:E:44:GLY:HA3	1:E:74:VAL:CG1	2.46	0.43
1:A:313:GLU:OE1	1:A:313:GLU:N	2.52	0.43
1:F:192:ASN:N	1:F:192:ASN:HD22	2.16	0.43
1:E:191:ALA:CA	1:E:197:SER:HB3	2.49	0.43
1:D:43:ILE:HG23	1:D:74:VAL:HG11	2.01	0.43
1:D:60:LEU:HD13	1:D:64:ARG:NH2	2.34	0.43
1:G:303:MET:HG2	1:G:308:PHE:HE2	1.83	0.43
1:C:294:LEU:HD22	1:C:321:VAL:HG22	2.01	0.43
1:C:281:SER:O	1:C:282:ALA:C	2.56	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:278:VAL:HG12	1:D:279:HIS:N	2.33	0.43
1:H:271:ARG:HG3	1:H:271:ARG:O	2.19	0.43
1:C:84:ALA:O	1:C:87:ARG:N	2.51	0.42
1:G:193:VAL:HG11	1:H:141:TYR:CD2	2.54	0.42
1:H:123:GLU:HG2	1:H:124:ARG:N	2.34	0.42
1:D:221:VAL:HG11	1:D:244:PHE:CZ	2.54	0.42
1:A:156:VAL:HG22	1:A:157:VAL:N	2.34	0.42
1:G:191:ALA:HA	1:G:197:SER:CB	2.49	0.42
1:E:32:ASP:HB3	1:E:34:HIS:CE1	2.54	0.42
1:C:22:ILE:CG2	1:C:26:LYS:HE2	2.49	0.42
1:E:152:GLY:O	1:E:153:GLU:HB2	2.19	0.42
1:E:259:LEU:CG	1:E:260:GLY:N	2.82	0.42
1:A:183:LYS:O	1:A:214:VAL:HG13	2.18	0.42
1:A:1:MET:O	1:A:34:HIS:HB3	2.18	0.42
1:E:134:ARG:NH2	1:E:242:ASN:OD1	2.50	0.42
1:B:245:GLY:O	1:B:247:ILE:N	2.51	0.42
1:A:188:VAL:HG13	1:A:221:VAL:HA	2.01	0.42
1:E:123:GLU:CD	1:E:123:GLU:H	2.23	0.42
1:A:105:LEU:HD12	1:A:105:LEU:N	2.33	0.42
1:B:78:LYS:C	1:B:80:ASP:H	2.23	0.42
1:B:336:VAL:HG12	1:B:337:ALA:N	2.34	0.42
1:G:323:ASP:HB3	1:G:354:LYS:HE2	2.00	0.42
1:B:43:ILE:HD13	1:B:54:PRO:O	2.19	0.42
1:E:28:VAL:HG11	1:E:313:GLU:HB3	2.01	0.42
1:H:194:LEU:HB2	1:H:197:SER:HB2	2.00	0.42
1:C:30:ASP:O	1:C:31:ASN:C	2.57	0.42
1:E:326:GLN:HB3	1:E:326:GLN:HE21	1.63	0.42
1:E:259:LEU:CD1	1:E:260:GLY:H	2.26	0.42
1:C:104:ASN:C	1:C:105:LEU:HD12	2.40	0.42
1:F:243:MET:O	1:F:247:ILE:HG12	2.20	0.42
1:H:252:ALA:O	1:H:255:ILE:HG12	2.19	0.42
1:G:342:VAL:HG23	1:G:343:SER:O	2.19	0.42
1:B:170:ILE:HG23	1:B:171:ILE:N	2.34	0.42
1:D:96:ARG:O	1:D:97:LYS:C	2.58	0.42
1:H:74:VAL:HG23	1:H:74:VAL:O	2.20	0.42
1:H:142:PHE:CD1	1:H:142:PHE:N	2.87	0.42
1:F:55:LEU:HG	1:F:55:LEU:O	2.19	0.42
1:C:355:LEU:O	1:C:356:ASN:CB	2.67	0.42
1:B:179:GLN:NE2	1:B:183:LYS:NZ	2.50	0.42
1:A:192:ASN:C	1:A:192:ASN:ND2	2.73	0.42
1:A:268:ARG:HG3	1:A:269:SER:H	1.81	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:139:GLY:HA2	1:F:160:LEU:HD13	1.98	0.42
1:A:156:VAL:HG11	1:B:196:SER:HA	2.01	0.42
1:D:170:ILE:CG2	1:D:171:ILE:N	2.82	0.42
1:E:1:MET:H3	1:E:34:HIS:CD2	2.37	0.42
1:F:156:VAL:O	1:F:157:VAL:HG13	2.20	0.42
1:A:14:GLY:O	1:A:17:VAL:HG22	2.19	0.42
1:C:32:ASP:OD1	1:C:32:ASP:N	2.53	0.42
1:B:259:LEU:CG	1:B:260:GLY:N	2.82	0.42
1:H:141:TYR:H	1:H:141:TYR:HD1	1.68	0.42
1:H:292:ASN:HB2	1:H:331:THR:OG1	2.19	0.42
1:B:190:LYS:HB3	1:B:194:LEU:HD12	2.01	0.42
1:G:107:PRO:HA	1:G:131:VAL:HA	2.02	0.42
1:F:102:PHE:CD2	1:F:169:ARG:HD2	2.54	0.42
1:G:259:LEU:C	1:G:261:MET:N	2.73	0.42
1:F:181:ARG:NH1	1:F:236:ASP:OD1	2.53	0.42
1:C:122:ARG:C	1:C:124:ARG:H	2.22	0.42
1:F:179:GLN:OE1	1:F:213:ASP:OD2	2.38	0.42
1:B:139:GLY:HA2	1:B:160:LEU:HD12	2.00	0.42
1:C:16:GLU:OE2	1:C:287:GLY:N	2.36	0.42
1:E:314:ALA:O	1:E:318:GLU:HG3	2.19	0.42
1:H:184:LYS:O	1:H:236:ASP:HB3	2.20	0.42
1:H:14:GLY:N	1:H:15:PRO:CD	2.83	0.42
1:G:305:ARG:NH2	1:G:318:GLU:OE2	2.52	0.42
1:A:281:SER:O	1:A:282:ALA:C	2.58	0.42
1:G:130:LEU:C	1:G:130:LEU:HD12	2.40	0.42
1:G:120:LEU:HD23	1:H:120:LEU:HD23	2.02	0.42
1:B:78:LYS:HD3	1:B:79:TRP:CZ2	2.55	0.42
1:D:259:LEU:HD12	1:D:260:GLY:N	2.34	0.42
1:B:282:ALA:HB1	1:B:285:ILE:HG21	2.01	0.42
1:B:70:LEU:HD21	1:B:303:MET:SD	2.60	0.42
1:D:140:LEU:HB2	1:D:160:LEU:HD13	2.02	0.42
1:B:177:LEU:CD1	1:B:181:ARG:HD2	2.50	0.42
1:H:229:ILE:HD11	1:H:251:LEU:HD21	2.01	0.42
1:A:27:THR:OG1	1:A:352:ILE:HD12	2.20	0.42
1:G:63:CYS:HB3	1:G:69:ILE:HD11	2.01	0.42
1:F:24:VAL:HG13	1:F:355:LEU:HD11	2.01	0.42
1:C:107:PRO:CB	1:C:131:VAL:HG22	2.49	0.42
1:C:8:LEU:HD13	1:C:69:ILE:HG23	2.02	0.42
1:D:93:LEU:C	1:D:93:LEU:HD23	2.40	0.42
1:H:172:GLU:OE1	1:H:211:TYR:OH	2.36	0.42
1:B:184:LYS:O	1:B:236:ASP:HB3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:29:LEU:HA	1:G:29:LEU:HD23	1.79	0.42
1:C:239:VAL:O	1:C:239:VAL:HG13	2.19	0.42
1:D:142:PHE:N	1:D:142:PHE:CD1	2.87	0.42
1:C:84:ALA:O	1:C:85:SER:C	2.57	0.42
1:B:55:LEU:CD1	1:B:60:LEU:HD21	2.40	0.42
1:E:82:ASN:O	1:E:87:ARG:CZ	2.68	0.42
1:D:256:THR:O	1:D:258:SER:N	2.53	0.42
1:C:164:ARG:NH1	1:C:203:ILE:CD1	2.83	0.42
1:B:129:ASP:O	1:B:182:ARG:NH2	2.51	0.42
1:A:101:LEU:HD13	1:A:266:SER:HB2	2.02	0.42
1:H:45:GLY:HA3	1:H:79:TRP:CZ2	2.55	0.42
1:F:114:LEU:HD11	1:F:261:MET:CE	2.50	0.41
1:F:126:GLU:CG	1:F:126:GLU:O	2.68	0.41
1:D:25:LEU:HD13	1:D:25:LEU:HA	1.83	0.41
1:C:106:ARG:O	1:C:131:VAL:HA	2.20	0.41
1:B:130:LEU:C	1:B:130:LEU:CD1	2.89	0.41
1:B:7:VAL:C	1:B:8:LEU:HD12	2.41	0.41
1:C:97:LYS:C	1:C:99:MET:H	2.23	0.41
1:G:141:TYR:N	1:G:141:TYR:HD1	2.18	0.41
1:B:99:MET:CE	1:B:272:PHE:CZ	3.03	0.41
1:E:130:LEU:C	1:E:130:LEU:HD12	2.40	0.41
1:E:22:ILE:O	1:E:26:LYS:HG3	2.20	0.41
1:A:96:ARG:HH21	1:A:136:LEU:CB	2.19	0.41
1:F:224:THR:O	1:F:228:LEU:HG	2.19	0.41
1:C:342:VAL:CB	1:C:346:GLU:CG	2.88	0.41
1:E:83:PRO:HD2	1:E:86:LEU:HB2	2.01	0.41
1:G:163:THR:HG23	1:G:166:GLU:OE1	2.21	0.41
1:C:82:ASN:CB	1:C:83:PRO:HD2	2.49	0.41
1:A:21:ALA:O	1:A:22:ILE:C	2.59	0.41
1:A:74:VAL:HG22	1:A:92:LEU:HD12	2.00	0.41
1:G:156:VAL:HG22	1:G:157:VAL:N	2.35	0.41
1:C:268:ARG:HE	1:C:270:ASP:CG	2.23	0.41
1:A:82:ASN:CB	1:A:83:PRO:HD2	2.29	0.41
1:E:39:GLU:CG	1:E:62:ILE:HD13	2.50	0.41
1:B:48:ILE:HG23	1:B:86:LEU:HD21	2.02	0.41
1:C:285:ILE:O	1:C:285:ILE:CG1	2.67	0.41
1:C:18:MET:HE2	1:C:21:ALA:HB3	2.02	0.41
1:E:107:PRO:HB3	1:E:131:VAL:HG22	2.02	0.41
1:A:10:GLY:HA3	1:A:73:ALA:O	2.21	0.41
1:A:99:MET:HE2	1:A:99:MET:HB3	1.79	0.41
1:C:345:ILE:HD13	1:C:349:ASP:OD1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:141:TYR:HB2	1:C:242:ASN:HD21	1.85	0.41
1:G:325:LEU:HD21	1:G:334:LEU:CD1	2.50	0.41
1:D:120:LEU:CD1	1:D:255:ILE:HB	2.49	0.41
1:G:353:GLU:O	1:G:354:LYS:C	2.56	0.41
1:G:141:TYR:N	1:G:141:TYR:CD1	2.88	0.41
1:B:140:LEU:HD13	1:B:160:LEU:HB2	2.02	0.41
1:D:130:LEU:HB3	1:D:235:PHE:O	2.20	0.41
1:H:16:GLU:OE2	1:H:287:GLY:N	2.47	0.41
1:E:342:VAL:HB	1:E:346:GLU:HB3	2.01	0.41
1:G:17:VAL:HB	1:G:296:THR:CG2	2.45	0.41
1:E:148:ARG:HD3	1:F:199:MET:HE3	2.00	0.41
1:A:193:VAL:HG11	1:B:141:TYR:CD1	2.55	0.41
1:H:168:GLU:HG2	1:H:203:ILE:HG21	2.03	0.41
1:E:124:ARG:NE	1:E:230:ALA:O	2.52	0.41
1:H:281:SER:O	1:H:282:ALA:C	2.59	0.41
1:A:25:LEU:O	1:A:27:THR:N	2.53	0.41
1:A:95:LEU:O	1:A:99:MET:HG2	2.21	0.41
1:E:60:LEU:O	1:E:64:ARG:HG3	2.20	0.41
1:B:89:GLU:H	1:B:89:GLU:CD	2.22	0.41
1:A:160:LEU:O	1:B:157:VAL:HA	2.21	0.41
1:G:192:ASN:HD22	1:G:193:VAL:N	2.18	0.41
1:D:261:MET:CE	1:D:294:LEU:HB3	2.48	0.41
1:F:192:ASN:C	1:F:192:ASN:HD22	2.24	0.41
1:H:18:MET:CE	1:H:70:LEU:HD22	2.51	0.41
1:H:305:ARG:NH2	1:H:318:GLU:OE2	2.54	0.41
1:A:25:LEU:C	1:A:27:THR:N	2.73	0.41
1:E:60:LEU:HD22	1:E:98:GLU:HG2	2.02	0.41
1:C:243:MET:O	1:C:246:ASP:HB3	2.20	0.41
1:F:355:LEU:O	1:F:357:ASN:N	2.51	0.41
1:C:254:VAL:HG13	1:D:226:MET:HE3	2.03	0.41
1:G:7:VAL:C	1:G:8:LEU:HD12	2.41	0.41
1:F:8:LEU:N	1:F:8:LEU:CD1	2.84	0.41
1:E:190:LYS:HA	1:E:220:LEU:HD22	2.03	0.41
1:A:102:PHE:CE2	1:A:268:ARG:HA	2.56	0.41
1:A:156:VAL:O	1:A:157:VAL:HG13	2.20	0.41
1:C:140:LEU:HD11	1:C:158:ASP:HB3	2.02	0.41
1:C:172:GLU:O	1:C:176:GLN:HG3	2.20	0.41
1:H:132:ILE:HG21	1:H:249:SER:OG	2.21	0.41
1:H:271:ARG:HG3	1:H:307:SER:HA	2.02	0.41
1:B:65:ARG:O	1:B:65:ARG:CG	2.68	0.41
1:F:336:VAL:HG23	1:F:336:VAL:H	1.58	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:79:TRP:HA	1:B:82:ASN:OD1	2.21	0.41
1:E:82:ASN:HB3	1:E:83:PRO:CD	2.50	0.41
1:F:192:ASN:C	1:F:192:ASN:ND2	2.72	0.41
1:A:107:PRO:HA	1:A:131:VAL:HA	2.03	0.41
1:H:164:ARG:NH1	1:H:168:GLU:OE2	2.53	0.41
1:D:77:PRO:HA	1:D:80:ASP:CG	2.41	0.41
1:B:122:ARG:O	1:B:126:GLU:CB	2.69	0.41
1:D:288:GLN:HB2	1:D:290:LYS:HG3	2.01	0.41
1:E:22:ILE:HG22	1:E:26:LYS:HD2	2.03	0.41
1:D:271:ARG:HA	1:D:271:ARG:HD3	1.82	0.41
1:F:220:LEU:HA	1:F:220:LEU:HD23	1.94	0.41
1:H:49:ASP:OD1	1:H:78:LYS:HE3	2.20	0.41
1:A:87:ARG:NH1	1:A:87:ARG:CB	2.77	0.41
1:B:27:THR:O	1:B:31:ASN:HB2	2.20	0.41
1:C:288:GLN:HB2	1:C:290:LYS:HE2	2.01	0.41
1:E:300:ALA:O	1:E:303:MET:HB3	2.20	0.41
1:A:342:VAL:HB	1:A:346:GLU:CG	2.51	0.41
1:G:285:ILE:HA	1:G:288:GLN:NE2	2.35	0.41
1:H:156:VAL:HG22	1:H:157:VAL:N	2.36	0.41
1:F:33:GLY:O	1:F:34:HIS:C	2.59	0.41
1:H:330:CYS:O	1:H:341:VAL:HA	2.20	0.41
1:G:142:PHE:CD1	1:G:142:PHE:N	2.89	0.41
1:E:323:ASP:O	1:E:326:GLN:HB2	2.21	0.40
1:F:140:LEU:HD23	1:F:243:MET:CE	2.51	0.40
1:B:282:ALA:O	1:B:285:ILE:HG23	2.22	0.40
1:C:128:VAL:HG23	1:C:233:GLY:HA2	2.02	0.40
1:E:281:SER:O	1:E:282:ALA:C	2.59	0.40
1:A:171:ILE:HD13	1:A:204:ALA:HB2	2.03	0.40
1:D:230:ALA:O	1:D:231:ASN:HB2	2.21	0.40
1:H:298:LEU:HA	1:H:298:LEU:HD23	1.92	0.40
1:B:331:THR:O	1:B:333:ASP:N	2.50	0.40
1:C:105:LEU:N	1:C:105:LEU:HD12	2.36	0.40
1:C:107:PRO:HG2	1:C:263:PRO:HG2	2.02	0.40
1:B:190:LYS:HD2	1:B:190:LYS:HA	1.89	0.40
1:D:324:VAL:CG2	1:D:351:LEU:HD23	2.52	0.40
1:E:107:PRO:HA	1:E:131:VAL:HA	2.03	0.40
1:F:16:GLU:OE1	1:F:289:GLY:HA2	2.21	0.40
1:C:349:ASP:O	1:C:353:GLU:HB2	2.22	0.40
1:C:43:ILE:HD12	1:C:54:PRO:O	2.21	0.40
1:H:58:GLU:O	1:H:58:GLU:CG	2.70	0.40
1:G:118:SER:HA	1:G:119:PRO:HD3	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:18:MET:CE	1:H:22:ILE:HG13	2.51	0.40
1:A:320:ALA:HB2	1:A:355:LEU:CD1	2.51	0.40
1:F:323:ASP:HB3	1:F:354:LYS:CE	2.51	0.40
1:A:28:VAL:C	1:A:30:ASP:N	2.75	0.40
1:C:164:ARG:HH12	1:C:203:ILE:HD11	1.86	0.40
1:B:228:LEU:O	1:B:232:PRO:HB3	2.20	0.40
1:D:134:ARG:HG3	1:D:245:GLY:HA3	2.03	0.40
1:G:329:TYR:CE2	1:G:350:ARG:CZ	3.05	0.40
1:A:32:ASP:HB3	1:A:34:HIS:HE1	1.87	0.40
1:H:60:LEU:CD1	1:H:98:GLU:HG2	2.52	0.40
1:D:356:ASN:HD22	1:D:356:ASN:HA	1.70	0.40
1:A:151:PRO:C	1:A:153:GLU:N	2.75	0.40
1:C:48:ILE:HD13	1:C:86:LEU:O	2.21	0.40
1:A:19:ASP:O	1:A:23:ARG:HG3	2.21	0.40
1:E:193:VAL:HG11	1:F:141:TYR:CD1	2.57	0.40
1:E:142:PHE:CD2	1:E:142:PHE:N	2.89	0.40
1:A:93:LEU:C	1:A:96:ARG:HB3	2.41	0.40
1:E:39:GLU:HG2	1:E:62:ILE:HD13	2.03	0.40
1:H:122:ARG:HD2	2:H:1002:SO4:S	2.62	0.40
1:H:44:GLY:HA2	1:H:88:PRO:HA	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	354/366 (97%)	298 (84%)	45 (13%)	11 (3%)	5	25
1	B	355/366 (97%)	289 (81%)	53 (15%)	13 (4%)	4	20
1	C	354/366 (97%)	284 (80%)	52 (15%)	18 (5%)	2	13
1	D	355/366 (97%)	307 (86%)	38 (11%)	10 (3%)	6	28

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	354/366 (97%)	319 (90%)	28 (8%)	7 (2%)	9	38
1	F	355/366 (97%)	309 (87%)	35 (10%)	11 (3%)	5	25
1	G	355/366 (97%)	311 (88%)	38 (11%)	6 (2%)	11	43
1	H	355/366 (97%)	316 (89%)	35 (10%)	4 (1%)	17	56
All	All	2837/2928 (97%)	2433 (86%)	324 (11%)	80 (3%)	6	28

All (80) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	336	VAL
1	A	337	ALA
1	A	339	GLY
1	B	39	GLU
1	B	78	LYS
1	B	84	ALA
1	B	337	ALA
1	C	68	ALA
1	C	255	ILE
1	C	288	GLN
1	E	339	GLY
1	F	127	ASN
1	F	337	ALA
1	G	31	ASN
1	G	337	ALA
1	A	33	GLY
1	A	270	ASP
1	B	285	ILE
1	B	332	GLY
1	B	340	LYS
1	C	33	GLY
1	C	51	ALA
1	C	152	GLY
1	C	270	ASP
1	C	339	GLY
1	D	32	ASP
1	D	129	ASP
1	D	191	ALA
1	D	339	GLY
1	E	84	ALA
1	E	337	ALA
1	F	141	TYR

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Mol	Chain	Res	Type
1	F	150	GLY
1	F	269	SER
1	F	270	ASP
1	F	338	ASN
1	G	355	LEU
1	H	84	ALA
1	A	126	GLU
1	A	311	GLU
1	A	355	LEU
1	B	183	LYS
1	B	246	ASP
1	C	49	ASP
1	C	80	ASP
1	C	98	GLU
1	C	126	GLU
1	C	280	GLY
1	D	207	THR
1	E	31	ASN
1	F	122	ARG
1	F	126	GLU
1	G	255	ILE
1	H	151	PRO
1	H	333	ASP
1	A	182	ARG
1	B	79	TRP
1	B	151	PRO
1	B	270	ASP
1	C	309	GLY
1	D	231	ASN
1	G	153	GLU
1	H	2	LYS
1	A	269	SER
1	C	123	GLU
1	C	256	THR
1	D	291	ALA
1	E	82	ASN
1	E	150	GLY
1	G	122	ARG
1	B	284	ASP
1	C	180	ILE
1	D	270	ASP
1	C	9	PRO

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Mol	Chain	Res	Type
1	F	143	GLY
1	F	193	VAL
1	A	54	PRO
1	D	28	VAL
1	E	221	VAL
1	D	193	VAL

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	286/296 (97%)	264 (92%)	22 (8%)	16	47
1	B	287/296 (97%)	267 (93%)	20 (7%)	19	53
1	C	289/296 (98%)	264 (91%)	25 (9%)	13	40
1	D	288/296 (97%)	274 (95%)	14 (5%)	31	68
1	E	286/296 (97%)	264 (92%)	22 (8%)	16	47
1	F	287/296 (97%)	265 (92%)	22 (8%)	16	47
1	G	289/296 (98%)	264 (91%)	25 (9%)	13	40
1	H	288/296 (97%)	268 (93%)	20 (7%)	19	54
All	All	2300/2368 (97%)	2130 (93%)	170 (7%)	17	49

All (170) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LYS
1	A	11	ASP
1	A	30	ASP
1	A	90	LYS
1	A	120	LEU
1	A	140	LEU
1	A	147	GLU
1	A	160	LEU
1	A	164	ARG

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Mol	Chain	Res	Type
1	A	175	PHE
1	A	176	GLN
1	A	177	LEU
1	A	192	ASN
1	A	213	ASP
1	A	241	GLU
1	A	243	MET
1	A	259	LEU
1	A	284	ASP
1	A	326	GLN
1	A	347	LEU
1	A	355	LEU
1	A	356	ASN
1	B	1	MET
1	B	30	ASP
1	B	32	ASP
1	B	35	GLU
1	B	43	ILE
1	B	80	ASP
1	B	97	LYS
1	B	106	ARG
1	B	149	ARG
1	B	177	LEU
1	B	192	ASN
1	B	222	ASP
1	B	241	GLU
1	B	256	THR
1	B	271	ARG
1	B	285	ILE
1	B	327	ASP
1	B	338	ASN
1	B	349	ASP
1	B	357	ASN
1	C	30	ASP
1	C	35	GLU
1	C	50	GLU
1	C	58	GLU
1	C	61	ASP
1	C	70	LEU
1	C	71	LEU
1	C	81	HIS
1	C	90	LYS

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Mol	Chain	Res	Type
1	C	106	ARG
1	C	109	LYS
1	C	177	LEU
1	C	181	ARG
1	C	198	ARG
1	C	209	LYS
1	C	215	GLU
1	C	250	ASP
1	C	259	LEU
1	C	276	GLU
1	C	285	ILE
1	C	310	LEU
1	C	319	LYS
1	C	345	ILE
1	C	349	ASP
1	C	356	ASN
1	D	2	LYS
1	D	25	LEU
1	D	32	ASP
1	D	38	PHE
1	D	43	ILE
1	D	58	GLU
1	D	71	LEU
1	D	192	ASN
1	D	210	LYS
1	D	241	GLU
1	D	250	ASP
1	D	270	ASP
1	D	327	ASP
1	D	331	THR
1	E	32	ASP
1	E	43	ILE
1	E	62	ILE
1	E	69	ILE
1	E	106	ARG
1	E	116	ASN
1	E	120	LEU
1	E	160	LEU
1	E	177	LEU
1	E	192	ASN
1	E	213	ASP
1	E	217	SER

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Mol	Chain	Res	Type
1	E	219	MET
1	E	234	GLN
1	E	241	GLU
1	E	251	LEU
1	E	256	THR
1	E	312	LYS
1	E	326	GLN
1	E	335	GLN
1	E	347	LEU
1	E	355	LEU
1	F	4	LYS
1	F	11	ASP
1	F	27	THR
1	F	42	LEU
1	F	50	GLU
1	F	79	TRP
1	F	82	ASN
1	F	99	MET
1	F	105	LEU
1	F	106	ARG
1	F	126	GLU
1	F	147	GLU
1	F	160	LEU
1	F	168	GLU
1	F	177	LEU
1	F	192	ASN
1	F	222	ASP
1	F	251	LEU
1	F	253	SER
1	F	333	ASP
1	F	346	GLU
1	F	357	ASN
1	G	26	LYS
1	G	32	ASP
1	G	65	ARG
1	G	86	LEU
1	G	87	ARG
1	G	106	ARG
1	G	160	LEU
1	G	165	GLU
1	G	177	LEU
1	G	183	LYS

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Mol	Chain	Res	Type
1	G	192	ASN
1	G	198	ARG
1	G	217	SER
1	G	234	GLN
1	G	241	GLU
1	G	243	MET
1	G	251	LEU
1	G	259	LEU
1	G	276	GLU
1	G	284	ASP
1	G	296	THR
1	G	319	LYS
1	G	336	VAL
1	G	347	LEU
1	G	355	LEU
1	H	2	LYS
1	H	19	ASP
1	H	27	THR
1	H	99	MET
1	H	113	THR
1	H	116	ASN
1	H	142	PHE
1	H	149	ARG
1	H	160	LEU
1	H	164	ARG
1	H	165	GLU
1	H	170	ILE
1	H	192	ASN
1	H	209	LYS
1	H	213	ASP
1	H	241	GLU
1	H	251	LEU
1	H	259	LEU
1	H	262	LEU
1	H	269	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (60) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	HIS
1	A	104	ASN
1	A	192	ASN

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Mol	Chain	Res	Type
1	A	227	GLN
1	A	335	GLN
1	A	356	ASN
1	B	40	ASN
1	B	104	ASN
1	B	176	GLN
1	B	179	GLN
1	B	192	ASN
1	B	288	GLN
1	B	326	GLN
1	B	356	ASN
1	B	357	ASN
1	C	31	ASN
1	C	34	HIS
1	C	104	ASN
1	C	154	ASN
1	C	176	GLN
1	C	179	GLN
1	C	192	ASN
1	C	227	GLN
1	C	242	ASN
1	C	338	ASN
1	C	356	ASN
1	D	176	GLN
1	D	179	GLN
1	D	192	ASN
1	D	218	HIS
1	D	356	ASN
1	E	34	HIS
1	E	104	ASN
1	E	154	ASN
1	E	192	ASN
1	E	227	GLN
1	E	234	GLN
1	E	326	GLN
1	F	104	ASN
1	F	176	GLN
1	F	192	ASN
1	F	227	GLN
1	F	234	GLN
1	F	356	ASN
1	F	357	ASN

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Mol	Chain	Res	Type
1	G	34	HIS
1	G	104	ASN
1	G	176	GLN
1	G	179	GLN
1	G	192	ASN
1	G	231	ASN
1	G	234	GLN
1	G	338	ASN
1	H	31	ASN
1	H	176	GLN
1	H	192	ASN
1	H	227	GLN
1	H	234	GLN
1	H	326	GLN
1	H	356	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

5 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	1005	-	4,4,4	0.32	0	6,6,6	0.07	0
2	SO4	C	1004	-	4,4,4	0.30	0	6,6,6	0.13	0
2	SO4	H	1001	-	4,4,4	0.24	0	6,6,6	0.20	0
2	SO4	H	1002	-	4,4,4	0.11	0	6,6,6	0.07	0
2	SO4	H	1003	-	4,4,4	0.34	0	6,6,6	0.19	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	1005	-	-	0/0/0/0	0/0/0/0
2	SO4	C	1004	-	-	0/0/0/0	0/0/0/0
2	SO4	H	1001	-	-	0/0/0/0	0/0/0/0
2	SO4	H	1002	-	-	0/0/0/0	0/0/0/0
2	SO4	H	1003	-	-	0/0/0/0	0/0/0/0

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.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	H	1002	SO4	2	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	356/366 (97%)	-0.11	3 (0%) 87 73	19, 37, 55, 70	0
1	B	357/366 (97%)	-0.05	10 (2%) 56 36	17, 35, 61, 71	0
1	C	356/366 (97%)	-0.08	2 (0%) 90 78	16, 37, 57, 66	0
1	D	357/366 (97%)	-0.23	0 100 100	16, 34, 52, 65	0
1	E	356/366 (97%)	-0.30	7 (1%) 68 48	13, 27, 47, 63	0
1	F	357/366 (97%)	-0.20	3 (0%) 87 73	12, 28, 51, 67	0
1	G	357/366 (97%)	-0.44	0 100 100	13, 25, 41, 56	0
1	H	357/366 (97%)	-0.26	4 (1%) 82 65	12, 28, 46, 71	0
All	All	2853/2928 (97%)	-0.21	29 (1%) 84 67	12, 31, 54, 71	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	86	LEU	4.3
1	H	339	GLY	4.2
1	E	83	PRO	4.1
1	F	339	GLY	4.1
1	H	334	LEU	3.6
1	B	85	SER	3.5
1	A	81	HIS	3.2
1	B	83	PRO	3.1
1	C	33	GLY	3.0
1	E	84	ALA	2.9
1	A	31	ASN	2.9
1	B	53	THR	2.8
1	B	52	GLY	2.6
1	B	150	GLY	2.6
1	B	81	HIS	2.5
1	B	87	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
1	E	51	ALA	2.4
1	F	334	LEU	2.4
1	E	80	ASP	2.3
1	B	84	ALA	2.2
1	B	154	ASN	2.2
1	A	83	PRO	2.2
1	H	1	MET	2.2
1	F	335	GLN	2.1
1	C	339	GLY	2.1
1	H	335	GLN	2.1
1	E	86	LEU	2.1
1	E	81	HIS	2.0
1	E	82	ASN	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, 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	LLDF	B-factors(Å ²)	Q<0.9
2	SO4	C	1004	5/5	0.92	0.23	1.58	72,73,73,74	0
2	SO4	H	1001	5/5	0.97	0.13	-1.26	40,40,41,41	0
2	SO4	H	1002	5/5	0.99	0.12	-4.05	37,37,37,38	0
2	SO4	H	1003	5/5	0.92	0.20	-	70,71,71,71	0
2	SO4	A	1005	5/5	0.96	0.19	-	87,88,88,89	0

6.5 Other polymers [i](#)

There are no such residues in this entry.