



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 13, 2020 – 12:26 PM BST

PDB ID : 3S6H
Title : Crystal structure of native mmNAGS/k
Authors : Shi, D.; Li, Y.; Cabrera-Luque, J.; Jin, Z.; Yu, X.; Allewell, N.M.; Tuchman, M.
Deposited on : 2011-05-25
Resolution : 3.10 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 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 : 2.14.4.dev1
buster-report : 1.1.7 (2018)
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) : 2.14.4.dev1

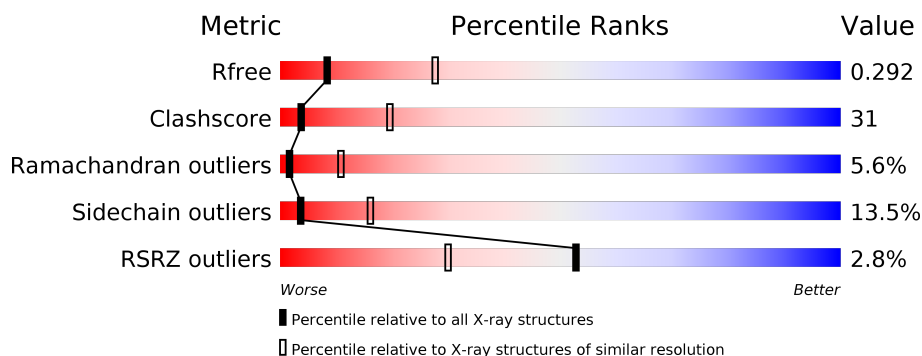
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)

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 respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	460	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> % 46% 38% 10% • 5% </div> </div>
1	B	460	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> 3% 45% 42% 8% 5% </div> </div>
1	X	460	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> % 44% 40% 10% • 5% </div> </div>
1	Y	460	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> 5% 38% 43% 7% • 11% </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 13266 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 N-acetylglutamate kinase / N-acetylglutamate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	436	Total	C	N	O	S	0	1	0
			3349	2107	605	631	6			
1	B	435	Total	C	N	O	S	0	0	0
			3334	2097	601	630	6			
1	X	435	Total	C	N	O	S	0	0	0
			3334	2097	601	630	6			
1	Y	408	Total	C	N	O	S	0	0	0
			3127	1972	560	589	6			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	EXPRESSION TAG	UNP Q0ASS9
A	-18	GLY	-	EXPRESSION TAG	UNP Q0ASS9
A	-17	SER	-	EXPRESSION TAG	UNP Q0ASS9
A	-16	SER	-	EXPRESSION TAG	UNP Q0ASS9
A	-15	HIS	-	EXPRESSION TAG	UNP Q0ASS9
A	-14	HIS	-	EXPRESSION TAG	UNP Q0ASS9
A	-13	HIS	-	EXPRESSION TAG	UNP Q0ASS9
A	-12	HIS	-	EXPRESSION TAG	UNP Q0ASS9
A	-11	HIS	-	EXPRESSION TAG	UNP Q0ASS9
A	-10	HIS	-	EXPRESSION TAG	UNP Q0ASS9
A	-9	SER	-	EXPRESSION TAG	UNP Q0ASS9
A	-8	SER	-	EXPRESSION TAG	UNP Q0ASS9
A	-7	GLY	-	EXPRESSION TAG	UNP Q0ASS9
A	-6	LEU	-	EXPRESSION TAG	UNP Q0ASS9
A	-5	VAL	-	EXPRESSION TAG	UNP Q0ASS9
A	-4	PRO	-	EXPRESSION TAG	UNP Q0ASS9
A	-3	ARG	-	EXPRESSION TAG	UNP Q0ASS9
A	-2	GLY	-	EXPRESSION TAG	UNP Q0ASS9
A	-1	SER	-	EXPRESSION TAG	UNP Q0ASS9
A	0	HIS	-	EXPRESSION TAG	UNP Q0ASS9
B	-19	MET	-	EXPRESSION TAG	UNP Q0ASS9

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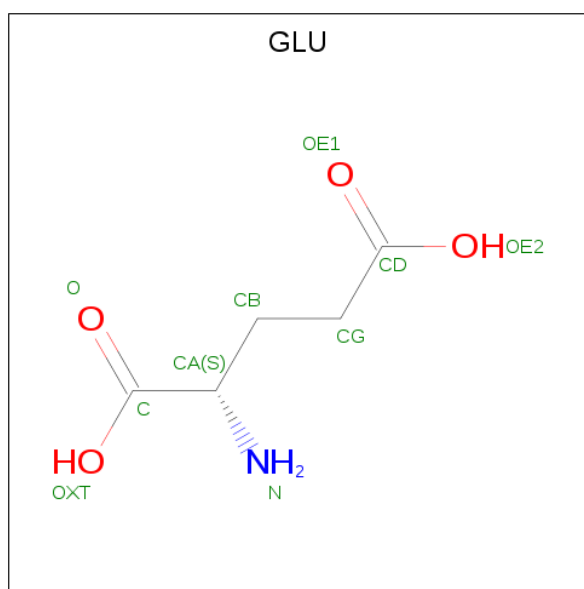
Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	EXPRESSION TAG	UNP Q0ASS9
B	-17	SER	-	EXPRESSION TAG	UNP Q0ASS9
B	-16	SER	-	EXPRESSION TAG	UNP Q0ASS9
B	-15	HIS	-	EXPRESSION TAG	UNP Q0ASS9
B	-14	HIS	-	EXPRESSION TAG	UNP Q0ASS9
B	-13	HIS	-	EXPRESSION TAG	UNP Q0ASS9
B	-12	HIS	-	EXPRESSION TAG	UNP Q0ASS9
B	-11	HIS	-	EXPRESSION TAG	UNP Q0ASS9
B	-10	HIS	-	EXPRESSION TAG	UNP Q0ASS9
B	-9	SER	-	EXPRESSION TAG	UNP Q0ASS9
B	-8	SER	-	EXPRESSION TAG	UNP Q0ASS9
B	-7	GLY	-	EXPRESSION TAG	UNP Q0ASS9
B	-6	LEU	-	EXPRESSION TAG	UNP Q0ASS9
B	-5	VAL	-	EXPRESSION TAG	UNP Q0ASS9
B	-4	PRO	-	EXPRESSION TAG	UNP Q0ASS9
B	-3	ARG	-	EXPRESSION TAG	UNP Q0ASS9
B	-2	GLY	-	EXPRESSION TAG	UNP Q0ASS9
B	-1	SER	-	EXPRESSION TAG	UNP Q0ASS9
B	0	HIS	-	EXPRESSION TAG	UNP Q0ASS9
X	-19	MET	-	EXPRESSION TAG	UNP Q0ASS9
X	-18	GLY	-	EXPRESSION TAG	UNP Q0ASS9
X	-17	SER	-	EXPRESSION TAG	UNP Q0ASS9
X	-16	SER	-	EXPRESSION TAG	UNP Q0ASS9
X	-15	HIS	-	EXPRESSION TAG	UNP Q0ASS9
X	-14	HIS	-	EXPRESSION TAG	UNP Q0ASS9
X	-13	HIS	-	EXPRESSION TAG	UNP Q0ASS9
X	-12	HIS	-	EXPRESSION TAG	UNP Q0ASS9
X	-11	HIS	-	EXPRESSION TAG	UNP Q0ASS9
X	-10	HIS	-	EXPRESSION TAG	UNP Q0ASS9
X	-9	SER	-	EXPRESSION TAG	UNP Q0ASS9
X	-8	SER	-	EXPRESSION TAG	UNP Q0ASS9
X	-7	GLY	-	EXPRESSION TAG	UNP Q0ASS9
X	-6	LEU	-	EXPRESSION TAG	UNP Q0ASS9
X	-5	VAL	-	EXPRESSION TAG	UNP Q0ASS9
X	-4	PRO	-	EXPRESSION TAG	UNP Q0ASS9
X	-3	ARG	-	EXPRESSION TAG	UNP Q0ASS9
X	-2	GLY	-	EXPRESSION TAG	UNP Q0ASS9
X	-1	SER	-	EXPRESSION TAG	UNP Q0ASS9
X	0	HIS	-	EXPRESSION TAG	UNP Q0ASS9
Y	-19	MET	-	EXPRESSION TAG	UNP Q0ASS9
Y	-18	GLY	-	EXPRESSION TAG	UNP Q0ASS9
Y	-17	SER	-	EXPRESSION TAG	UNP Q0ASS9

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Chain	Residue	Modelled	Actual	Comment	Reference
Y	-16	SER	-	EXPRESSION TAG	UNP Q0ASS9
Y	-15	HIS	-	EXPRESSION TAG	UNP Q0ASS9
Y	-14	HIS	-	EXPRESSION TAG	UNP Q0ASS9
Y	-13	HIS	-	EXPRESSION TAG	UNP Q0ASS9
Y	-12	HIS	-	EXPRESSION TAG	UNP Q0ASS9
Y	-11	HIS	-	EXPRESSION TAG	UNP Q0ASS9
Y	-10	HIS	-	EXPRESSION TAG	UNP Q0ASS9
Y	-9	SER	-	EXPRESSION TAG	UNP Q0ASS9
Y	-8	SER	-	EXPRESSION TAG	UNP Q0ASS9
Y	-7	GLY	-	EXPRESSION TAG	UNP Q0ASS9
Y	-6	LEU	-	EXPRESSION TAG	UNP Q0ASS9
Y	-5	VAL	-	EXPRESSION TAG	UNP Q0ASS9
Y	-4	PRO	-	EXPRESSION TAG	UNP Q0ASS9
Y	-3	ARG	-	EXPRESSION TAG	UNP Q0ASS9
Y	-2	GLY	-	EXPRESSION TAG	UNP Q0ASS9
Y	-1	SER	-	EXPRESSION TAG	UNP Q0ASS9
Y	0	HIS	-	EXPRESSION TAG	UNP Q0ASS9

- Molecule 2 is GLUTAMIC ACID (three-letter code: GLU) (formula: C₅H₉NO₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			10	5	1	4		
2	Y	1	Total	C	N	O	0	0
			10	5	1	4		

- Molecule 3 is COENZYME A (three-letter code: COA) (formula: C₂₁H₃₆N₇O₁₆P₃S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	X	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
3	Y	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		

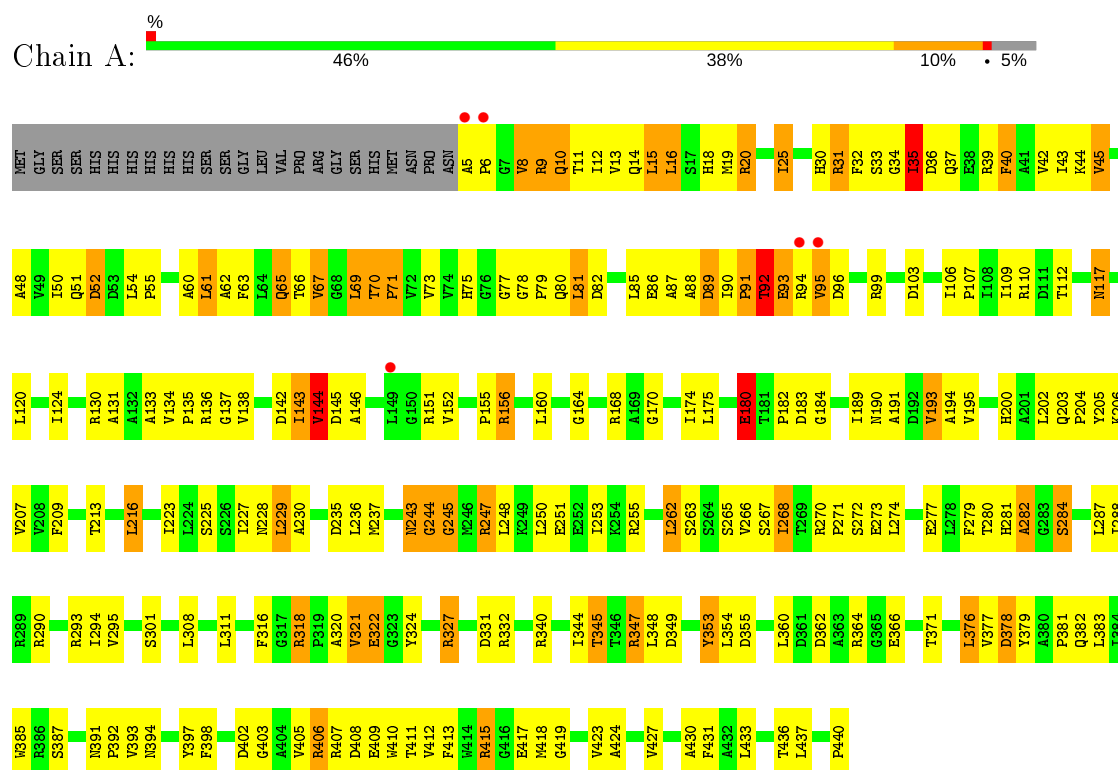
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	2	Total	0	0
			2		
4	X	3	Total	0	0
			3		
4	Y	1	Total	0	0
			1		

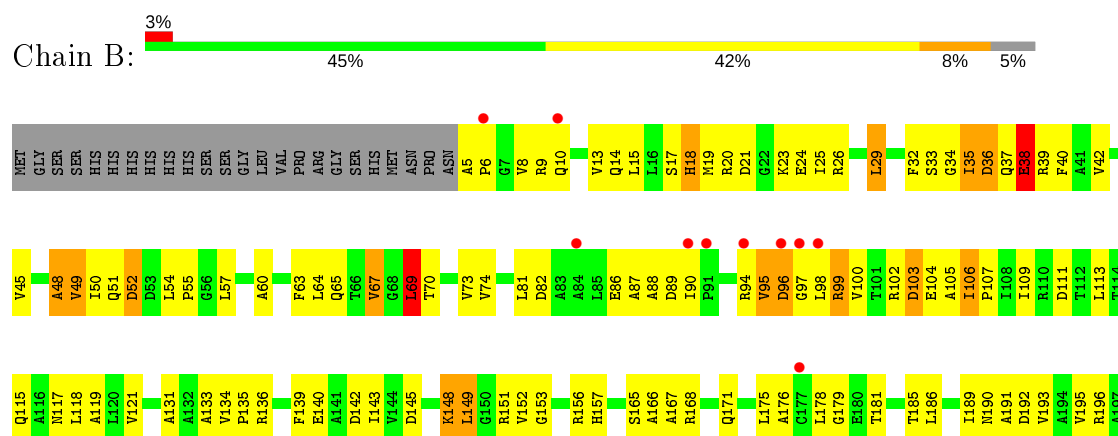
3 Residue-property plots

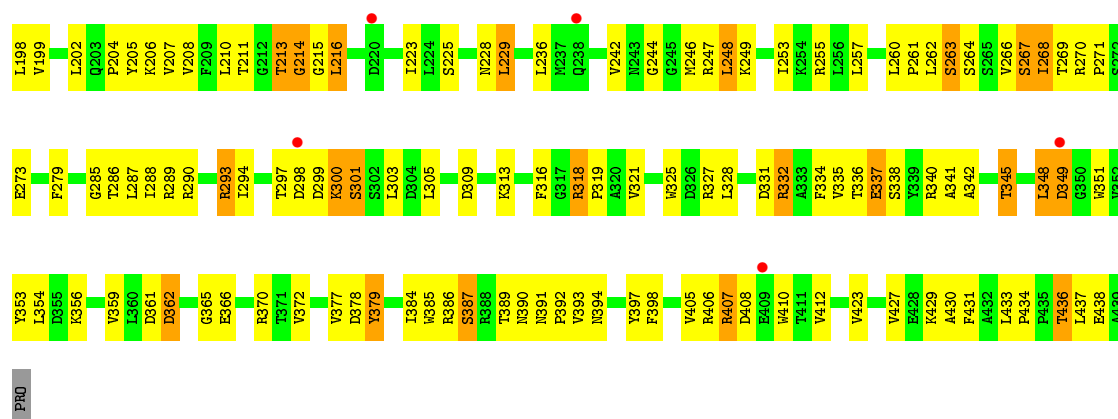
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

- Molecule 1: N-acetylglutamate kinase / N-acetylglutamate synthase

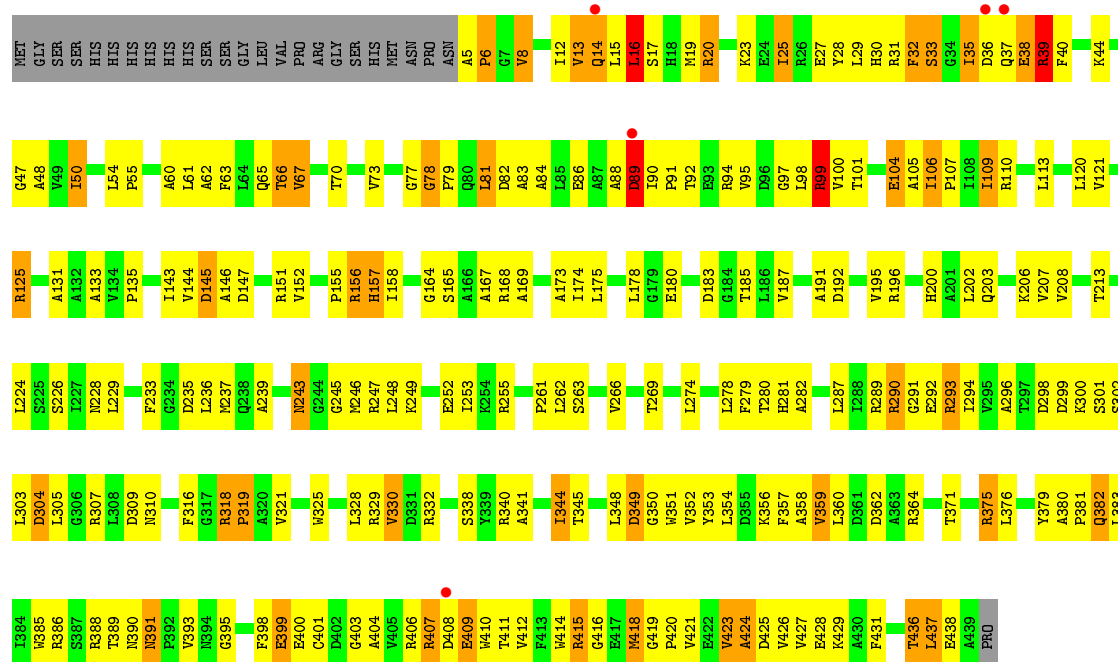
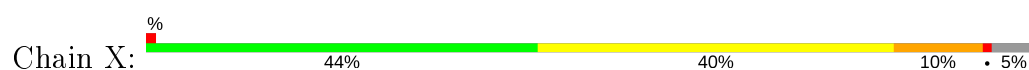


- Molecule 1: N-acetylglutamate kinase / N-acetylglutamate synthase

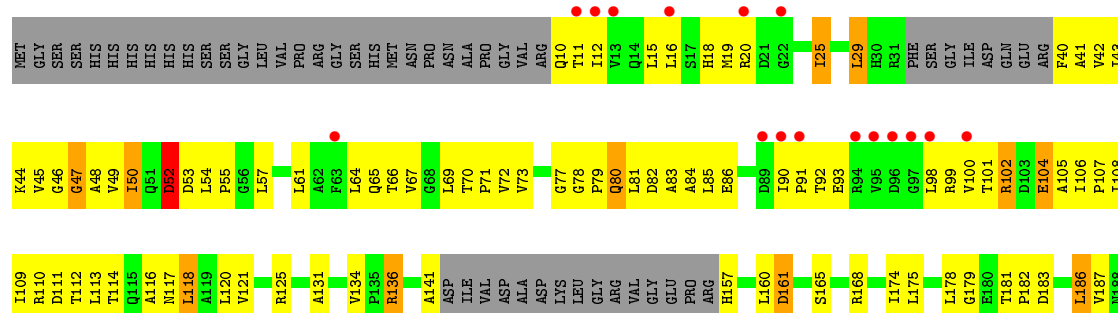


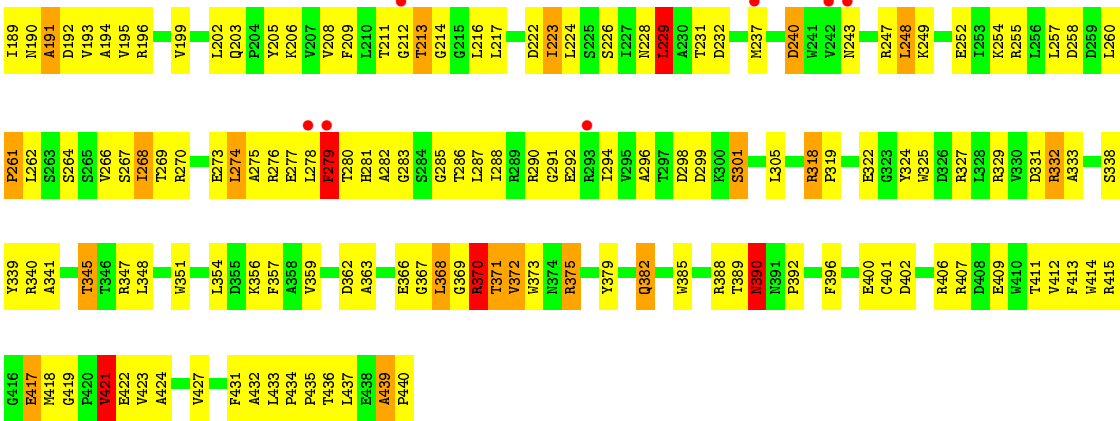


• Molecule 1: N-acetylglutamate kinase / N-acetylglutamate synthase



• Molecule 1: N-acetylglutamate kinase / N-acetylglutamate synthase





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	114.59Å 118.21Å 152.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.80 – 3.10 32.80 – 3.10	Depositor EDS
% Data completeness (in resolution range)	95.4 (32.80-3.10) 95.4 (32.80-3.10)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.22 (at 3.12Å)	Xtriage
Refinement program	PHENIX 1.7.1 _743	Depositor
R, R_{free}	0.186 , 0.297 0.179 , 0.292	Depositor DCC
R_{free} test set	1812 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	85.1	Xtriage
Anisotropy	0.681	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 59.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.019 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13266	wwPDB-VP
Average B, all atoms (Å ²)	118.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.10% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.48	0/3412	0.71	0/4639
1	B	0.36	0/3393	0.57	0/4613
1	X	0.45	0/3393	0.68	0/4613
1	Y	0.39	0/3182	0.60	0/4327
All	All	0.42	0/13380	0.64	0/18192

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	X	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	X	33	SER	Peptide

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	3349	0	3352	201	0
1	B	3334	0	3332	215	0
1	X	3334	0	3332	228	0
1	Y	3127	0	3126	203	0
2	A	10	0	5	1	0
2	Y	10	0	5	2	0
3	X	48	0	31	9	0
3	Y	48	0	31	7	0
4	B	2	0	0	0	0
4	X	3	0	0	0	0
4	Y	1	0	0	0	0
All	All	13266	0	13214	822	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 31.

All (822) 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:Y:439:ALA:HB1	1:Y:440:PRO:HD2	1.35	1.07
1:X:415:ARG:HG3	1:X:415:ARG:HH11	1.04	1.07
1:X:20:ARG:HH11	1:X:20:ARG:HG2	1.17	1.02
1:B:266:VAL:HG12	1:B:267:SER:H	1.28	0.96
1:X:415:ARG:CG	1:X:415:ARG:HH11	1.79	0.96
1:X:375:ARG:HG3	1:X:375:ARG:HH11	1.28	0.95
1:X:38:GLU:HG2	1:X:167:ALA:HB2	1.47	0.95
1:A:34:GLY:O	1:A:36:ASP:N	2.01	0.93
1:X:409:GLU:HG2	1:X:410:TRP:HD1	1.35	0.91
1:A:164:GLY:O	1:A:168:ARG:HB2	1.71	0.91
1:X:36:ASP:HB2	1:X:39:ARG:HG3	1.52	0.90
1:X:409:GLU:HG2	1:X:410:TRP:CD1	2.06	0.90
1:A:88:ALA:O	1:A:89:ASP:HB2	1.73	0.88
1:X:415:ARG:HG3	1:X:415:ARG:NH1	1.87	0.87
1:B:293:ARG:HH11	1:B:294:ILE:H	1.22	0.87
1:Y:332:ARG:H	1:Y:345:THR:HG22	1.40	0.86
1:X:319:PRO:HD2	1:X:438:GLU:HG2	1.55	0.86
1:B:269:THR:HG22	1:B:285:GLY:HA3	1.58	0.85
1:X:375:ARG:HH11	1:X:375:ARG:CG	1.90	0.85
1:A:39:ARG:HH21	1:A:203:GLN:HB2	1.40	0.85
1:X:62:ALA:O	1:X:66:THR:HG23	1.79	0.83
1:B:29:LEU:HD22	1:B:279:PHE:HE1	1.42	0.83
1:B:204:PRO:HD2	1:B:260:LEU:HD21	1.61	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:262:LEU:HD11	1:A:290:ARG:NH2	1.94	0.82
1:Y:294:ILE:HD11	1:Y:371:THR:HG22	1.62	0.82
1:B:20:ARG:CZ	1:Y:20:ARG:HB2	2.11	0.81
1:B:430:ALA:HA	1:B:433:LEU:HD13	1.63	0.81
1:X:243:ASN:OD1	1:X:245:GLY:N	2.13	0.80
1:X:44:LYS:HE2	1:X:191:ALA:CB	2.12	0.80
1:B:257:LEU:HD21	1:B:266:VAL:HG23	1.63	0.80
1:B:405:VAL:HG13	3:Y:501:COA:H133	1.62	0.80
1:X:354:LEU:HD21	1:X:357:PHE:HB2	1.63	0.79
1:A:294:ILE:HD11	1:A:371:THR:HG22	1.64	0.79
1:B:405:VAL:HG13	3:Y:501:COA:CDP	2.12	0.79
1:A:236:LEU:HD23	1:A:250:LEU:HD11	1.64	0.79
1:Y:331:ASP:HB3	1:Y:345:THR:HG23	1.62	0.79
1:Y:370:ARG:CG	1:Y:370:ARG:HH11	1.95	0.79
1:A:16:LEU:HD13	1:A:25:ILE:HG22	1.66	0.78
1:X:156:ARG:O	1:X:157:HIS:HB2	1.83	0.78
1:X:391:ASN:OD1	1:X:393:VAL:HG23	1.83	0.78
1:X:340:ARG:HG2	1:X:360:LEU:HD12	1.66	0.76
1:A:106:ILE:O	1:A:109:ILE:HG22	1.84	0.76
1:Y:101:THR:HG23	1:Y:102:ARG:HH21	1.48	0.76
1:B:266:VAL:HG12	1:B:267:SER:N	2.00	0.76
1:Y:269:THR:HG22	1:Y:285:GLY:HA3	1.67	0.75
1:A:62:ALA:O	1:A:66:THR:HG23	1.87	0.75
1:X:20:ARG:NH1	1:X:20:ARG:HG2	1.97	0.75
1:X:418:MET:HG3	1:X:423:VAL:HG13	1.67	0.74
1:X:106:ILE:HD11	1:X:151:ARG:HG2	1.69	0.74
1:A:90:ILE:N	1:A:91:PRO:HD3	2.01	0.74
1:A:25:ILE:HG13	1:A:279:PHE:CD1	2.22	0.74
1:X:44:LYS:HE2	1:X:191:ALA:HB1	1.70	0.74
1:A:280:THR:HG21	1:X:20:ARG:HE	1.53	0.73
1:A:332:ARG:H	1:A:345:THR:HG22	1.53	0.73
1:A:320:ALA:HA	1:A:437:LEU:HD23	1.68	0.73
1:Y:64:LEU:HD11	1:Y:278:LEU:CD1	2.18	0.73
1:Y:418:MET:HG3	1:Y:423:VAL:HG13	1.69	0.73
1:A:65:GLN:HG2	1:A:130:ARG:H	1.53	0.73
1:B:248:LEU:HG	1:B:249:LYS:N	2.03	0.73
1:Y:370:ARG:HH11	1:Y:370:ARG:HG3	1.54	0.72
1:Y:439:ALA:HB1	1:Y:440:PRO:CD	2.15	0.72
1:X:293:ARG:HD2	1:X:293:ARG:H	1.53	0.72
1:Y:12:ILE:HA	1:Y:15:LEU:HD21	1.70	0.72
1:A:281:HIS:O	1:A:282:ALA:HB2	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:15:LEU:O	1:X:17:SER:N	2.19	0.72
1:A:331:ASP:OD2	1:A:379:TYR:OH	2.07	0.72
1:B:196:ARG:HD3	1:B:255:ARG:NH1	2.05	0.71
1:X:249:LYS:O	1:X:253:ILE:HG13	1.91	0.71
1:B:287:LEU:HD12	1:B:288:ILE:H	1.56	0.71
1:X:20:ARG:HH11	1:X:20:ARG:CG	2.01	0.71
1:B:69:LEU:HD11	1:B:279:PHE:HZ	1.56	0.71
1:A:321:VAL:HG22	1:A:436:THR:O	1.91	0.71
1:A:32:PHE:CE1	1:A:40:PHE:HA	2.25	0.71
1:B:35:ILE:HG21	1:B:39:ARG:NH1	2.05	0.71
1:B:86:GLU:C	1:B:88:ALA:H	1.94	0.71
1:X:294:ILE:HD11	1:X:371:THR:HG22	1.73	0.71
1:B:242:VAL:HG13	1:B:246:MET:HG2	1.71	0.70
1:Y:412:VAL:HG23	1:Y:431:PHE:CE1	2.25	0.70
1:B:29:LEU:HD22	1:B:279:PHE:CE1	2.25	0.70
1:Y:298:ASP:HB3	1:Y:332:ARG:NH1	2.05	0.70
1:A:318:ARG:HH21	1:A:440:PRO:HD3	1.56	0.70
1:Y:252:GLU:HG2	1:Y:255:ARG:NH2	2.06	0.70
1:A:415:ARG:HH11	1:A:415:ARG:HB3	1.56	0.70
1:B:331:ASP:OD2	1:B:379:TYR:OH	2.09	0.70
1:X:32:PHE:HD1	1:X:32:PHE:O	1.74	0.70
1:Y:47:GLY:O	1:Y:50:ILE:HG13	1.91	0.70
1:A:182:PRO:O	1:B:107:PRO:HG3	1.92	0.69
1:B:38:GLU:HA	1:B:38:GLU:OE2	1.89	0.69
1:B:348:LEU:HD21	1:B:433:LEU:HD11	1.72	0.69
1:A:190:ASN:OD1	1:A:193:VAL:HG13	1.92	0.69
1:B:94:ARG:NH1	1:B:148:LYS:O	2.23	0.69
1:X:412:VAL:HG23	1:X:431:PHE:CE1	2.27	0.69
1:Y:44:LYS:HE2	1:Y:191:ALA:HB1	1.75	0.69
1:X:344:ILE:HG13	1:X:356:LYS:HB2	1.74	0.69
1:X:351:TRP:CD1	1:X:426:VAL:HG21	2.27	0.68
1:B:37:GLN:O	1:B:38:GLU:HB2	1.93	0.68
1:B:52:ASP:N	1:B:52:ASP:OD1	2.27	0.68
1:X:12:ILE:HA	1:X:15:LEU:HB3	1.75	0.68
1:X:375:ARG:NH1	1:X:375:ARG:HG3	2.01	0.68
1:X:25:ILE:HD13	1:X:279:PHE:CD1	2.29	0.68
1:A:417:GLU:O	1:A:418:MET:HG3	1.94	0.67
1:A:405:VAL:CG1	3:X:501:COA:H131	2.25	0.67
1:Y:340:ARG:HB3	1:Y:363:ALA:HB2	1.77	0.67
1:X:32:PHE:CD1	1:X:32:PHE:O	2.48	0.67
1:B:293:ARG:NH1	1:B:294:ILE:H	1.92	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:253:ILE:HD13	1:A:288:ILE:CD1	2.26	0.66
1:A:86:GLU:HA	1:A:91:PRO:HG3	1.78	0.66
1:X:35:ILE:HG23	1:X:40:PHE:CZ	2.31	0.66
1:X:39:ARG:HD2	1:X:202:LEU:O	1.96	0.66
1:Y:79:PRO:HA	1:Y:82:ASP:HB2	1.78	0.66
1:A:81:LEU:HD23	1:A:112:THR:HG21	1.78	0.66
1:A:117:ASN:C	1:A:117:ASN:HD22	1.99	0.66
1:A:354:LEU:HD22	1:A:376:LEU:HD21	1.77	0.65
1:X:47:GLY:HA2	1:X:50:ILE:HD11	1.77	0.65
1:X:23:LYS:O	1:X:27:GLU:HG3	1.94	0.65
1:A:39:ARG:HH21	1:A:203:GLN:CB	2.09	0.65
1:B:113:LEU:HD12	1:B:178:LEU:HD21	1.77	0.65
1:B:210:LEU:HD13	1:B:271:PRO:HG3	1.78	0.65
1:X:36:ASP:O	1:X:39:ARG:HG2	1.96	0.65
1:X:409:GLU:CD	1:X:409:GLU:H	2.00	0.65
1:X:89:ASP:C	1:X:91:PRO:HD3	2.17	0.65
1:A:281:HIS:O	1:A:282:ALA:CB	2.44	0.65
1:Y:83:ALA:C	1:Y:85:LEU:H	2.01	0.65
1:A:42:VAL:HG12	1:A:42:VAL:O	1.96	0.64
1:X:407:ARG:NH2	1:X:428:GLU:OE1	2.30	0.64
1:A:318:ARG:HH21	1:A:440:PRO:CD	2.10	0.64
1:A:44:LYS:HD2	1:A:45:VAL:N	2.11	0.64
1:Y:318:ARG:CB	1:Y:319:PRO:HD2	2.27	0.64
1:Y:274:LEU:HD22	1:Y:278:LEU:HD11	1.79	0.64
1:A:204:PRO:HB2	1:A:206:LYS:O	1.98	0.64
1:A:354:LEU:HB2	1:A:383:LEU:HD11	1.80	0.64
1:Y:214:GLY:H	1:Y:270:ARG:NH1	1.96	0.64
1:X:292:GLU:OE2	1:X:340:ARG:NH2	2.31	0.64
1:Y:385:TRP:CZ3	1:Y:415:ARG:HG3	2.33	0.64
1:A:376:LEU:O	1:A:378:ASP:N	2.31	0.63
1:B:313:LYS:HG3	1:B:319:PRO:HG3	1.79	0.63
1:X:415:ARG:CG	1:X:415:ARG:NH1	2.45	0.63
1:A:340:ARG:HG2	1:A:360:LEU:HD12	1.81	0.63
1:B:156:ARG:HG2	1:B:157:HIS:ND1	2.13	0.63
1:A:407:ARG:HG3	1:A:431:PHE:CE1	2.33	0.63
1:X:329:ARG:O	1:X:330:VAL:HB	1.98	0.63
1:B:86:GLU:O	1:B:88:ALA:N	2.32	0.63
1:B:260:LEU:HD13	1:B:264:SER:HB3	1.81	0.63
1:B:318:ARG:NH1	1:B:438:GLU:O	2.32	0.63
1:B:261:PRO:HD2	1:B:264:SER:OG	1.98	0.62
1:B:48:ALA:O	1:B:50:ILE:N	2.33	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:340:ARG:HH12	1:Y:366:GLU:CD	2.02	0.62
1:B:429:LYS:O	1:B:433:LEU:HD12	1.99	0.62
1:X:88:ALA:C	1:X:90:ILE:H	2.02	0.62
1:X:243:ASN:ND2	1:X:246:MET:H	1.97	0.62
1:Y:389:THR:HG23	1:Y:409:GLU:O	1.98	0.62
1:X:151:ARG:O	1:X:187:VAL:HG23	1.99	0.62
1:Y:212:GLY:O	1:Y:270:ARG:NH1	2.32	0.62
1:X:243:ASN:HD21	1:X:246:MET:H	1.48	0.62
1:Y:417:GLU:HG2	3:Y:501:COA:O5A	1.99	0.62
1:X:35:ILE:HG23	1:X:40:PHE:CE2	2.35	0.62
3:X:501:COA:O1A	3:X:501:COA:H142	2.00	0.62
1:B:45:VAL:HG11	1:B:57:LEU:HD21	1.82	0.61
1:X:94:ARG:HB3	1:X:100:VAL:HG22	1.81	0.61
1:X:351:TRP:HD1	1:X:426:VAL:HG21	1.62	0.61
1:A:13:VAL:C	1:A:15:LEU:H	2.03	0.61
1:B:38:GLU:C	1:B:40:PHE:H	2.04	0.61
1:A:144:VAL:HG22	1:A:145:ASP:N	2.15	0.61
1:X:389:THR:HG21	1:X:407:ARG:O	2.00	0.61
1:B:32:PHE:HE2	1:B:205:TYR:CE2	2.19	0.61
1:B:213:THR:O	1:B:215:GLY:N	2.33	0.61
1:X:15:LEU:HG	1:X:16:LEU:H	1.66	0.61
1:Y:110:ARG:O	1:Y:114:THR:OG1	2.11	0.61
1:Y:367:GLY:O	1:Y:369:GLY:N	2.34	0.61
1:X:412:VAL:HG23	1:X:431:PHE:CZ	2.36	0.60
1:Y:25:ILE:O	1:Y:29:LEU:HB2	2.01	0.60
1:A:430:ALA:HA	1:A:433:LEU:HD12	1.81	0.60
1:B:133:ALA:C	1:B:135:PRO:HD3	2.21	0.60
1:Y:104:GLU:O	1:Y:107:PRO:HD2	2.01	0.60
1:A:318:ARG:HH21	1:A:440:PRO:HG3	1.66	0.60
1:A:61:LEU:HD13	1:A:73:VAL:HG21	1.83	0.60
1:Y:102:ARG:NE	1:Y:102:ARG:HA	2.16	0.60
1:B:205:TYR:O	1:B:264:SER:HA	2.02	0.60
1:X:15:LEU:C	1:X:17:SER:H	2.05	0.60
1:A:133:ALA:C	1:A:135:PRO:HD3	2.21	0.60
1:Y:318:ARG:HB2	1:Y:319:PRO:HD2	1.84	0.60
1:A:412:VAL:HG23	1:A:431:PHE:CZ	2.36	0.60
1:X:340:ARG:HG2	1:X:360:LEU:CD1	2.31	0.60
1:Y:419:GLY:O	1:Y:423:VAL:HG22	2.02	0.59
1:B:253:ILE:HG23	1:B:266:VAL:HG21	1.84	0.59
1:B:223:ILE:HD12	1:B:223:ILE:H	1.66	0.59
1:X:341:ALA:CB	1:X:359:VAL:HG13	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:423:VAL:HB	1:X:427:VAL:HG23	1.84	0.59
1:Y:136:ARG:HH11	1:Y:136:ARG:HG3	1.66	0.59
1:X:44:LYS:HE2	1:X:191:ALA:HB3	1.85	0.59
1:Y:260:LEU:HB3	1:Y:261:PRO:HD2	1.84	0.59
1:Y:47:GLY:HA2	1:Y:50:ILE:HD11	1.85	0.59
1:Y:179:GLY:O	1:Y:186:LEU:HD23	2.01	0.59
1:B:149:LEU:HD12	1:B:152:VAL:HB	1.84	0.59
1:B:35:ILE:O	1:B:35:ILE:HG23	2.03	0.59
1:Y:338:SER:O	1:Y:339:TYR:HB2	2.03	0.59
1:Y:331:ASP:HB3	1:Y:345:THR:CG2	2.32	0.59
1:A:411:THR:HG22	1:A:413:PHE:CE2	2.38	0.58
1:X:86:GLU:O	1:X:91:PRO:HD2	2.03	0.58
1:Y:99:ARG:HB3	1:Y:100:VAL:HG13	1.85	0.58
1:X:293:ARG:CD	1:X:293:ARG:H	2.14	0.58
1:X:299:ASP:O	1:X:302:SER:HB3	2.03	0.58
1:Y:269:THR:HG23	1:Y:277:GLU:HG2	1.84	0.58
1:Y:439:ALA:CB	1:Y:440:PRO:HD2	2.23	0.58
1:A:81:LEU:O	1:A:81:LEU:HD22	2.03	0.58
3:Y:501:COA:H143	3:Y:501:COA:O5A	2.04	0.58
1:A:379:TYR:O	1:A:381:PRO:HD2	2.04	0.58
1:B:179:GLY:HA3	1:B:189:ILE:HD11	1.84	0.58
1:X:25:ILE:HD13	1:X:279:PHE:CG	2.39	0.58
1:Y:257:LEU:HD21	1:Y:266:VAL:HG23	1.85	0.58
1:X:304:ASP:HB3	1:X:307:ARG:HB3	1.85	0.58
1:Y:113:LEU:O	1:Y:116:ALA:HB3	2.04	0.58
1:A:136:ARG:NH1	1:A:137:GLY:H	2.02	0.57
1:A:332:ARG:N	1:A:345:THR:HG22	2.18	0.57
1:B:86:GLU:C	1:B:88:ALA:N	2.58	0.57
1:B:338:SER:OG	1:B:340:ARG:HB2	2.04	0.57
1:X:382:GLN:HA	1:X:416:GLY:CA	2.34	0.57
1:Y:331:ASP:HB3	1:Y:345:THR:O	2.04	0.57
1:B:32:PHE:C	1:B:34:GLY:H	2.08	0.57
1:X:91:PRO:O	1:X:92:THR:OG1	2.20	0.57
1:X:237:MET:O	1:X:247:ARG:NH1	2.37	0.57
1:X:237:MET:SD	1:X:247:ARG:HG2	2.44	0.57
1:X:390:ASN:O	1:X:391:ASN:C	2.43	0.57
1:X:173:ALA:HB1	1:X:175:LEU:HD11	1.86	0.57
1:X:229:LEU:O	1:X:233:PHE:HB3	2.05	0.57
1:X:262:LEU:HG	1:X:290:ARG:HH12	1.69	0.57
1:X:175:LEU:N	1:X:175:LEU:HD12	2.20	0.57
1:X:300:LYS:C	1:X:302:SER:H	2.07	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:199:VAL:HG13	1:Y:260:LEU:HD21	1.85	0.56
1:A:19:MET:HE2	1:X:19:MET:HG3	1.86	0.56
1:A:207:VAL:HB	1:A:266:VAL:HG22	1.87	0.56
1:Y:189:ILE:HD12	1:Y:194:ALA:HB2	1.87	0.56
1:X:125:ARG:NH2	1:X:131:ALA:O	2.39	0.56
1:X:97:GLY:O	1:X:98:LEU:HG	2.05	0.56
1:Y:175:LEU:N	1:Y:175:LEU:HD12	2.20	0.56
1:A:209:PHE:HB2	1:A:268:ILE:HB	1.86	0.56
1:A:265:SER:HB2	1:A:287:LEU:HD21	1.86	0.56
1:A:78:GLY:O	1:A:81:LEU:HB3	2.05	0.56
1:B:15:LEU:O	1:B:19:MET:HG2	2.05	0.56
1:B:321:VAL:HG12	1:B:438:GLU:HG2	1.88	0.56
1:A:332:ARG:HG3	1:A:332:ARG:HH11	1.70	0.56
1:B:266:VAL:CG1	1:B:267:SER:H	2.08	0.56
1:X:409:GLU:CD	1:X:409:GLU:N	2.59	0.56
1:X:81:LEU:HD12	1:X:82:ASP:N	2.20	0.56
1:Y:54:LEU:N	1:Y:55:PRO:HD2	2.20	0.56
1:Y:25:ILE:HG12	1:Y:279:PHE:CG	2.40	0.56
1:A:318:ARG:HH21	1:A:440:PRO:CG	2.18	0.55
1:X:65:GLN:NE2	1:X:66:THR:HG22	2.21	0.55
1:A:183:ASP:O	1:B:151:ARG:NH1	2.37	0.55
1:X:403:GLY:HA3	1:X:414:TRP:CE2	2.40	0.55
1:Y:141:ALA:HB3	1:Y:187:VAL:HG21	1.88	0.55
1:B:405:VAL:HG13	3:Y:501:COA:H132	1.88	0.55
1:A:91:PRO:O	1:A:92:THR:OG1	2.22	0.55
1:A:81:LEU:HD11	1:A:109:ILE:CD1	2.37	0.55
1:Y:105:ALA:O	1:Y:109:ILE:HG13	2.07	0.55
1:Y:385:TRP:HZ3	1:Y:415:ARG:HG3	1.71	0.55
1:X:395:GLY:O	1:X:399:GLU:HG3	2.07	0.55
1:Y:331:ASP:O	1:Y:332:ARG:NH1	2.39	0.55
1:Y:411:THR:HG22	1:Y:413:PHE:CE2	2.42	0.55
1:Y:269:THR:CG2	1:Y:277:GLU:HG2	2.36	0.55
1:B:215:GLY:HA2	1:B:268:ILE:HG12	1.87	0.55
1:X:292:GLU:OE1	1:X:338:SER:N	2.40	0.55
1:X:38:GLU:C	1:X:40:PHE:H	2.10	0.55
1:A:189:ILE:CG2	1:A:194:ALA:HB2	2.36	0.55
1:A:244:GLY:O	1:A:247:ARG:N	2.39	0.55
1:A:180:GLU:CD	1:B:136:ARG:HH12	2.09	0.55
1:B:334:PHE:CD2	1:B:334:PHE:N	2.75	0.55
1:X:381:PRO:O	1:X:416:GLY:HA2	2.07	0.55
1:X:54:LEU:HB3	1:X:55:PRO:HD3	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:277:GLU:HG3	1:Y:277:GLU:O	2.07	0.55
1:B:106:ILE:HD12	1:B:151:ARG:CZ	2.38	0.54
1:B:32:PHE:HE2	1:B:205:TYR:CD2	2.25	0.54
1:X:354:LEU:HB2	1:X:383:LEU:HD11	1.90	0.54
1:Y:269:THR:CG2	1:Y:285:GLY:HA3	2.36	0.54
1:A:143:ILE:HG12	1:A:152:VAL:O	2.07	0.54
1:B:165:SER:HA	1:B:168:ARG:NH1	2.22	0.54
1:B:48:ALA:O	1:B:49:VAL:C	2.45	0.54
1:A:191:ALA:O	1:A:195:VAL:HG23	2.07	0.54
1:A:86:GLU:HG2	1:A:91:PRO:CG	2.37	0.54
1:Y:81:LEU:HD23	1:Y:112:THR:HB	1.89	0.54
1:B:117:ASN:HD22	1:B:176:ALA:HB2	1.71	0.54
1:B:386:ARG:HD2	1:B:410:TRP:CE3	2.43	0.54
1:B:287:LEU:HD12	1:B:288:ILE:N	2.21	0.54
1:X:120:LEU:HD23	1:X:174:ILE:CG2	2.38	0.54
1:X:15:LEU:HG	1:X:16:LEU:N	2.22	0.54
1:X:165:SER:HB2	1:Y:118:LEU:HD11	1.90	0.54
1:A:134:VAL:N	1:A:135:PRO:HD3	2.23	0.54
1:A:308:LEU:HD13	1:A:344:ILE:HD11	1.90	0.54
1:B:398:PHE:CZ	1:Y:406:ARG:HD3	2.43	0.54
1:X:207:VAL:O	1:X:266:VAL:HG13	2.08	0.54
1:Y:65:GLN:C	1:Y:67:VAL:H	2.11	0.54
1:B:36:ASP:C	1:B:38:GLU:H	2.11	0.54
1:A:109:ILE:HG23	1:A:110:ARG:N	2.22	0.54
1:A:31:ARG:HD3	1:A:32:PHE:CZ	2.43	0.54
1:B:166:ALA:HB1	1:B:171:GLN:HG3	1.89	0.54
1:B:268:ILE:HG23	1:B:286:THR:HB	1.90	0.54
1:B:294:ILE:HG12	1:B:336:THR:HA	1.90	0.54
1:Y:370:ARG:CG	1:Y:370:ARG:NH1	2.63	0.54
1:A:180:GLU:OE2	1:B:136:ARG:NH1	2.41	0.54
1:B:38:GLU:HG2	1:B:167:ALA:HB2	1.89	0.54
1:A:40:PHE:CD1	1:A:69:LEU:HD22	2.43	0.53
1:B:393:VAL:HG12	1:B:397:TYR:CE2	2.43	0.53
1:A:5:ALA:HB3	1:A:6:PRO:HD3	1.90	0.53
1:Y:80:GLN:HG2	1:Y:80:GLN:O	2.07	0.53
1:B:348:LEU:O	1:B:351:TRP:N	2.40	0.53
1:X:382:GLN:HA	1:X:416:GLY:HA2	1.91	0.53
1:X:38:GLU:OE1	1:X:70:THR:HG22	2.08	0.53
1:Y:81:LEU:HD23	1:Y:112:THR:CB	2.39	0.53
1:Y:113:LEU:O	1:Y:116:ALA:N	2.41	0.53
1:B:54:LEU:O	1:B:54:LEU:HD23	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:40:PHE:CZ	1:B:69:LEU:HD13	2.44	0.53
1:X:348:LEU:O	1:X:350:GLY:N	2.41	0.53
1:Y:341:ALA:HB1	1:Y:359:VAL:HG22	1.89	0.53
1:B:35:ILE:HG21	1:B:39:ARG:HH11	1.72	0.53
1:X:38:GLU:OE2	1:X:38:GLU:HA	2.08	0.53
1:X:423:VAL:O	1:X:424:ALA:C	2.47	0.53
1:X:423:VAL:O	1:X:425:ASP:N	2.41	0.53
1:B:38:GLU:OE1	1:B:70:THR:HB	2.09	0.53
1:Y:190:ASN:C	1:Y:192:ASP:H	2.12	0.53
1:B:35:ILE:HG23	1:B:39:ARG:HB2	1.91	0.53
1:X:143:ILE:HD12	1:X:152:VAL:O	2.09	0.53
1:Y:370:ARG:O	1:Y:371:THR:C	2.47	0.53
1:Y:81:LEU:HD21	1:Y:109:ILE:HA	1.91	0.53
1:A:331:ASP:OD1	1:A:347:ARG:HD2	2.09	0.53
1:B:95:VAL:O	1:B:96:ASP:C	2.46	0.53
1:B:166:ALA:O	1:B:171:GLN:HG2	2.08	0.52
1:Y:432:ALA:O	1:Y:433:LEU:C	2.47	0.52
1:X:235:ASP:O	1:X:239:ALA:HB2	2.09	0.52
1:Y:106:ILE:HB	1:Y:107:PRO:HD3	1.92	0.52
1:Y:203:GLN:OE1	1:Y:260:LEU:HA	2.08	0.52
1:Y:356:LYS:NZ	1:Y:436:THR:OG1	2.42	0.52
1:X:121:VAL:HG21	1:X:133:ALA:HB2	1.91	0.52
1:Y:228:ASN:HB3	1:Y:231:THR:OG1	2.07	0.52
1:B:362:ASP:OD2	1:B:362:ASP:N	2.33	0.52
1:X:95:VAL:CG1	1:X:98:LEU:HD23	2.39	0.52
1:A:109:ILE:CG2	1:A:110:ARG:N	2.71	0.52
1:A:270:ARG:HG2	1:A:271:PRO:HD2	1.92	0.52
1:B:190:ASN:OD1	1:B:193:VAL:HG23	2.10	0.52
1:X:48:ALA:HB2	1:X:79:PRO:HG2	1.92	0.52
1:A:415:ARG:CB	1:A:415:ARG:HH11	2.23	0.52
1:A:423:VAL:O	1:A:427:VAL:HG23	2.10	0.52
1:B:121:VAL:HG13	1:B:131:ALA:HB3	1.91	0.52
1:B:318:ARG:NH2	1:B:437:LEU:HB3	2.24	0.52
1:X:418:MET:CG	1:X:423:VAL:HG13	2.38	0.52
1:X:98:LEU:O	1:X:99:ARG:CB	2.58	0.52
1:X:207:VAL:HB	1:X:266:VAL:HG22	1.90	0.52
1:A:94:ARG:O	1:A:96:ASP:N	2.42	0.52
1:B:309:ASP:OD2	1:B:325:TRP:CD1	2.63	0.52
1:Y:44:LYS:NZ	1:Y:192:ASP:OD2	2.40	0.52
1:Y:43:ILE:HG13	1:Y:208:VAL:HB	1.91	0.52
1:X:98:LEU:O	1:X:99:ARG:HB2	2.08	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:357:PHE:N	2:Y:502:GLU:OXT	2.35	0.51
1:A:318:ARG:NH2	1:A:440:PRO:HG3	2.24	0.51
1:X:406:ARG:HH11	1:X:411:THR:HG21	1.75	0.51
1:Y:372:VAL:HG12	1:Y:373:TRP:N	2.25	0.51
1:X:300:LYS:C	1:X:302:SER:N	2.64	0.51
1:A:32:PHE:HZ	1:A:205:TYR:CB	2.23	0.51
1:B:354:LEU:HB3	1:B:385:TRP:HB3	1.91	0.51
1:A:39:ARG:O	1:A:204:PRO:HA	2.11	0.51
1:X:164:GLY:O	1:X:168:ARG:HG3	2.10	0.51
1:A:184:GLY:HA3	1:B:151:ARG:HH22	1.75	0.51
1:A:82:ASP:CG	1:A:99:ARG:HH22	2.14	0.51
1:B:300:LYS:NZ	1:B:328:LEU:O	2.34	0.51
1:B:412:VAL:HG23	1:B:431:PHE:CZ	2.45	0.51
1:A:409:GLU:HB3	1:A:410:TRP:HD1	1.76	0.51
1:B:165:SER:HA	1:B:168:ARG:HH12	1.75	0.51
1:X:95:VAL:HG13	1:X:98:LEU:HA	1.92	0.51
1:B:206:LYS:HE3	1:B:267:SER:CB	2.41	0.51
1:B:49:VAL:HG12	1:B:57:LEU:HD22	1.93	0.51
1:Y:12:ILE:N	1:Y:12:ILE:HD13	2.25	0.51
1:Y:216:LEU:N	1:Y:286:THR:OG1	2.42	0.51
1:X:13:VAL:C	1:X:15:LEU:H	2.15	0.51
1:X:38:GLU:HG2	1:X:167:ALA:CB	2.30	0.50
1:B:5:ALA:HB3	1:B:6:PRO:HD3	1.93	0.50
1:A:280:THR:HG21	1:X:20:ARG:NE	2.25	0.50
1:X:156:ARG:NH1	1:X:156:ARG:HB3	2.26	0.50
1:X:208:VAL:HG11	1:X:274:LEU:HD13	1.93	0.50
1:X:37:GLN:O	1:X:40:PHE:CE2	2.64	0.50
1:A:405:VAL:CG1	3:X:501:COA:CDP	2.89	0.50
1:Y:243:ASN:O	1:Y:247:ARG:HB2	2.11	0.50
1:B:223:ILE:N	1:B:223:ILE:HD12	2.26	0.50
1:X:296:ALA:HB1	1:X:332:ARG:HH12	1.77	0.50
1:X:354:LEU:HD13	1:X:376:LEU:HD21	1.94	0.50
1:Y:189:ILE:O	1:Y:189:ILE:HG13	2.11	0.50
1:A:243:ASN:OD1	1:A:243:ASN:N	2.43	0.50
1:A:244:GLY:O	1:A:245:GLY:C	2.50	0.50
1:X:77:GLY:O	1:X:78:GLY:O	2.29	0.50
1:Y:274:LEU:CD2	1:Y:278:LEU:HD11	2.40	0.50
1:Y:296:ALA:HA	1:Y:333:ALA:O	2.12	0.50
1:A:136:ARG:NH2	1:A:180:GLU:HB3	2.26	0.50
1:B:102:ARG:O	1:B:103:ASP:HB2	2.11	0.50
1:B:263:SER:HA	1:B:289:ARG:HH22	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:393:VAL:O	1:B:393:VAL:CG1	2.60	0.50
1:X:70:THR:HG21	1:X:167:ALA:HA	1.93	0.50
1:X:200:HIS:O	1:X:203:GLN:HG2	2.11	0.50
1:Y:205:TYR:O	1:Y:264:SER:HA	2.11	0.50
1:Y:64:LEU:HD11	1:Y:278:LEU:HD12	1.93	0.50
1:B:13:VAL:O	1:B:13:VAL:HG12	2.12	0.50
1:Y:318:ARG:CB	1:Y:319:PRO:CD	2.89	0.50
1:B:341:ALA:O	1:B:372:VAL:HG21	2.12	0.50
1:B:351:TRP:HB3	1:B:384:ILE:HD13	1.94	0.50
1:Y:223:ILE:H	1:Y:223:ILE:HD12	1.77	0.50
1:X:375:ARG:CB	1:X:375:ARG:HH11	2.25	0.49
1:Y:418:MET:HG3	1:Y:423:VAL:CG1	2.40	0.49
1:B:21:ASP:O	1:B:24:GLU:HG2	2.12	0.49
1:Y:216:LEU:HB2	1:Y:286:THR:OG1	2.12	0.49
1:A:69:LEU:O	1:A:71:PRO:HD3	2.12	0.49
1:B:299:ASP:C	1:B:301:SER:H	2.16	0.49
1:X:309:ASP:HA	1:X:325:TRP:CZ2	2.47	0.49
1:Y:57:LEU:HD23	1:Y:120:LEU:HD11	1.93	0.49
1:A:353:TYR:CD2	1:A:353:TYR:C	2.86	0.49
1:X:5:ALA:HB3	1:X:6:PRO:HD3	1.94	0.49
1:A:362:ASP:O	1:A:366:GLU:HG3	2.13	0.49
1:A:407:ARG:HG3	1:A:431:PHE:CZ	2.46	0.49
1:A:398:PHE:CZ	1:X:406:ARG:NH1	2.81	0.49
1:Y:10:GLN:HG2	1:Y:10:GLN:O	2.12	0.49
1:Y:322:GLU:O	1:Y:327:ARG:NH2	2.45	0.49
1:A:16:LEU:O	1:A:18:HIS:N	2.46	0.49
1:A:54:LEU:HB3	1:A:55:PRO:HD3	1.94	0.49
1:X:156:ARG:O	1:X:157:HIS:CB	2.57	0.49
1:Y:101:THR:CG2	1:Y:102:ARG:HH21	2.20	0.49
1:A:331:ASP:HB3	1:A:345:THR:HG23	1.93	0.49
1:A:91:PRO:C	1:A:92:THR:OG1	2.51	0.49
1:B:105:ALA:O	1:B:109:ILE:HG12	2.12	0.49
1:B:299:ASP:O	1:B:301:SER:N	2.46	0.49
1:Y:12:ILE:HA	1:Y:15:LEU:CD2	2.42	0.49
1:Y:209:PHE:O	1:Y:268:ILE:HA	2.12	0.49
1:Y:78:GLY:C	1:Y:80:GLN:H	2.16	0.49
1:Y:83:ALA:O	1:Y:85:LEU:N	2.42	0.49
1:A:415:ARG:NH1	1:A:415:ARG:HB3	2.26	0.49
1:A:40:PHE:CE1	1:A:69:LEU:HD22	2.48	0.49
1:B:297:THR:OG1	1:B:298:ASP:N	2.46	0.49
1:B:356:LYS:HE3	1:B:437:LEU:HD11	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:18:HIS:HB2	1:Y:19:MET:SD	2.53	0.49
1:B:65:GLN:C	1:B:67:VAL:H	2.16	0.49
1:Y:294:ILE:HD12	1:Y:375:ARG:HD3	1.94	0.49
1:A:136:ARG:CD	1:A:137:GLY:H	2.25	0.48
1:A:418:MET:HE2	1:A:423:VAL:HG22	1.94	0.48
1:B:213:THR:C	1:B:215:GLY:H	2.16	0.48
1:B:389:THR:OG1	1:B:410:TRP:O	2.30	0.48
1:B:51:GLN:HB2	1:B:52:ASP:OD1	2.13	0.48
1:Y:117:ASN:OD1	1:Y:174:ILE:HG22	2.13	0.48
1:Y:54:LEU:N	1:Y:55:PRO:CD	2.76	0.48
1:A:406:ARG:HD3	1:X:398:PHE:CE1	2.48	0.48
1:B:257:LEU:CD2	1:B:266:VAL:HG23	2.39	0.48
1:B:29:LEU:CD2	1:B:279:PHE:CE1	2.94	0.48
1:B:361:ASP:O	1:B:365:GLY:N	2.45	0.48
1:X:120:LEU:HD23	1:X:174:ILE:HG21	1.95	0.48
1:A:136:ARG:HH11	1:A:137:GLY:H	1.62	0.48
1:B:17:SER:HA	1:B:26:ARG:NH1	2.28	0.48
1:Y:102:ARG:HE	1:Y:102:ARG:HA	1.76	0.48
1:Y:354:LEU:HD21	1:Y:357:PHE:HB2	1.96	0.48
1:Y:42:VAL:C	1:Y:43:ILE:HD12	2.34	0.48
1:Y:77:GLY:HA3	1:Y:81:LEU:HB3	1.95	0.48
1:A:16:LEU:HA	1:A:19:MET:CG	2.44	0.48
1:A:45:VAL:CG2	1:A:75:HIS:HB3	2.44	0.48
1:X:81:LEU:C	1:X:81:LEU:HD12	2.34	0.48
1:A:136:ARG:HD2	1:A:137:GLY:H	1.78	0.48
1:A:408:ASP:OD1	3:X:501:COA:H3B	2.14	0.48
1:B:335:VAL:HG22	1:B:342:ALA:CB	2.42	0.48
1:Y:46:GLY:O	1:Y:49:VAL:HG13	2.13	0.48
1:Y:86:GLU:CG	1:Y:91:PRO:HA	2.43	0.48
1:A:32:PHE:HZ	1:A:205:TYR:HB2	1.78	0.48
1:X:13:VAL:O	1:X:15:LEU:N	2.41	0.48
1:X:341:ALA:HB1	1:X:359:VAL:HG13	1.95	0.48
1:A:403:GLY:HA2	1:X:404:ALA:O	2.13	0.48
1:Y:224:LEU:HD21	1:Y:226:SER:O	2.14	0.48
1:Y:248:LEU:HD23	1:Y:249:LYS:N	2.28	0.48
1:A:33:SER:O	1:A:37:GLN:NE2	2.46	0.48
1:B:25:ILE:HG12	1:B:279:PHE:O	2.14	0.48
1:X:316:PHE:CE2	1:X:358:ALA:HB2	2.48	0.48
1:Y:421:VAL:HG22	1:Y:422:GLU:N	2.28	0.48
1:Y:92:THR:O	1:Y:101:THR:HG22	2.13	0.48
1:X:38:GLU:OE2	1:X:70:THR:HB	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:78:GLY:C	1:Y:80:GLN:N	2.67	0.48
1:B:32:PHE:CG	1:B:40:PHE:HE1	2.32	0.48
1:B:406:ARG:N	1:Y:402:ASP:O	2.45	0.48
1:B:73:VAL:HG12	1:B:74:VAL:N	2.28	0.48
1:X:175:LEU:CD1	1:X:175:LEU:N	2.77	0.48
1:X:298:ASP:OD1	1:X:298:ASP:N	2.47	0.48
1:Y:178:LEU:HD22	1:Y:186:LEU:HD21	1.96	0.48
1:Y:41:ALA:HB2	1:Y:69:LEU:HD13	1.96	0.48
1:X:90:ILE:N	1:X:91:PRO:HD3	2.29	0.47
1:Y:190:ASN:O	1:Y:192:ASP:N	2.47	0.47
1:B:213:THR:O	1:B:213:THR:OG1	2.31	0.47
1:B:214:GLY:H	1:B:270:ARG:NH2	2.13	0.47
1:B:98:LEU:N	1:B:98:LEU:HD12	2.29	0.47
1:X:16:LEU:HD13	1:X:16:LEU:O	2.13	0.47
1:X:61:LEU:HD13	1:X:73:VAL:HG21	1.96	0.47
1:Y:72:VAL:HG12	1:Y:72:VAL:O	2.14	0.47
1:X:420:PRO:HD3	3:X:501:COA:OAP	2.14	0.47
1:Y:421:VAL:O	1:Y:424:ALA:HB3	2.15	0.47
1:A:273:GLU:HB3	1:A:284:SER:CB	2.44	0.47
1:B:262:LEU:HD12	1:B:290:ARG:NH2	2.29	0.47
1:Y:25:ILE:H	1:Y:25:ILE:HD12	1.79	0.47
1:A:273:GLU:HB3	1:A:284:SER:HB2	1.97	0.47
1:X:30:HIS:O	1:X:33:SER:HB2	2.15	0.47
1:X:36:ASP:HB2	1:X:39:ARG:CG	2.36	0.47
1:Y:195:VAL:HG12	1:Y:195:VAL:O	2.14	0.47
1:A:318:ARG:NH2	1:A:440:PRO:HD3	2.28	0.47
1:B:20:ARG:NE	1:Y:20:ARG:HB2	2.28	0.47
1:B:353:TYR:C	1:B:353:TYR:CD2	2.88	0.47
1:B:40:PHE:CE2	1:B:69:LEU:HB3	2.50	0.47
1:X:156:ARG:NH1	1:X:156:ARG:O	2.33	0.47
1:X:262:LEU:HG	1:X:290:ARG:NH1	2.29	0.47
1:X:293:ARG:HD2	1:X:293:ARG:N	2.26	0.47
1:A:81:LEU:HD21	1:A:109:ILE:HD12	1.97	0.47
1:B:332:ARG:HD2	1:B:334:PHE:CZ	2.50	0.47
1:X:169:ALA:HB2	1:Y:125:ARG:NH1	2.29	0.47
1:Y:385:TRP:CH2	1:Y:415:ARG:HG3	2.49	0.47
1:A:316:PHE:CZ	2:A:501:GLU:HA	2.50	0.47
1:B:293:ARG:HA	1:B:293:ARG:HD2	1.37	0.47
1:B:294:ILE:HG22	1:B:294:ILE:O	2.13	0.47
1:B:82:ASP:N	1:B:82:ASP:OD1	2.45	0.47
1:X:100:VAL:O	1:X:101:THR:HG23	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:254:LYS:NZ	1:Y:258:ASP:OD2	2.48	0.47
1:Y:373:TRP:CD1	1:Y:396:PHE:HZ	2.33	0.47
1:A:409:GLU:HB3	1:A:410:TRP:CD1	2.49	0.47
1:X:403:GLY:HA3	1:X:414:TRP:CD2	2.50	0.47
1:Y:269:THR:HB	1:Y:273:GLU:HB2	1.97	0.46
1:A:13:VAL:C	1:A:15:LEU:N	2.68	0.46
1:A:430:ALA:HA	1:A:433:LEU:CD1	2.46	0.46
1:Y:199:VAL:CG1	1:Y:260:LEU:HD21	2.44	0.46
1:A:13:VAL:O	1:A:15:LEU:N	2.49	0.46
1:A:52:ASP:OD1	1:A:52:ASP:N	2.47	0.46
1:X:304:ASP:O	1:X:307:ARG:N	2.48	0.46
1:Y:90:ILE:N	1:Y:91:PRO:HD3	2.30	0.46
1:B:95:VAL:HG23	1:B:97:GLY:O	2.15	0.46
1:X:229:LEU:O	1:X:233:PHE:CB	2.63	0.46
1:X:388:ARG:C	1:X:390:ASN:H	2.18	0.46
1:A:237:MET:CE	1:A:251:GLU:HG3	2.45	0.46
1:A:25:ILE:HG13	1:A:279:PHE:CE1	2.50	0.46
1:B:423:VAL:O	1:B:427:VAL:HG23	2.15	0.46
1:X:35:ILE:HA	1:X:40:PHE:CZ	2.50	0.46
1:X:436:THR:O	1:X:437:LEU:HD12	2.16	0.46
1:A:354:LEU:HB3	1:A:385:TRP:HB3	1.97	0.46
1:B:10:GLN:O	1:B:14:GLN:HG3	2.15	0.46
1:B:142:ASP:O	1:B:153:GLY:HA2	2.15	0.46
1:B:98:LEU:O	1:B:99:ARG:C	2.53	0.46
1:Y:83:ALA:C	1:Y:85:LEU:N	2.67	0.46
1:B:102:ARG:HE	1:B:104:GLU:HG3	1.81	0.46
1:B:216:LEU:HD12	1:B:216:LEU:HA	1.77	0.46
1:X:180:GLU:OE2	1:Y:136:ARG:NE	2.48	0.46
1:X:345:THR:HA	1:X:353:TYR:O	2.16	0.46
1:A:253:ILE:HG21	1:A:288:ILE:HD13	1.96	0.46
1:B:293:ARG:O	1:B:337:GLU:HB3	2.16	0.46
1:B:398:PHE:CE2	1:Y:406:ARG:NH1	2.84	0.46
1:X:229:LEU:HB2	1:X:289:ARG:O	2.16	0.46
1:A:216:LEU:HD12	1:A:216:LEU:HA	1.71	0.46
1:B:40:PHE:CZ	1:B:69:LEU:HB3	2.51	0.46
1:X:319:PRO:HD2	1:X:438:GLU:CG	2.37	0.46
1:A:155:PRO:HD3	1:A:189:ILE:HD12	1.97	0.46
1:A:189:ILE:HA	1:A:189:ILE:HD13	1.81	0.46
1:X:121:VAL:O	1:X:125:ARG:HG3	2.16	0.46
1:X:77:GLY:O	1:X:78:GLY:C	2.54	0.46
1:A:236:LEU:HD23	1:A:250:LEU:CD1	2.41	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:402:ASP:HB2	1:A:415:ARG:HA	1.97	0.45
1:B:63:PHE:HD2	1:B:64:LEU:HD12	1.81	0.45
1:Y:382:GLN:HA	1:Y:415:ARG:O	2.15	0.45
1:B:121:VAL:HG21	1:B:133:ALA:HB2	1.98	0.45
1:Y:341:ALA:CB	1:Y:359:VAL:HG22	2.46	0.45
1:Y:46:GLY:O	1:Y:48:ALA:N	2.49	0.45
1:A:262:LEU:CD1	1:A:290:ARG:NH2	2.72	0.45
1:B:134:VAL:N	1:B:135:PRO:HD3	2.31	0.45
1:B:63:PHE:CD2	1:B:64:LEU:HD12	2.51	0.45
1:B:89:ASP:HB3	1:B:90:ILE:H	1.52	0.45
1:B:18:HIS:CE1	1:Y:276:ARG:HE	2.35	0.45
1:A:393:VAL:HG22	1:A:393:VAL:O	2.16	0.45
1:B:38:GLU:CD	1:B:70:THR:HB	2.37	0.45
1:X:39:ARG:CD	1:X:202:LEU:O	2.64	0.45
1:A:9:ARG:O	1:A:10:GLN:C	2.54	0.45
1:A:332:ARG:NH1	1:A:332:ARG:HG3	2.31	0.45
1:Y:228:ASN:OD1	1:Y:291:GLY:HA3	2.16	0.45
1:A:106:ILE:HB	1:A:107:PRO:HD3	1.98	0.45
1:A:174:ILE:HG22	1:A:174:ILE:O	2.16	0.45
1:Y:101:THR:O	1:Y:102:ARG:HB2	2.16	0.45
1:A:16:LEU:C	1:A:18:HIS:N	2.68	0.45
1:B:266:VAL:O	1:B:267:SER:HB2	2.17	0.45
1:B:316:PHE:CD2	1:B:316:PHE:N	2.84	0.45
1:B:331:ASP:HB3	1:B:345:THR:O	2.16	0.45
1:B:348:LEU:O	1:B:349:ASP:C	2.54	0.45
1:X:348:LEU:C	1:X:350:GLY:N	2.69	0.45
1:X:416:GLY:HA3	1:X:418:MET:SD	2.57	0.45
1:Y:12:ILE:O	1:Y:12:ILE:HG22	2.14	0.45
1:Y:52:ASP:OD1	1:Y:53:ASP:N	2.49	0.45
1:A:106:ILE:HD12	1:A:151:ARG:CZ	2.46	0.45
1:B:362:ASP:O	1:B:365:GLY:N	2.49	0.45
1:X:113:LEU:HD12	1:X:178:LEU:CD2	2.47	0.45
1:X:206:LYS:HE3	1:X:278:LEU:HD23	1.98	0.45
1:X:349:ASP:OD1	1:X:429:LYS:HE3	2.17	0.45
1:Y:255:ARG:CB	1:Y:255:ARG:HH11	2.30	0.45
1:Y:262:LEU:CD2	1:Y:290:ARG:HH21	2.30	0.45
1:Y:288:ILE:HD12	1:Y:288:ILE:N	2.32	0.45
1:B:196:ARG:HE	1:B:196:ARG:HB2	1.61	0.45
1:X:307:ARG:O	1:X:310:ASN:HB2	2.16	0.45
1:B:181:THR:OG1	1:B:185:THR:HB	2.17	0.45
1:B:20:ARG:CD	1:Y:20:ARG:HD2	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:79:PRO:O	1:X:83:ALA:HB3	2.17	0.45
1:Y:61:LEU:HD22	1:Y:71:PRO:HB3	1.99	0.45
1:A:138:VAL:HG11	1:A:175:LEU:HD23	1.99	0.44
1:X:228:ASN:OD1	1:X:291:GLY:HA3	2.16	0.44
1:X:94:ARG:HD2	1:X:95:VAL:N	2.32	0.44
1:A:406:ARG:HB3	1:A:406:ARG:HE	1.65	0.44
1:B:257:LEU:HD21	1:B:266:VAL:H	1.83	0.44
1:B:390:ASN:O	1:B:392:PRO:HD3	2.17	0.44
1:X:302:SER:O	1:X:302:SER:OG	2.30	0.44
1:Y:412:VAL:HB	1:Y:427:VAL:HG13	1.99	0.44
3:Y:501:COA:H71	3:Y:501:COA:HN4	1.67	0.44
1:A:340:ARG:HD2	1:A:362:ASP:OD2	2.17	0.44
1:A:90:ILE:O	1:A:90:ILE:HG22	2.18	0.44
1:B:299:ASP:C	1:B:301:SER:N	2.71	0.44
1:X:133:ALA:C	1:X:135:PRO:HD3	2.37	0.44
1:X:15:LEU:CG	1:X:16:LEU:N	2.81	0.44
1:X:419:GLY:CA	3:X:501:COA:N8P	2.80	0.44
1:Y:237:MET:HE1	1:Y:247:ARG:O	2.17	0.44
1:A:144:VAL:HG13	1:A:145:ASP:H	1.82	0.44
1:B:40:PHE:HZ	1:B:69:LEU:HD13	1.83	0.44
1:A:424:ALA:HB2	1:X:420:PRO:HB2	2.00	0.44
1:A:407:ARG:HE	3:X:501:COA:H122	1.83	0.44
1:B:391:ASN:O	1:B:394:ASN:HB2	2.17	0.44
1:X:304:ASP:O	1:X:305:LEU:C	2.56	0.44
1:Y:110:ARG:HG2	1:Y:111:ASP:OD2	2.17	0.44
1:Y:165:SER:N	1:Y:168:ARG:NH2	2.65	0.44
1:Y:359:VAL:HG21	1:Y:369:GLY:HA2	1.99	0.44
1:A:120:LEU:HD11	1:A:124:ILE:HD11	1.98	0.44
1:X:105:ALA:O	1:X:109:ILE:HG13	2.18	0.44
1:X:63:PHE:O	1:X:67:VAL:HB	2.18	0.44
1:Y:286:THR:HG22	1:Y:287:LEU:N	2.33	0.44
1:Y:262:LEU:HD21	1:Y:290:ARG:HH21	1.83	0.44
1:B:140:GLU:OE1	1:B:157:HIS:HB2	2.18	0.44
1:B:42:VAL:HG23	1:B:204:PRO:HG3	1.99	0.44
1:B:340:ARG:NH2	1:B:366:GLU:OE2	2.50	0.44
1:X:421:VAL:HG23	1:X:421:VAL:O	2.14	0.44
1:A:391:ASN:HA	1:A:392:PRO:HD2	1.85	0.44
1:X:109:ILE:H	1:X:109:ILE:HG13	1.50	0.44
1:X:329:ARG:O	1:X:330:VAL:CB	2.62	0.44
1:X:88:ALA:C	1:X:90:ILE:N	2.71	0.44
1:A:106:ILE:O	1:A:107:PRO:C	2.57	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:43:ILE:HB	1:A:73:VAL:HG22	1.99	0.43
1:B:175:LEU:N	1:B:175:LEU:HD12	2.33	0.43
1:B:38:GLU:C	1:B:40:PHE:N	2.70	0.43
1:B:407:ARG:HD3	1:B:431:PHE:CZ	2.53	0.43
1:X:13:VAL:HG12	1:X:14:GLN:N	2.33	0.43
1:A:44:LYS:NZ	1:A:191:ALA:HB1	2.33	0.43
1:B:32:PHE:C	1:B:34:GLY:N	2.70	0.43
1:Y:213:THR:O	1:Y:213:THR:OG1	2.32	0.43
1:A:13:VAL:HA	1:A:16:LEU:HD12	2.00	0.43
1:A:60:ALA:O	1:A:63:PHE:N	2.51	0.43
1:B:244:GLY:HA2	1:B:247:ARG:HG3	2.00	0.43
1:X:20:ARG:CG	1:X:20:ARG:NH1	2.68	0.43
1:X:419:GLY:HA3	3:X:501:COA:H72	1.99	0.43
1:A:63:PHE:HE1	1:X:15:LEU:HD12	1.84	0.43
1:B:175:LEU:H	1:B:175:LEU:HD12	1.82	0.43
1:Y:255:ARG:HB2	1:Y:255:ARG:NH1	2.33	0.43
1:Y:98:LEU:O	1:Y:99:ARG:HG3	2.18	0.43
1:B:206:LYS:HE3	1:B:267:SER:HB2	2.00	0.43
1:B:225:SER:O	1:B:286:THR:HA	2.19	0.43
1:B:13:VAL:HG13	1:B:26:ARG:HD2	2.00	0.43
1:B:95:VAL:CG2	1:B:98:LEU:HB2	2.49	0.43
1:X:28:TYR:O	1:X:32:PHE:N	2.44	0.43
1:X:341:ALA:HB2	1:X:359:VAL:HG13	2.00	0.43
1:Y:25:ILE:HD11	1:Y:279:PHE:HB2	2.00	0.43
1:B:214:GLY:H	1:B:270:ARG:HH21	1.67	0.43
1:X:95:VAL:HG13	1:X:98:LEU:HD23	1.99	0.43
1:B:362:ASP:O	1:B:366:GLU:HG2	2.18	0.43
1:B:95:VAL:HG21	1:B:98:LEU:HB2	2.01	0.43
1:X:192:ASP:HB3	1:X:252:GLU:OE2	2.19	0.43
1:Y:100:VAL:O	1:Y:100:VAL:HG23	2.19	0.43
1:Y:106:ILE:CB	1:Y:107:PRO:HD3	2.49	0.43
1:Y:160:LEU:O	1:Y:161:ASP:C	2.57	0.43
1:B:289:ARG:NH1	1:B:289:ARG:HB3	2.34	0.43
1:X:279:PHE:O	1:X:280:THR:CG2	2.67	0.43
1:Y:165:SER:HA	1:Y:168:ARG:NH2	2.34	0.43
1:Y:356:LYS:HA	2:Y:502:GLU:OXT	2.19	0.43
1:A:227:ILE:CG2	1:A:229:LEU:HD23	2.49	0.42
1:A:331:ASP:HB3	1:A:345:THR:CG2	2.49	0.42
1:A:60:ALA:O	1:A:62:ALA:N	2.52	0.42
1:X:386:ARG:HD2	1:X:410:TRP:CE3	2.54	0.42
1:Y:217:LEU:HA	1:Y:222:ASP:O	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:131:ALA:HB1	1:A:174:ILE:HD13	2.01	0.42
1:B:54:LEU:N	1:B:55:PRO:CD	2.81	0.42
1:X:94:ARG:HB3	1:X:100:VAL:CG2	2.48	0.42
1:Y:136:ARG:HH11	1:Y:136:ARG:CG	2.32	0.42
1:Y:267:SER:C	1:Y:268:ILE:HG13	2.39	0.42
1:Y:40:PHE:HB3	1:Y:69:LEU:HD22	2.01	0.42
1:A:20:ARG:NE	1:X:20:ARG:HH12	2.17	0.42
1:A:387:SER:OG	1:A:394:ASN:OD1	2.15	0.42
1:B:106:ILE:HB	1:B:107:PRO:HD3	2.01	0.42
1:B:433:LEU:HA	1:B:434:PRO:HD3	1.86	0.42
1:X:400:GLU:O	1:X:415:ARG:NH1	2.51	0.42
1:B:139:PHE:HB3	1:B:189:ILE:CD1	2.50	0.42
1:X:376:LEU:O	1:X:379:TYR:HB3	2.19	0.42
1:X:383:LEU:HG	1:X:385:TRP:CE3	2.55	0.42
1:Y:292:GLU:OE2	1:Y:368:LEU:HD21	2.19	0.42
1:Y:61:LEU:HD13	1:Y:73:VAL:HG21	2.01	0.42
1:A:92:THR:O	1:A:93:GLU:O	2.38	0.42
1:B:102:ARG:HG3	1:B:103:ASP:N	2.33	0.42
1:B:118:LEU:O	1:B:119:ALA:C	2.56	0.42
1:Y:362:ASP:O	1:Y:366:GLU:HG3	2.19	0.42
1:A:142:ASP:OD2	1:A:156:ARG:HD2	2.19	0.42
1:B:301:SER:C	1:B:303:LEU:H	2.23	0.42
1:B:81:LEU:HA	1:B:81:LEU:HD23	1.81	0.42
1:X:354:LEU:HD13	1:X:376:LEU:CD2	2.49	0.42
1:Y:388:ARG:O	1:Y:389:THR:C	2.57	0.42
1:Y:417:GLU:OE2	3:Y:501:COA:H62	2.20	0.42
1:A:376:LEU:O	1:A:379:TYR:N	2.52	0.42
1:B:32:PHE:O	1:B:34:GLY:N	2.44	0.42
1:B:336:THR:O	1:B:338:SER:N	2.52	0.42
1:X:106:ILE:HG22	1:X:107:PRO:N	2.34	0.42
1:X:196:ARG:NH1	1:X:255:ARG:HD2	2.34	0.42
1:Y:273:GLU:C	1:Y:275:ALA:H	2.23	0.42
1:A:136:ARG:HH21	1:A:180:GLU:HG2	1.85	0.42
1:A:287:LEU:HD13	1:A:287:LEU:C	2.40	0.42
1:B:95:VAL:O	1:B:97:GLY:N	2.53	0.42
1:X:158:ILE:HA	1:X:158:ILE:HD13	1.69	0.42
1:Y:134:VAL:O	1:Y:175:LEU:HA	2.20	0.42
1:Y:372:VAL:O	1:Y:375:ARG:N	2.52	0.42
1:X:388:ARG:C	1:X:390:ASN:N	2.73	0.42
1:X:91:PRO:HB3	1:X:104:GLU:OE1	2.19	0.42
1:Y:121:VAL:HG13	1:Y:131:ALA:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:190:ASN:C	1:Y:192:ASP:N	2.73	0.42
1:Y:81:LEU:HA	1:Y:112:THR:HG21	2.01	0.42
1:A:90:ILE:N	1:A:91:PRO:CD	2.78	0.42
1:B:229:LEU:HD23	1:B:229:LEU:HA	1.82	0.42
1:B:335:VAL:HG22	1:B:342:ALA:HB2	2.01	0.42
1:X:106:ILE:CD1	1:X:151:ARG:HG2	2.45	0.42
1:X:300:LYS:O	1:X:302:SER:N	2.52	0.42
1:X:303:LEU:O	1:X:305:LEU:N	2.50	0.42
1:X:37:GLN:O	1:X:40:PHE:HE2	2.02	0.42
1:Y:400:GLU:O	1:Y:415:ARG:HD2	2.20	0.42
1:A:35:ILE:HD13	1:A:35:ILE:N	2.35	0.41
1:B:192:ASP:OD1	1:B:192:ASP:N	2.49	0.41
1:X:144:VAL:O	1:X:145:ASP:HB3	2.20	0.41
1:A:160:LEU:HD11	1:A:202:LEU:HD23	2.02	0.41
1:A:322:GLU:O	1:A:327:ARG:NH2	2.52	0.41
1:X:229:LEU:HD23	1:X:229:LEU:HA	1.82	0.41
1:X:383:LEU:HG	1:X:385:TRP:HE3	1.85	0.41
1:X:419:GLY:O	1:X:423:VAL:HG22	2.20	0.41
1:X:419:GLY:HA3	3:X:501:COA:N8P	2.35	0.41
1:Y:189:ILE:CD1	1:Y:194:ALA:HB2	2.48	0.41
1:A:79:PRO:C	1:A:81:LEU:N	2.74	0.41
1:A:9:ARG:O	1:A:11:THR:N	2.54	0.41
1:B:36:ASP:O	1:B:36:ASP:CG	2.59	0.41
1:X:109:ILE:O	1:X:110:ARG:C	2.58	0.41
1:X:88:ALA:O	1:X:90:ILE:N	2.53	0.41
1:A:348:LEU:HD22	1:A:353:TYR:CD1	2.55	0.41
1:A:324:TYR:OH	1:A:355:ASP:OD2	2.26	0.41
1:A:63:PHE:O	1:A:67:VAL:HG22	2.20	0.41
1:A:70:THR:HA	1:A:71:PRO:HD2	1.90	0.41
1:A:8:VAL:HG12	1:A:9:ARG:N	2.35	0.41
1:X:29:LEU:HA	1:X:29:LEU:HD23	1.82	0.41
1:B:37:GLN:O	1:B:37:GLN:HG2	2.19	0.41
1:Y:324:TYR:CZ	1:Y:356:LYS:HE3	2.55	0.41
1:Y:434:PRO:HA	1:Y:435:PRO:HD3	1.92	0.41
1:A:228:ASN:O	1:A:230:ALA:N	2.54	0.41
1:A:235:ASP:N	1:A:235:ASP:OD1	2.54	0.41
1:B:185:THR:HG22	1:B:186:LEU:O	2.21	0.41
1:B:225:SER:O	1:B:287:LEU:N	2.42	0.41
1:Y:11:THR:C	1:Y:12:ILE:HD13	2.41	0.41
1:Y:82:ASP:O	1:Y:85:LEU:HB2	2.21	0.41
1:A:318:ARG:N	1:A:318:ARG:CD	2.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:44:LYS:HD3	1:X:195:VAL:HG21	2.02	0.41
1:Y:108:ILE:O	1:Y:109:ILE:C	2.58	0.41
1:Y:299:ASP:OD1	1:Y:301:SER:HB3	2.21	0.41
1:Y:305:LEU:HD13	1:Y:325:TRP:HB3	2.03	0.41
1:A:180:GLU:CD	1:B:136:ARG:NH1	2.74	0.41
1:B:111:ASP:O	1:B:115:GLN:HB2	2.20	0.41
1:X:107:PRO:HG3	1:Y:182:PRO:O	2.19	0.41
1:X:351:TRP:HD1	1:X:426:VAL:CG2	2.33	0.41
1:Y:269:THR:HB	1:Y:270:ARG:H	1.50	0.41
1:A:183:ASP:O	1:B:151:ARG:NH2	2.54	0.41
1:A:267:SER:HB3	1:A:277:GLU:OE2	2.21	0.41
1:A:48:ALA:O	1:A:51:GLN:HB3	2.21	0.41
1:Y:181:THR:C	1:Y:183:ASP:H	2.23	0.41
1:A:376:LEU:C	1:A:378:ASP:H	2.24	0.41
1:A:92:THR:HB	1:A:93:GLU:H	1.28	0.41
1:B:207:VAL:HG12	1:B:208:VAL:N	2.36	0.41
1:B:262:LEU:HD12	1:B:290:ARG:HH21	1.86	0.41
1:B:354:LEU:HB3	1:B:385:TRP:CB	2.50	0.41
1:X:38:GLU:CG	1:X:167:ALA:HB2	2.34	0.41
1:Y:390:ASN:O	1:Y:392:PRO:HD3	2.21	0.41
1:A:223:ILE:HA	1:A:223:ILE:HD12	1.74	0.41
1:B:195:VAL:O	1:B:199:VAL:HG23	2.20	0.41
1:B:316:PHE:H	1:B:316:PHE:HD2	1.68	0.41
1:X:28:TYR:HH	1:X:281:HIS:CD2	2.39	0.41
1:Y:331:ASP:OD2	1:Y:379:TYR:OH	2.32	0.41
1:Y:332:ARG:H	1:Y:345:THR:CG2	2.22	0.41
1:Y:348:LEU:O	1:Y:351:TRP:HB2	2.20	0.41
1:Y:318:ARG:HD3	1:Y:437:LEU:HB3	2.02	0.41
1:A:32:PHE:CE1	1:A:40:PHE:CA	3.01	0.40
1:A:417:GLU:C	1:A:418:MET:HG3	2.41	0.40
1:A:50:ILE:HD11	1:A:80:GLN:OE1	2.21	0.40
1:A:94:ARG:O	1:A:95:VAL:C	2.59	0.40
1:B:379:TYR:O	1:B:379:TYR:CD1	2.74	0.40
1:X:89:ASP:O	1:X:91:PRO:HD3	2.21	0.40
1:B:236:LEU:HA	1:B:236:LEU:HD23	1.91	0.40
1:B:36:ASP:C	1:B:38:GLU:N	2.74	0.40
1:X:248:LEU:O	1:X:249:LYS:C	2.59	0.40
1:Y:407:ARG:CZ	1:Y:431:PHE:CD2	3.04	0.40
1:Y:407:ARG:NE	1:Y:431:PHE:CE2	2.90	0.40
1:A:411:THR:CG2	1:A:413:PHE:CE2	3.04	0.40
1:B:13:VAL:CG1	1:B:13:VAL:O	2.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:436:THR:O	1:B:437:LEU:HD12	2.21	0.40
1:X:352:VAL:HG11	1:X:380:ALA:HB2	2.03	0.40
1:Y:228:ASN:O	1:Y:229:LEU:C	2.59	0.40
1:A:18:HIS:CE1	1:X:60:ALA:HA	2.57	0.40
1:A:253:ILE:HD13	1:A:288:ILE:HD13	2.02	0.40
1:A:397:TYR:HB3	1:A:413:PHE:CE1	2.57	0.40
1:A:65:GLN:NE2	1:A:170:GLY:O	2.54	0.40
1:B:270:ARG:O	1:B:273:GLU:N	2.36	0.40
1:B:377:VAL:HG23	1:B:378:ASP:N	2.36	0.40
1:B:39:ARG:CZ	1:B:39:ARG:HB3	2.52	0.40
1:B:60:ALA:O	1:B:63:PHE:HB3	2.22	0.40
1:X:318:ARG:HA	1:X:319:PRO:HD3	1.90	0.40
1:A:321:VAL:HG23	1:A:324:TYR:HB2	2.03	0.40
1:A:60:ALA:O	1:A:61:LEU:C	2.60	0.40
1:A:70:THR:OG1	1:A:70:THR:O	2.30	0.40
1:B:262:LEU:CD1	1:B:290:ARG:HH21	2.34	0.40
1:X:28:TYR:OH	1:X:281:HIS:CD2	2.74	0.40
1:Y:240:ASP:N	1:Y:240:ASP:OD1	2.54	0.40
1:Y:318:ARG:HB2	1:Y:319:PRO:CD	2.51	0.40
1:Y:69:LEU:HD23	1:Y:69:LEU:HA	1.87	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	435/460 (95%)	348 (80%)	59 (14%)	28 (6%)	1	8
1	B	433/460 (94%)	331 (76%)	79 (18%)	23 (5%)	2	12
1	X	433/460 (94%)	335 (77%)	74 (17%)	24 (6%)	2	11
1	Y	402/460 (87%)	314 (78%)	67 (17%)	21 (5%)	2	12
All	All	1703/1840 (93%)	1328 (78%)	279 (16%)	96 (6%)	2	11

All (96) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	35	ILE
1	A	89	ASP
1	A	92	THR
1	A	93	GLU
1	A	95	VAL
1	A	144	VAL
1	A	282	ALA
1	A	376	LEU
1	A	377	VAL
1	B	49	VAL
1	B	87	ALA
1	B	349	ASP
1	X	16	LEU
1	X	78	GLY
1	X	84	ALA
1	X	145	ASP
1	X	157	HIS
1	X	330	VAL
1	X	424	ALA
1	Y	232	ASP
1	Y	261	PRO
1	Y	368	LEU
1	A	10	GLN
1	A	14	GLN
1	A	77	GLY
1	A	87	ALA
1	A	91	PRO
1	A	146	ALA
1	A	229	LEU
1	A	245	GLY
1	A	311	LEU
1	A	419	GLY
1	B	38	GLU
1	B	48	ALA
1	B	96	ASP
1	B	99	ARG
1	B	103	ASP
1	B	145	ASP
1	B	191	ALA
1	B	214	GLY
1	B	300	LYS
1	X	8	VAL

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Mol	Chain	Res	Type
1	X	13	VAL
1	X	99	ARG
1	X	349	ASP
1	Y	52	ASP
1	Y	84	ALA
1	Y	268	ILE
1	Y	283	GLY
1	Y	371	THR
1	A	9	ARG
1	A	61	LEU
1	A	180	GLU
1	A	243	ASN
1	A	349	ASP
1	B	9	ARG
1	B	33	SER
1	B	305	LEU
1	B	337	GLU
1	B	408	ASP
1	X	6	PRO
1	X	14	GLN
1	X	146	ALA
1	X	261	PRO
1	X	282	ALA
1	Y	66	THR
1	Y	191	ALA
1	Y	370	ARG
1	A	30	HIS
1	A	71	PRO
1	B	267	SER
1	X	35	ILE
1	X	89	ASP
1	X	304	ASP
1	X	328	LEU
1	Y	47	GLY
1	Y	93	GLU
1	Y	282	ALA
1	Y	439	ALA
1	A	244	GLY
1	B	35	ILE
1	B	69	LEU
1	B	387	SER
1	X	39	ARG

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Mol	Chain	Res	Type
1	X	301	SER
1	Y	161	ASP
1	Y	279	PHE
1	Y	390	ASN
1	Y	421	VAL
1	B	106	ILE
1	Y	229	LEU
1	Y	372	VAL
1	X	155	PRO
1	B	8	VAL
1	A	8	VAL
1	X	391	ASN

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	346/366 (94%)	293 (85%)	53 (15%)	2	12
1	B	344/366 (94%)	307 (89%)	37 (11%)	6	25
1	X	344/366 (94%)	293 (85%)	51 (15%)	3	13
1	Y	323/366 (88%)	281 (87%)	42 (13%)	4	18
All	All	1357/1464 (93%)	1174 (86%)	183 (14%)	4	16

All (183) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	ILE
1	A	15	LEU
1	A	16	LEU
1	A	20	ARG
1	A	25	ILE
1	A	31	ARG
1	A	35	ILE
1	A	40	PHE
1	A	45	VAL

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Mol	Chain	Res	Type
1	A	52	ASP
1	A	65	GLN
1	A	67	VAL
1	A	69	LEU
1	A	70	THR
1	A	81	LEU
1	A	85	LEU
1	A	92	THR
1	A	103	ASP
1	A	117	ASN
1	A	143	ILE
1	A	144	VAL
1	A	156	ARG
1	A	180	GLU
1	A	193	VAL
1	A	200	HIS
1	A	213	THR
1	A	216	LEU
1	A	225	SER
1	A	247	ARG
1	A	248	LEU
1	A	255	ARG
1	A	262	LEU
1	A	263	SER
1	A	268	ILE
1	A	272	SER
1	A	274	LEU
1	A	284	SER
1	A	293	ARG
1	A	295	VAL
1	A	301	SER
1	A	318	ARG
1	A	321	VAL
1	A	322	GLU
1	A	327	ARG
1	A	345	THR
1	A	347	ARG
1	A	353	TYR
1	A	364[A]	ARG
1	A	364[B]	ARG
1	A	378	ASP
1	A	382	GLN

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Mol	Chain	Res	Type
1	A	406	ARG
1	A	415	ARG
1	B	18	HIS
1	B	23	LYS
1	B	29	LEU
1	B	36	ASP
1	B	38	GLU
1	B	52	ASP
1	B	67	VAL
1	B	69	LEU
1	B	95	VAL
1	B	100	VAL
1	B	143	ILE
1	B	148	LYS
1	B	149	LEU
1	B	198	LEU
1	B	202	LEU
1	B	211	THR
1	B	213	THR
1	B	216	LEU
1	B	228	ASN
1	B	229	LEU
1	B	248	LEU
1	B	263	SER
1	B	268	ILE
1	B	293	ARG
1	B	301	SER
1	B	318	ARG
1	B	327	ARG
1	B	332	ARG
1	B	345	THR
1	B	348	LEU
1	B	359	VAL
1	B	362	ASP
1	B	370	ARG
1	B	379	TYR
1	B	387	SER
1	B	407	ARG
1	B	436	THR
1	X	8	VAL
1	X	16	LEU
1	X	20	ARG

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Mol	Chain	Res	Type
1	X	25	ILE
1	X	31	ARG
1	X	32	PHE
1	X	38	GLU
1	X	39	ARG
1	X	50	ILE
1	X	66	THR
1	X	67	VAL
1	X	81	LEU
1	X	89	ASP
1	X	99	ARG
1	X	104	GLU
1	X	106	ILE
1	X	109	ILE
1	X	125	ARG
1	X	147	ASP
1	X	156	ARG
1	X	183	ASP
1	X	185	THR
1	X	213	THR
1	X	224	LEU
1	X	226	SER
1	X	236	LEU
1	X	243	ASN
1	X	263	SER
1	X	269	THR
1	X	287	LEU
1	X	290	ARG
1	X	293	ARG
1	X	318	ARG
1	X	319	PRO
1	X	321	VAL
1	X	344	ILE
1	X	359	VAL
1	X	362	ASP
1	X	364	ARG
1	X	375	ARG
1	X	382	GLN
1	X	399	GLU
1	X	401	CYS
1	X	407	ARG
1	X	408	ASP

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Mol	Chain	Res	Type
1	X	409	GLU
1	X	415	ARG
1	X	418	MET
1	X	423	VAL
1	X	436	THR
1	X	437	LEU
1	Y	16	LEU
1	Y	25	ILE
1	Y	29	LEU
1	Y	45	VAL
1	Y	50	ILE
1	Y	52	ASP
1	Y	70	THR
1	Y	80	GLN
1	Y	102	ARG
1	Y	104	GLU
1	Y	118	LEU
1	Y	136	ARG
1	Y	157	HIS
1	Y	186	LEU
1	Y	193	VAL
1	Y	196	ARG
1	Y	202	LEU
1	Y	206	LYS
1	Y	211	THR
1	Y	213	THR
1	Y	223	ILE
1	Y	229	LEU
1	Y	240	ASP
1	Y	248	LEU
1	Y	274	LEU
1	Y	279	PHE
1	Y	280	THR
1	Y	281	HIS
1	Y	301	SER
1	Y	318	ARG
1	Y	329	ARG
1	Y	332	ARG
1	Y	345	THR
1	Y	347	ARG
1	Y	370	ARG
1	Y	375	ARG

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Mol	Chain	Res	Type
1	Y	382	GLN
1	Y	390	ASN
1	Y	401	CYS
1	Y	414	TRP
1	Y	417	GLU
1	Y	421	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	117	ASN
1	X	65	GLN
1	Y	18	HIS

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](#)

4 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
3	COA	Y	501	-	41,50,50	2.74	11 (26%)	52,75,75	1.76	13 (25%)
3	COA	X	501	-	41,50,50	2.71	11 (26%)	52,75,75	1.84	13 (25%)
2	GLU	A	501	-	2,9,9	0.28	0	2,11,11	1.39	0
2	GLU	Y	502	-	2,9,9	0.30	0	2,11,11	0.90	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
3	COA	Y	501	-	-	16/44/64/64	0/3/3/3
3	COA	X	501	-	-	23/44/64/64	0/3/3/3
2	GLU	A	501	-	-	1/3/9/9	-
2	GLU	Y	502	-	-	3/3/9/9	-

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	Y	501	COA	C2A-N3A	9.53	1.47	1.32
3	X	501	COA	C2A-N3A	9.13	1.46	1.32
3	X	501	COA	C9P-N8P	7.53	1.50	1.33
3	Y	501	COA	C9P-N8P	7.12	1.49	1.33
3	X	501	COA	C5P-N4P	6.18	1.47	1.33
3	Y	501	COA	C5P-N4P	6.02	1.47	1.33
3	Y	501	COA	O4B-C1B	4.79	1.47	1.41
3	X	501	COA	O4B-C1B	4.18	1.46	1.41
3	X	501	COA	C2A-N1A	3.97	1.41	1.33
3	Y	501	COA	C2A-N1A	3.93	1.41	1.33
3	X	501	COA	C8A-N7A	3.73	1.41	1.34
3	X	501	COA	C2B-C1B	3.57	1.59	1.53
3	Y	501	COA	C8A-N7A	3.53	1.41	1.34
3	Y	501	COA	C6A-N6A	3.50	1.46	1.34
3	X	501	COA	C6A-N6A	3.45	1.46	1.34
3	Y	501	COA	C4A-N3A	3.41	1.40	1.35
3	Y	501	COA	C2B-C1B	3.16	1.58	1.53
3	X	501	COA	C4A-N3A	2.97	1.39	1.35
3	Y	501	COA	C5A-N7A	2.72	1.49	1.39
3	X	501	COA	C5A-N7A	2.54	1.49	1.39
3	Y	501	COA	P1A-O1A	2.08	1.58	1.50
3	X	501	COA	P1A-O1A	2.07	1.58	1.50

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	Y	501	COA	N3A-C2A-N1A	-5.32	120.36	128.68
3	X	501	COA	O6A-CCP-CBP	5.31	119.08	110.55
3	X	501	COA	N3A-C2A-N1A	-5.26	120.46	128.68
3	Y	501	COA	O6A-CCP-CBP	4.71	118.12	110.55
3	X	501	COA	O2B-C2B-C3B	3.79	121.94	111.17
3	X	501	COA	P2A-O3A-P1A	-3.62	120.41	132.83
3	Y	501	COA	C3B-C2B-C1B	3.15	106.87	99.89
3	Y	501	COA	O3B-C3B-C4B	3.04	121.08	110.08
3	Y	501	COA	O2B-C2B-C3B	2.96	119.58	111.17
3	Y	501	COA	C2P-C3P-N4P	2.95	119.04	112.31
3	X	501	COA	O3B-C3B-C2B	2.90	122.19	111.68
3	Y	501	COA	C6P-C7P-N8P	2.89	117.73	111.90
3	X	501	COA	CDP-CBP-CAP	2.73	113.56	108.82
3	X	501	COA	O2B-C2B-C1B	2.71	120.87	110.85
3	X	501	COA	O4B-C4B-C5B	2.69	118.22	109.37
3	X	501	COA	C2P-C3P-N4P	2.68	118.42	112.31
3	X	501	COA	CEP-CBP-CCP	2.62	112.51	108.23
3	Y	501	COA	P2A-O3A-P1A	-2.57	124.01	132.83
3	Y	501	COA	C6P-C5P-N4P	2.48	120.60	116.42
3	Y	501	COA	O4B-C4B-C5B	2.38	117.19	109.37
3	X	501	COA	O3B-C3B-C4B	2.30	118.41	110.08
3	X	501	COA	O5B-C5B-C4B	2.28	116.85	108.99
3	Y	501	COA	O2B-C2B-C1B	2.28	119.26	110.85
3	X	501	COA	OAP-CAP-CBP	2.25	115.55	110.25
3	Y	501	COA	O5B-C5B-C4B	2.17	116.47	108.99
3	Y	501	COA	C5B-C4B-C3B	2.10	121.37	114.40

There are no chirality outliers.

All (43) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	Y	501	COA	C3B-O3B-P3B-O7A
3	Y	501	COA	C5B-O5B-P1A-O1A
3	Y	501	COA	CBP-CCP-O6A-P2A
3	Y	501	COA	CDP-CBP-CCP-O6A
3	Y	501	COA	CAP-CBP-CCP-O6A
3	Y	501	COA	O9P-C9P-CAP-OAP
3	Y	501	COA	CAP-C9P-N8P-C7P
3	Y	501	COA	O9P-C9P-N8P-C7P
3	Y	501	COA	C5P-C6P-C7P-N8P
3	X	501	COA	C3B-O3B-P3B-O7A

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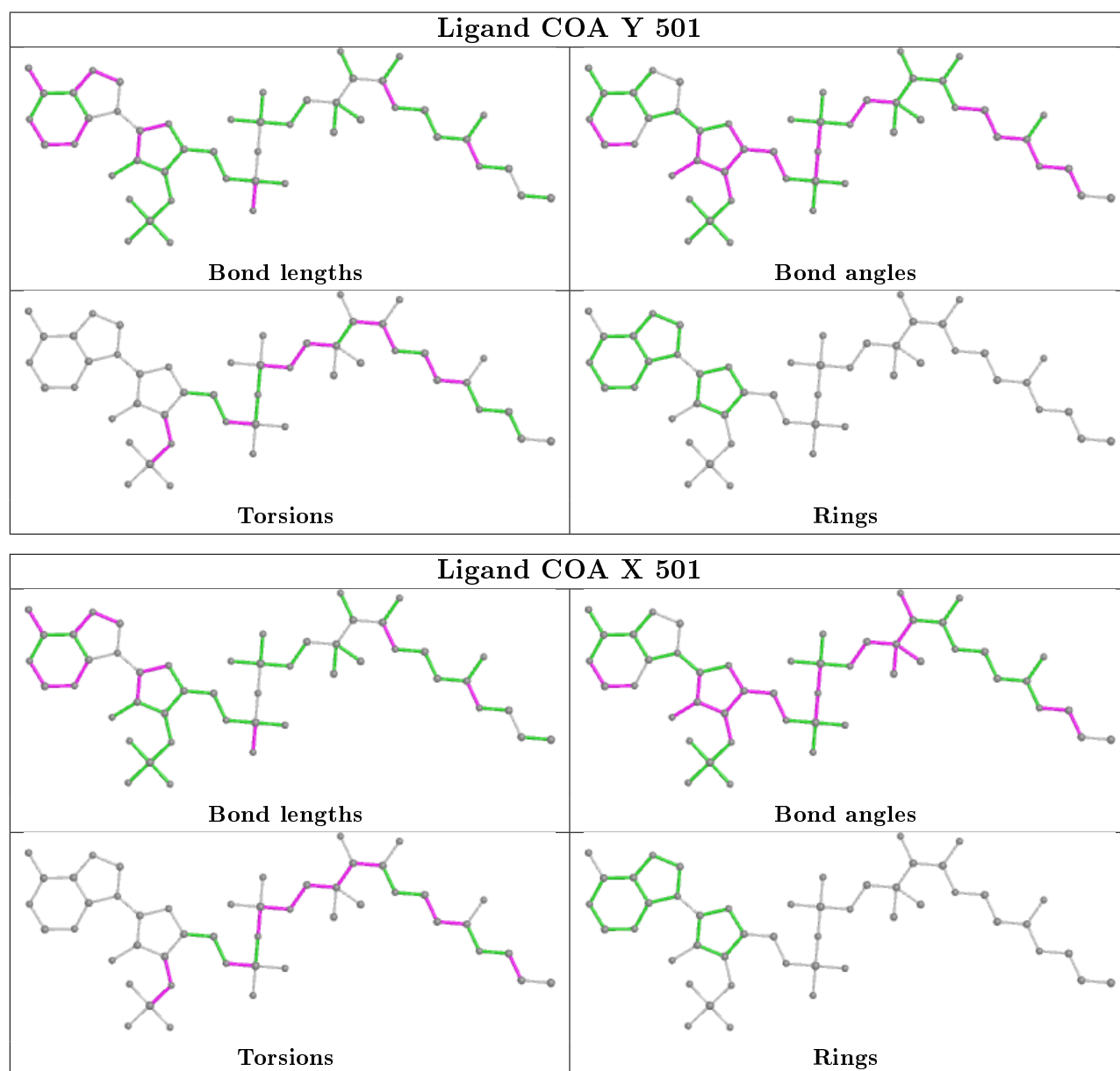
Mol	Chain	Res	Type	Atoms
3	X	501	COA	C5B-O5B-P1A-O1A
3	X	501	COA	C5B-O5B-P1A-O2A
3	X	501	COA	C5B-O5B-P1A-O3A
3	X	501	COA	CCP-O6A-P2A-O3A
3	X	501	COA	CCP-O6A-P2A-O4A
3	X	501	COA	CBP-CCP-O6A-P2A
3	X	501	COA	CAP-CBP-CCP-O6A
3	X	501	COA	C5P-C6P-C7P-N8P
3	X	501	COA	S1P-C2P-C3P-N4P
2	A	501	GLU	N-CA-CB-CG
2	Y	502	GLU	N-CA-CB-CG
2	Y	502	GLU	C-CA-CB-CG
3	X	501	COA	C2B-C3B-O3B-P3B
3	X	501	COA	C4B-C3B-O3B-P3B
3	Y	501	COA	CEP-CBP-CCP-O6A
2	Y	502	GLU	CA-CB-CG-CD
3	X	501	COA	O9P-C9P-CAP-OAP
3	X	501	COA	O5P-C5P-C6P-C7P
3	Y	501	COA	N4P-C5P-C6P-C7P
3	X	501	COA	P1A-O3A-P2A-O6A
3	X	501	COA	C9P-CAP-CBP-CEP
3	Y	501	COA	C5B-O5B-P1A-O3A
3	Y	501	COA	C5B-O5B-P1A-O2A
3	X	501	COA	CEP-CBP-CCP-O6A
3	Y	501	COA	O5P-C5P-C6P-C7P
3	X	501	COA	N4P-C5P-C6P-C7P
3	Y	501	COA	C2B-C3B-O3B-P3B
3	X	501	COA	N8P-C9P-CAP-OAP
3	X	501	COA	C9P-CAP-CBP-CDP
3	X	501	COA	C3B-O3B-P3B-O8A
3	Y	501	COA	CCP-O6A-P2A-O4A
3	X	501	COA	CDP-CBP-CCP-O6A
3	X	501	COA	C9P-CAP-CBP-CCP

There are no ring outliers.

4 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	Y	501	COA	7	0
3	X	501	COA	9	0
2	A	501	GLU	1	0
2	Y	502	GLU	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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	436/460 (94%)	-0.43	5 (1%) 80 64	54, 88, 153, 217	0
1	B	435/460 (94%)	-0.13	15 (3%) 45 24	72, 130, 192, 238	0
1	X	435/460 (94%)	-0.36	5 (1%) 80 64	62, 99, 160, 230	0
1	Y	408/460 (88%)	-0.07	23 (5%) 24 11	62, 124, 231, 301	0
All	All	1714/1840 (93%)	-0.25	48 (2%) 53 30	54, 110, 200, 301	0

All (48) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Y	97	GLY	6.0
1	B	98	LEU	5.9
1	B	10	GLN	4.1
1	B	96	ASP	4.0
1	Y	237	MET	3.8
1	A	6	PRO	3.8
1	A	149	LEU	3.8
1	B	90	ILE	3.7
1	Y	279	PHE	3.7
1	X	408	ASP	3.6
1	Y	13	VAL	3.6
1	Y	20	ARG	3.6
1	Y	11	THR	3.6
1	Y	100	VAL	3.4
1	B	91	PRO	3.3
1	Y	278	LEU	3.1
1	X	37	GLN	3.0
1	Y	90	ILE	3.0
1	Y	96	ASP	3.0
1	Y	91	PRO	2.9
1	B	6	PRO	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	298	ASP	2.8
1	Y	98	LEU	2.8
1	Y	12	ILE	2.7
1	A	5	ALA	2.6
1	X	36	ASP	2.6
1	B	94	ARG	2.5
1	Y	63	PHE	2.5
1	B	220	ASP	2.5
1	Y	243	ASN	2.5
1	Y	89	ASP	2.4
1	B	349	ASP	2.4
1	Y	242	VAL	2.3
1	Y	16	LEU	2.3
1	Y	94	ARG	2.3
1	Y	22	GLY	2.2
1	B	177	CYS	2.2
1	A	94	ARG	2.2
1	X	89	ASP	2.2
1	A	95	VAL	2.2
1	B	84	ALA	2.1
1	Y	293	ARG	2.1
1	Y	212	GLY	2.1
1	B	409	GLU	2.1
1	B	238	GLN	2.1
1	Y	95	VAL	2.1
1	X	14	GLN	2.1
1	B	97	GLY	2.1

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.

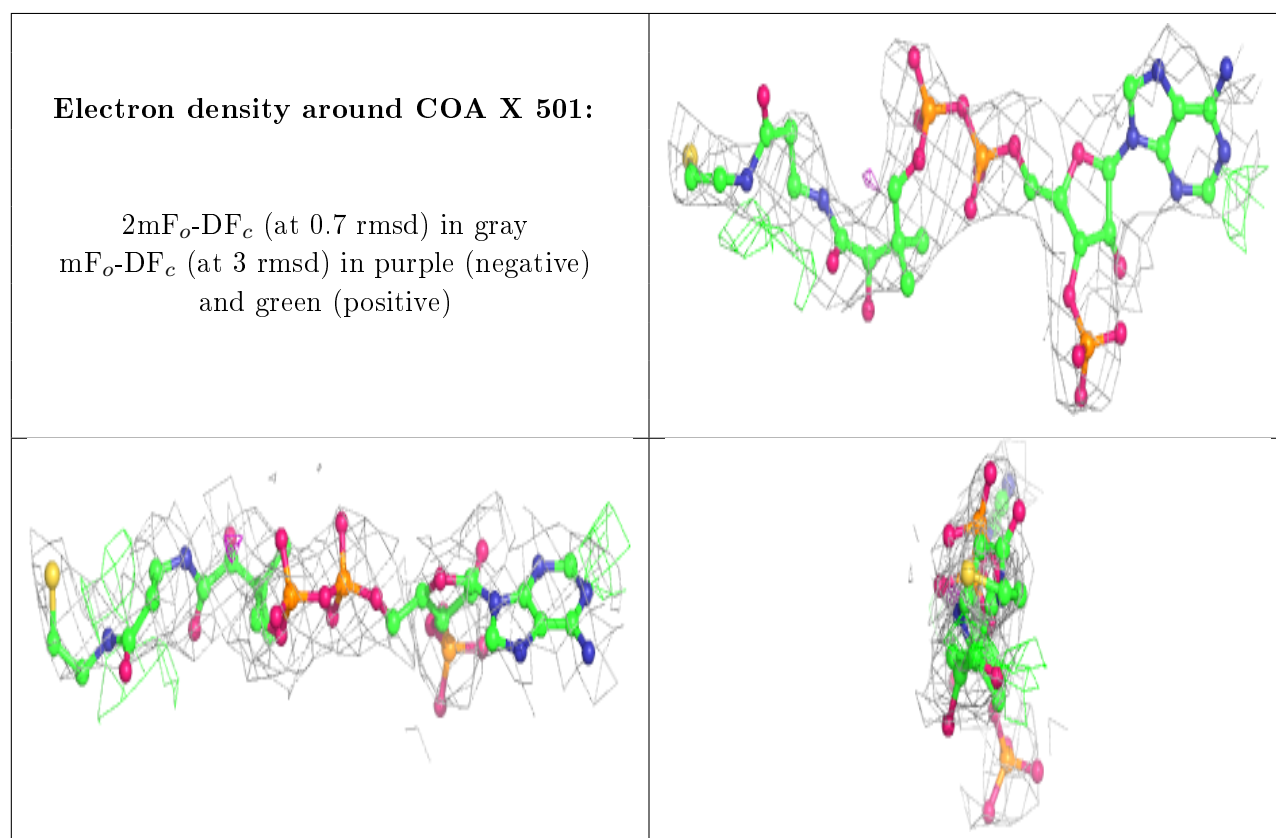
6.4 Ligands [i](#)

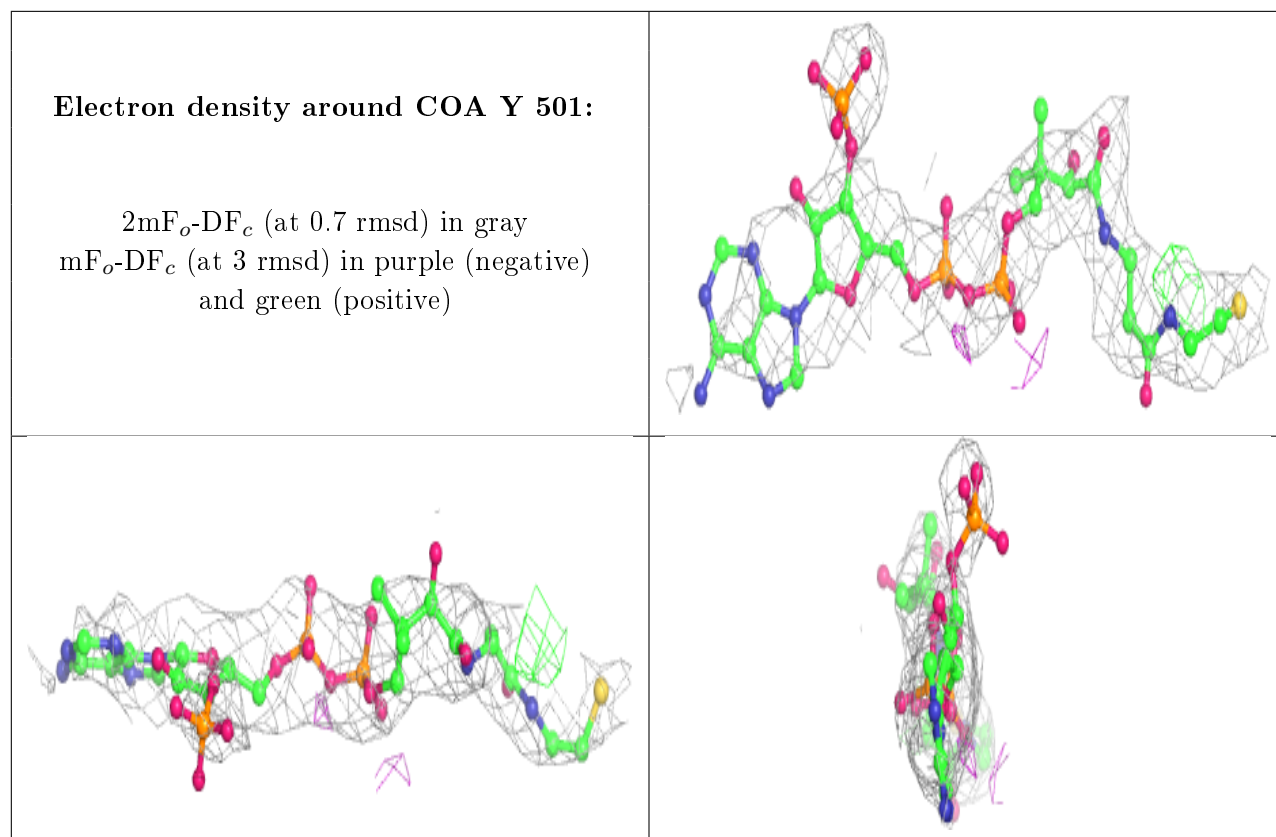
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	COA	X	501	48/48	0.83	0.24	91,175,214,449	0
3	COA	Y	501	48/48	0.89	0.27	78,141,256,434	0
2	GLU	Y	502	10/10	0.90	0.34	56,106,120,128	0
2	GLU	A	501	10/10	0.91	0.24	54,102,117,128	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





6.5 Other polymers [i](#)

There are no such residues in this entry.