



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 02:14 pm GMT

PDB ID : 3DC2
Title : Crystal structure of serine bound D-3-phosphoglycerate dehydrogenase from Mycobacterium tuberculosis
Authors : Dey, S.; Sacchettini, J.C.
Deposited on : 2008-06-03
Resolution : 2.70 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

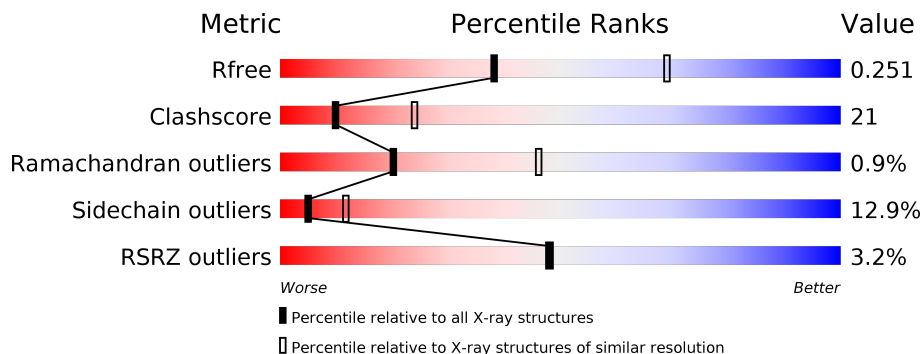
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	100719	2259 (2.70-2.70)
Clashscore	112137	2590 (2.70-2.70)
Ramachandran outliers	110173	2550 (2.70-2.70)
Sidechain outliers	110143	2550 (2.70-2.70)
RSRZ outliers	101464	2275 (2.70-2.70)

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	529	<div> <div>4%</div> <div> <div></div> <div>62%</div> <div>31%</div> <div>5% ..</div> </div> </div>
1	B	529	<div> <div>2%</div> <div> <div></div> <div>60%</div> <div>32%</div> <div>6% •</div> </div> </div>

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	SER	B	600	-	-	-	X
3	TLA	B	700	-	-	-	X
3	TLA	B	701	-	-	-	X

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7761 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

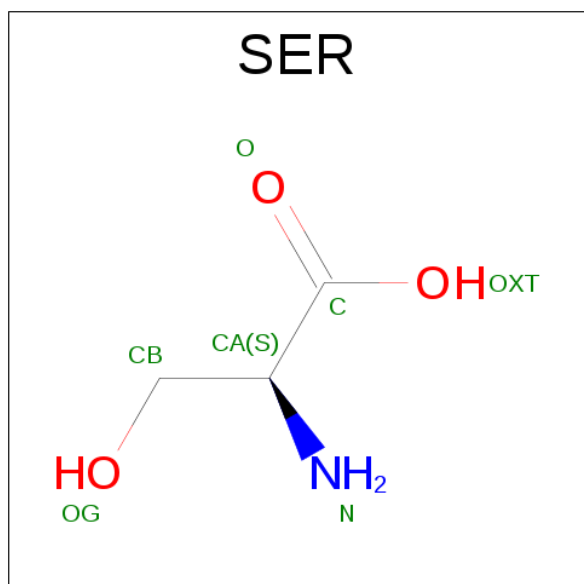
- Molecule 1 is a protein called D-3-phosphoglycerate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	526	Total	C	N	O	S	0	0	0
			3830	2413	672	743	2			
1	B	523	Total	C	N	O	S	0	0	0
			3810	2401	669	738	2			

There are 4 discrepancies between the modelled and reference sequences:

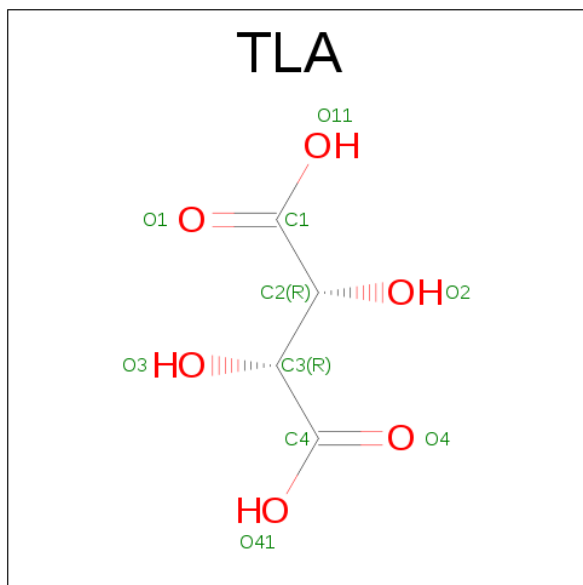
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	EXPRESSION TAG	UNP P0A544
A	2	VAL	-	EXPRESSION TAG	UNP P0A544
B	1	MET	-	EXPRESSION TAG	UNP P0A544
B	2	VAL	-	EXPRESSION TAG	UNP P0A544

- Molecule 2 is SERINE (three-letter code: SER) (formula: C₃H₇NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			7	3	1	3		
2	B	1	Total	C	N	O	0	0
			7	3	1	3		

- Molecule 3 is L(+)-TARTARIC ACID (three-letter code: TLA) (formula: C₄H₆O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			10	4	6		
3	B	1	Total	C	O	0	0
			10	4	6		
3	B	1	Total	C	O	0	0
			10	4	6		

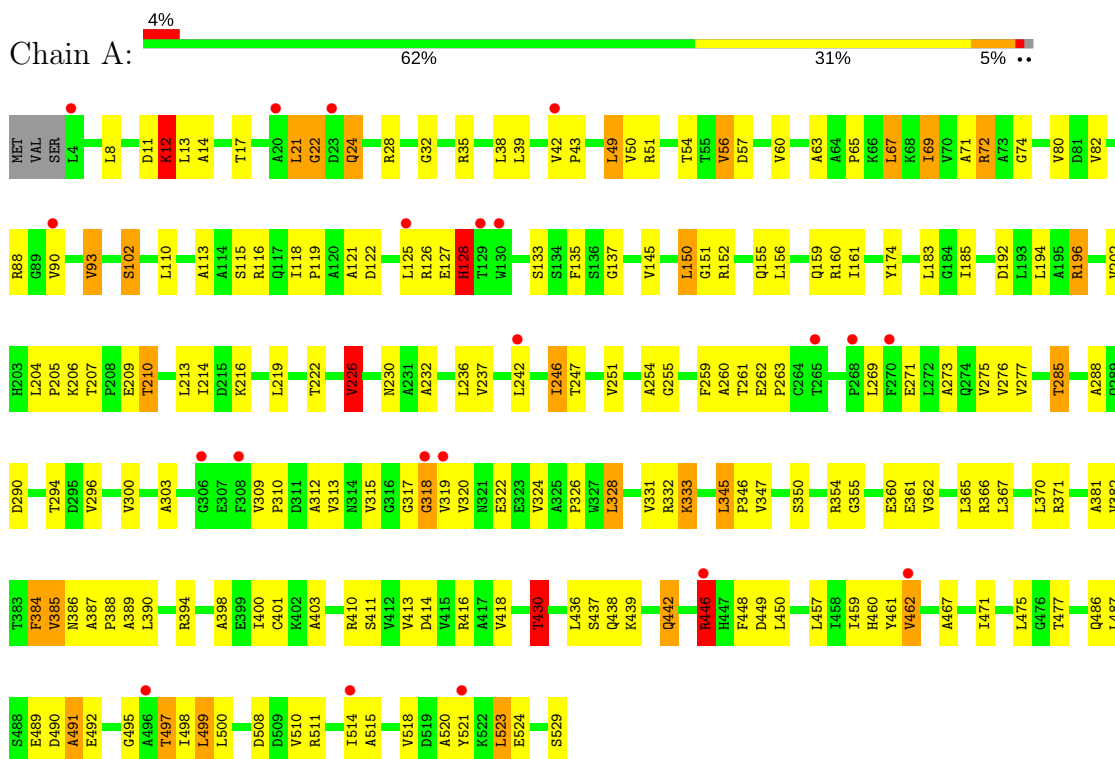
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	40	Total	O	0	0
			40	40		
4	B	37	Total	O	0	0
			37	37		

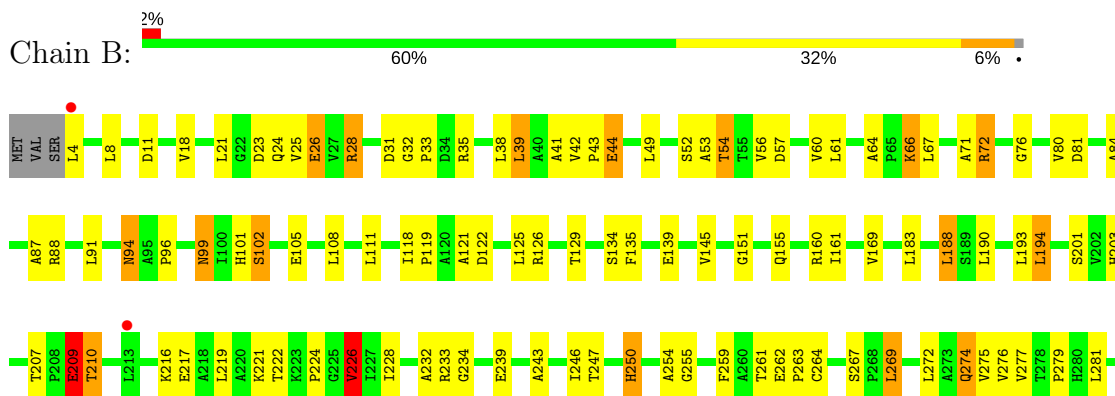
3 Residue-property plots

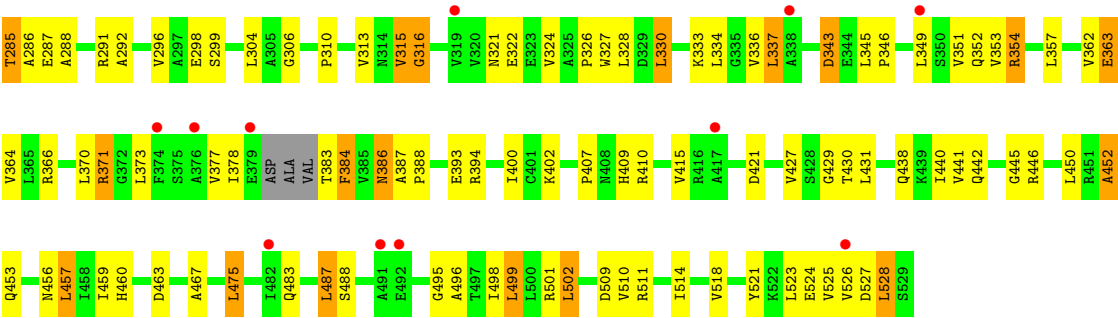
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

• Molecule 1: D-3-phosphoglycerate dehydrogenase



• Molecule 1: D-3-phosphoglycerate dehydrogenase





4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	165.19Å 165.19Å 218.89Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.57 – 2.70 46.59 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.2 (46.57-2.70) 99.2 (46.59-2.70)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.65 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.222 , 0.263 0.210 , 0.251	Depositor DCC
R_{free} test set	2452 reflections (5.32%)	DCC
Wilson B-factor (Å ²)	67.7	Xtriage
Anisotropy	0.632	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 66.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7761	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.10% 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: TLA

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	0.87	6/3884 (0.2%)	0.90	6/5308 (0.1%)
1	B	1.02	18/3863 (0.5%)	0.86	3/5277 (0.1%)
All	All	0.95	24/7747 (0.3%)	0.88	9/10585 (0.1%)

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

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

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	393	GLU	CD-OE1	16.65	1.44	1.25
1	A	128	HIS	CE1-NE2	15.61	1.68	1.32
1	B	217	GLU	CD-OE2	13.02	1.40	1.25
1	A	446	ARG	CZ-NH1	11.88	1.48	1.33
1	B	393	GLU	CD-OE2	11.65	1.38	1.25
1	B	44	GLU	CD-OE2	10.79	1.37	1.25
1	A	128	HIS	CG-ND1	10.14	1.61	1.38
1	B	44	GLU	CG-CD	9.70	1.66	1.51
1	B	66	LYS	CE-NZ	9.68	1.73	1.49
1	B	44	GLU	CD-OE1	9.66	1.36	1.25
1	B	226	VAL	CB-CG2	9.53	1.72	1.52
1	B	217	GLU	CD-OE1	9.35	1.35	1.25
1	B	26	GLU	CG-CD	9.15	1.65	1.51
1	B	250	HIS	CG-CD2	8.69	1.50	1.35
1	B	250	HIS	CE1-NE2	8.23	1.51	1.32
1	A	477	THR	CB-OG1	7.47	1.58	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	221	LYS	CE-NZ	6.78	1.66	1.49
1	B	28	ARG	CG-CD	6.29	1.67	1.51
1	A	477	THR	CB-CG2	5.58	1.70	1.52
1	B	216	LYS	CB-CG	5.58	1.67	1.52
1	A	159	GLN	CD-OE1	5.53	1.36	1.24
1	B	221	LYS	CD-CE	5.47	1.65	1.51
1	B	28	ARG	NE-CZ	5.29	1.40	1.33
1	B	250	HIS	CG-ND1	5.01	1.49	1.38

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	446	ARG	NE-CZ-NH2	-15.04	112.78	120.30
1	A	430	THR	CB-CA-C	-6.42	94.26	111.60
1	A	446	ARG	NE-CZ-NH1	6.31	123.46	120.30
1	B	221	LYS	CD-CE-NZ	-6.22	97.38	111.70
1	A	128	HIS	ND1-CG-CD2	5.43	116.41	108.80
1	A	345	LEU	CA-CB-CG	5.11	127.06	115.30
1	B	99	ASN	N-CA-CB	-5.02	101.57	110.60
1	A	226	VAL	CB-CA-C	-5.01	101.88	111.40
1	B	44	GLU	CB-CG-CD	-5.00	100.69	114.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	209	GLU	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	3830	0	3916	161	0
1	B	3810	0	3897	178	0
2	A	7	0	4	0	0
2	B	7	0	4	0	0
3	A	10	0	4	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	20	0	8	0	0
4	A	40	0	0	6	0
4	B	37	0	0	5	0
All	All	7761	0	7833	331	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 21.

All (331) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:66:LYS:CE	1:B:66:LYS:NZ	1.73	1.49
1:A:128:HIS:CE1	1:A:128:HIS:NE2	1.68	1.45
1:A:285:THR:HG22	1:A:288:ALA:H	1.06	1.20
1:A:332:ARG:HG2	1:A:332:ARG:HH21	1.18	1.08
1:B:285:THR:HG22	1:B:288:ALA:H	1.16	1.07
1:B:352:GLN:HE21	1:B:354:ARG:HD3	1.12	1.06
1:B:42:VAL:HG12	1:B:64:ALA:HB2	1.38	1.03
1:A:246:ILE:HD12	1:A:251:VAL:HG22	1.44	0.99
1:B:42:VAL:N	1:B:43:PRO:HD2	1.79	0.97
1:B:345:LEU:HD12	1:B:346:PRO:HD3	1.44	0.97
1:B:345:LEU:HD12	1:B:346:PRO:CD	2.01	0.91
1:B:511:ARG:NH2	1:B:525:VAL:HB	1.88	0.89
1:B:352:GLN:NE2	1:B:354:ARG:HD3	1.87	0.88
1:B:407:PRO:HD2	4:B:829:HOH:O	1.74	0.87
1:B:118:ILE:HB	1:B:119:PRO:HD3	1.57	0.87
1:B:430:THR:HG22	1:B:431:LEU:N	1.89	0.85
1:A:285:THR:CG2	1:A:288:ALA:H	1.88	0.85
1:A:332:ARG:NH2	1:A:332:ARG:HG2	1.85	0.85
1:B:371:ARG:HH12	1:B:384:PHE:HE1	1.26	0.84
1:B:315:VAL:HG13	1:B:316:GLY:N	1.91	0.84
1:A:285:THR:HG22	1:A:288:ALA:N	1.90	0.84
1:A:411:SER:O	1:A:430:THR:HG23	1.80	0.81
1:A:205:PRO:O	1:A:210:THR:HG21	1.82	0.80
1:B:285:THR:CG2	1:B:288:ALA:H	1.94	0.80
1:B:371:ARG:NH1	1:B:384:PHE:HE1	1.80	0.80
1:A:246:ILE:CD1	1:A:251:VAL:HG22	2.10	0.80
1:A:69:ILE:HD12	1:A:303:ALA:HB3	1.65	0.79
1:A:88:ARG:HH21	1:A:88:ARG:HB3	1.48	0.78
1:A:490:ASP:O	1:A:491:ALA:C	2.23	0.77
1:B:285:THR:HG22	1:B:288:ALA:N	1.98	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:69:ILE:HD13	1:A:303:ALA:HB1	1.68	0.75
1:B:81:ASP:OD2	1:B:84:ALA:HB2	1.87	0.75
1:B:315:VAL:HG13	1:B:316:GLY:H	1.50	0.75
1:B:274:GLN:H	1:B:274:GLN:HE21	1.35	0.74
1:A:72:ARG:NH2	1:A:74:GLY:HA3	2.03	0.74
1:B:41:ALA:C	1:B:43:PRO:HD2	2.08	0.74
1:A:226:VAL:HG23	1:A:251:VAL:HB	1.71	0.73
1:B:101:HIS:O	1:B:105:GLU:HG3	1.88	0.73
1:A:88:ARG:NH2	1:A:88:ARG:HB3	2.03	0.72
1:A:460:HIS:HD2	1:A:497:THR:HG23	1.55	0.72
1:A:411:SER:O	1:A:430:THR:CG2	2.37	0.72
1:A:72:ARG:HH21	1:A:74:GLY:HA3	1.53	0.72
1:B:274:GLN:N	1:B:274:GLN:HE21	1.88	0.72
1:A:49:LEU:HD22	1:A:71:ALA:HB3	1.72	0.71
1:B:352:GLN:HE21	1:B:354:ARG:CD	2.00	0.70
1:B:371:ARG:NH2	4:B:819:HOH:O	2.22	0.70
1:B:52:SER:HB3	1:B:72:ARG:NH1	2.06	0.70
1:A:461:TYR:O	1:A:495:GLY:HA2	1.92	0.70
1:B:11:ASP:OD2	1:B:54:THR:HG23	1.90	0.70
1:B:386:ASN:C	1:B:386:ASN:OD1	2.28	0.70
1:A:361:GLU:HA	4:A:808:HOH:O	1.90	0.69
1:B:362:VAL:HG22	1:B:402:LYS:HD3	1.72	0.69
1:A:206:LYS:CB	4:A:832:HOH:O	2.41	0.69
1:B:38:LEU:O	1:B:42:VAL:HG23	1.93	0.68
1:A:310:PRO:O	1:A:384:PHE:CE1	2.45	0.68
1:B:334:LEU:HB3	1:B:415:VAL:CG2	2.24	0.68
1:B:23:ASP:HB3	1:B:24:GLN:NE2	2.08	0.68
1:A:69:ILE:CD1	1:A:303:ALA:CB	2.71	0.68
1:B:209:GLU:OE2	1:B:209:GLU:HA	1.93	0.68
1:B:42:VAL:N	1:B:43:PRO:CD	2.57	0.68
1:A:12:LYS:HB2	4:A:821:HOH:O	1.94	0.68
1:A:102:SER:HG	1:A:285:THR:HG21	1.59	0.67
1:B:334:LEU:HB3	1:B:415:VAL:HG21	1.74	0.67
1:B:349:LEU:HD13	1:B:373:LEU:HG	1.77	0.67
1:A:69:ILE:CD1	1:A:303:ALA:HB1	2.25	0.67
1:B:169:VAL:HB	1:B:188:LEU:HD22	1.75	0.66
1:A:21:LEU:O	1:A:22:GLY:O	2.14	0.66
1:A:514:ILE:O	1:A:518:VAL:HG22	1.97	0.65
1:B:457:LEU:HD11	1:B:459:ILE:HD11	1.79	0.65
1:B:23:ASP:HB3	1:B:24:GLN:HE21	1.62	0.65
1:B:371:ARG:NH1	1:B:384:PHE:CE1	2.63	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:121:ALA:HA	1:B:135:PHE:CZ	2.31	0.65
1:B:333:LYS:HE2	1:B:528:LEU:O	1.97	0.65
1:A:255:GLY:HA2	1:A:276:VAL:O	1.96	0.64
1:B:457:LEU:HD11	1:B:459:ILE:CG1	2.26	0.64
1:B:315:VAL:CG1	1:B:316:GLY:N	2.59	0.64
1:A:310:PRO:O	1:A:384:PHE:HE1	1.80	0.64
1:A:457:LEU:HD23	1:A:500:LEU:HD13	1.78	0.64
1:B:430:THR:HG22	1:B:431:LEU:H	1.61	0.64
1:A:102:SER:OG	1:B:139:GLU:HG3	1.98	0.64
1:B:430:THR:CG2	1:B:431:LEU:N	2.61	0.64
1:A:230:ASN:ND2	1:A:232:ALA:H	1.96	0.63
1:A:69:ILE:HD12	1:A:303:ALA:CB	2.29	0.63
1:B:145:VAL:HG11	1:B:161:ILE:HD12	1.81	0.63
1:B:364:VAL:HG22	1:B:384:PHE:HE2	1.63	0.62
1:B:327:TRP:CD2	1:B:357:LEU:HD11	2.34	0.62
1:B:11:ASP:CG	1:B:54:THR:HG23	2.20	0.62
1:B:409:HIS:NE2	1:B:441:VAL:HG11	2.14	0.62
1:A:102:SER:OG	1:A:285:THR:HG21	1.99	0.61
1:B:56:VAL:HB	1:B:80:VAL:HG22	1.82	0.61
1:B:151:GLY:O	1:B:155:GLN:HG3	2.00	0.61
1:B:194:LEU:O	1:B:222:THR:HA	2.00	0.61
1:B:336:VAL:HG12	1:B:526:VAL:HG21	1.81	0.61
1:A:246:ILE:HG22	1:A:247:THR:N	2.15	0.61
1:A:63:ALA:O	1:A:65:PRO:HD3	2.00	0.61
1:B:207:THR:O	1:B:210:THR:HG22	2.01	0.61
1:A:461:TYR:HB2	1:A:518:VAL:HB	1.83	0.61
1:B:145:VAL:HG11	1:B:161:ILE:CD1	2.31	0.61
1:B:363:GLU:OE1	1:B:366:ARG:NH1	2.35	0.60
1:A:387:ALA:HB3	1:A:388:PRO:HD3	1.84	0.60
1:B:42:VAL:HG12	1:B:64:ALA:CB	2.24	0.60
1:A:333:LYS:HE2	1:A:438:GLN:OE1	2.01	0.59
1:A:271:GLU:OE1	1:A:271:GLU:HA	2.01	0.59
1:B:274:GLN:NE2	1:B:274:GLN:H	1.98	0.59
1:B:35:ARG:O	1:B:39:LEU:HD13	2.02	0.59
1:B:354:ARG:HD2	4:B:836:HOH:O	2.01	0.59
1:A:49:LEU:HD21	1:A:300:VAL:HG21	1.85	0.59
1:A:386:ASN:HB3	1:A:389:ALA:HB3	1.85	0.59
1:A:125:LEU:HD12	1:B:277:VAL:HG23	1.84	0.59
1:A:207:THR:O	1:A:210:THR:N	2.24	0.58
1:A:459:ILE:HG12	1:A:523:LEU:HD22	1.84	0.58
1:B:31:ASP:OD1	1:B:33:PRO:HG2	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:457:LEU:HB3	1:B:502:LEU:HD21	1.85	0.58
1:A:56:VAL:HG13	1:A:80:VAL:HG13	1.85	0.58
1:A:50:VAL:HG12	1:A:51:ARG:N	2.18	0.58
1:B:84:ALA:O	1:B:87:ALA:HB3	2.03	0.58
1:A:332:ARG:NH2	1:A:332:ARG:CG	2.60	0.58
1:A:324:VAL:CG2	1:A:360:GLU:HB3	2.34	0.57
1:B:310:PRO:HD2	4:B:811:HOH:O	2.02	0.57
1:B:269:LEU:HD12	1:B:272:LEU:HD12	1.87	0.57
1:A:214:ILE:HB	1:A:237:VAL:HG22	1.87	0.57
1:A:116:ARG:NH1	1:B:102:SER:O	2.38	0.57
1:A:206:LYS:N	4:A:832:HOH:O	2.25	0.57
1:B:122:ASP:O	1:B:126:ARG:HG2	2.04	0.57
1:B:190:LEU:O	1:B:194:LEU:HD22	2.04	0.57
1:A:35:ARG:HH22	1:A:60:VAL:HG23	1.70	0.56
1:B:243:ALA:HB2	1:B:269:LEU:CD1	2.35	0.56
1:A:204:LEU:HB2	1:A:236:LEU:HD13	1.88	0.56
1:A:259:PHE:HB2	1:A:262:GLU:HG2	1.88	0.55
1:A:370:LEU:HD21	1:A:398:ALA:HB2	1.88	0.55
1:A:332:ARG:CG	1:A:332:ARG:HH21	2.00	0.55
1:B:457:LEU:HD11	1:B:459:ILE:CD1	2.37	0.55
1:A:207:THR:OG1	1:A:209:GLU:HB2	2.07	0.55
1:B:145:VAL:HG21	1:B:161:ILE:HG21	1.88	0.54
1:A:206:LYS:HB3	4:A:832:HOH:O	2.06	0.54
1:B:25:VAL:CG1	1:B:26:GLU:N	2.70	0.54
1:A:56:VAL:CG1	1:A:80:VAL:HG22	2.38	0.54
1:A:50:VAL:HG13	1:A:54:THR:HB	1.89	0.54
1:B:343:ASP:OD1	1:B:343:ASP:N	2.34	0.54
1:A:152:ARG:NH2	1:A:152:ARG:HG3	2.22	0.54
1:A:42:VAL:N	1:A:43:PRO:CD	2.70	0.54
1:A:459:ILE:HB	1:A:498:ILE:CG2	2.37	0.54
1:B:201:SER:OG	1:B:203:HIS:CE1	2.60	0.54
1:B:487:LEU:HB3	1:B:498:ILE:HG13	1.90	0.53
1:A:313:VAL:HG13	1:A:382:VAL:HA	1.89	0.53
1:B:243:ALA:HB2	1:B:269:LEU:HD13	1.90	0.53
1:A:69:ILE:CD1	1:A:303:ALA:HB3	2.33	0.53
1:B:450:LEU:HD13	1:B:499:LEU:HD22	1.90	0.53
1:A:113:ALA:HA	1:A:118:ILE:HG13	1.89	0.53
1:A:442:GLN:HA	1:A:446:ARG:O	2.09	0.53
1:A:150:LEU:HD22	1:A:155:GLN:HG2	1.92	0.52
1:B:510:VAL:O	1:B:514:ILE:HG12	2.10	0.52
1:A:309:VAL:O	1:A:312:ALA:HB2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:GLY:O	1:A:155:GLN:HG3	2.10	0.52
1:B:118:ILE:HB	1:B:119:PRO:CD	2.36	0.52
1:B:94:ASN:HD22	1:B:94:ASN:H	1.58	0.52
1:A:350:SER:HB3	1:A:416:ARG:HB2	1.91	0.52
1:B:334:LEU:HD22	1:B:427:VAL:HG12	1.92	0.52
1:B:193:LEU:C	1:B:193:LEU:HD23	2.31	0.51
1:B:203:HIS:HA	1:B:232:ALA:HB2	1.91	0.51
1:B:91:LEU:N	1:B:91:LEU:HD12	2.26	0.51
1:A:331:VAL:HG22	1:A:413:VAL:HG11	1.93	0.51
1:B:502:LEU:N	1:B:502:LEU:HD13	2.25	0.51
1:A:14:ALA:O	1:A:17:THR:HB	2.11	0.51
1:A:487:LEU:HA	1:A:497:THR:O	2.10	0.51
1:B:345:LEU:HD12	1:B:346:PRO:HD2	1.88	0.51
1:A:24:GLN:HA	1:A:24:GLN:NE2	2.25	0.50
1:B:285:THR:HG22	1:B:285:THR:O	2.11	0.50
1:A:222:THR:HB	4:A:818:HOH:O	2.10	0.50
1:A:312:ALA:O	1:A:384:PHE:CD1	2.63	0.50
1:A:152:ARG:HG3	1:A:152:ARG:HH21	1.74	0.50
1:A:82:VAL:HG21	1:A:381:ALA:HB1	1.94	0.50
1:B:23:ASP:CB	1:B:24:GLN:HE21	2.24	0.50
1:A:487:LEU:HB3	1:A:498:ILE:HD12	1.94	0.49
1:A:467:ALA:HB1	1:A:518:VAL:HG12	1.93	0.49
1:A:93:VAL:HG23	1:A:312:ALA:HA	1.95	0.49
1:A:135:PHE:HB2	1:B:281:LEU:HD21	1.95	0.49
1:B:328:LEU:HD21	1:B:364:VAL:HG13	1.93	0.49
1:A:50:VAL:CG1	1:A:54:THR:HB	2.42	0.49
1:A:492:GLU:HA	1:A:492:GLU:OE2	2.12	0.49
1:B:228:ILE:O	1:B:254:ALA:HA	2.13	0.49
1:B:111:LEU:HD23	1:B:111:LEU:C	2.33	0.49
1:A:523:LEU:C	1:A:523:LEU:CD1	2.81	0.49
1:B:267:SER:OG	1:B:269:LEU:HB2	2.13	0.49
1:A:275:VAL:HG12	1:A:277:VAL:HG13	1.94	0.48
1:A:367:LEU:HD13	1:A:384:PHE:CD2	2.48	0.48
1:B:362:VAL:CG2	1:B:402:LYS:HD3	2.42	0.48
1:B:321:ASN:HB3	1:B:324:VAL:HG23	1.95	0.48
1:A:354:ARG:NH2	1:A:414:ASP:OD1	2.47	0.48
1:A:324:VAL:HG21	1:A:360:GLU:HB3	1.96	0.48
1:A:50:VAL:CG1	1:A:51:ARG:N	2.77	0.48
1:A:439:LYS:NZ	1:A:449:ASP:OD1	2.43	0.48
1:B:334:LEU:CB	1:B:415:VAL:HG21	2.43	0.48
1:B:11:ASP:OD1	1:B:54:THR:HG23	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:336:VAL:CG1	1:B:526:VAL:HG21	2.44	0.47
1:B:298:GLU:HA	1:B:298:GLU:OE2	2.14	0.47
1:B:456:ASN:ND2	1:B:528:LEU:HD23	2.29	0.47
1:B:94:ASN:O	1:B:96:PRO:HD3	2.14	0.47
1:B:487:LEU:HD22	1:B:488:SER:N	2.30	0.47
1:A:461:TYR:N	1:A:461:TYR:CD1	2.80	0.47
1:A:362:VAL:HB	1:A:365:LEU:HD12	1.97	0.47
1:B:275:VAL:HG12	1:B:277:VAL:HG13	1.97	0.47
1:B:421:ASP:OD1	1:B:421:ASP:N	2.47	0.47
1:B:207:THR:O	1:B:207:THR:HG22	2.14	0.47
1:B:377:VAL:HG12	1:B:378:ILE:HG13	1.97	0.47
1:A:384:PHE:O	1:A:385:VAL:HG13	2.15	0.46
1:B:523:LEU:O	1:B:524:GLU:HG2	2.15	0.46
1:A:345:LEU:HD22	1:A:346:PRO:HD2	1.97	0.46
1:A:38:LEU:O	1:A:42:VAL:HG13	2.14	0.46
1:B:511:ARG:NH2	1:B:525:VAL:CB	2.69	0.46
1:B:226:VAL:HG11	4:B:803:HOH:O	2.15	0.46
1:A:192:ASP:O	1:A:196:ARG:HB2	2.15	0.46
1:A:317:GLY:C	1:A:319:VAL:H	2.20	0.45
1:A:400:ILE:HG22	1:A:401:CYS:N	2.32	0.45
1:A:366:ARG:HB2	1:A:400:ILE:HG12	1.97	0.45
1:B:155:GLN:HB3	1:B:183:LEU:HD13	1.98	0.45
1:A:354:ARG:HG2	1:A:403:ALA:HB3	1.98	0.45
1:B:330:LEU:HD23	1:B:438:GLN:HB3	1.99	0.45
1:B:445:GLY:O	1:B:446:ARG:HD2	2.17	0.45
1:B:32:GLY:HA3	1:B:54:THR:CG2	2.47	0.45
1:A:230:ASN:HD22	1:A:232:ALA:H	1.65	0.45
1:A:448:PHE:CD1	1:A:486:GLN:CD	2.90	0.45
1:B:460:HIS:O	1:B:521:TYR:N	2.47	0.45
1:B:459:ILE:HB	1:B:498:ILE:HG22	1.99	0.45
1:A:259:PHE:O	1:A:260:ALA:C	2.55	0.45
1:A:460:HIS:HD2	1:A:497:THR:CG2	2.28	0.45
1:B:483:GLN:OE1	1:B:501:ARG:HG2	2.17	0.45
1:A:446:ARG:HH21	1:A:491:ALA:H	1.64	0.45
1:A:156:LEU:O	1:A:160:ARG:HD2	2.17	0.45
1:A:32:GLY:HA3	1:A:54:THR:OG1	2.17	0.45
1:B:209:GLU:CA	1:B:209:GLU:OE2	2.64	0.45
1:A:122:ASP:OD1	1:A:126:ARG:NH2	2.50	0.44
1:A:246:ILE:CD1	1:A:251:VAL:CG2	2.89	0.44
1:A:322:GLU:O	1:A:326:PRO:HD3	2.17	0.44
1:B:487:LEU:HD22	1:B:487:LEU:C	2.37	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:487:LEU:CB	1:B:498:ILE:HG13	2.47	0.44
1:B:262:GLU:HA	1:B:263:PRO:C	2.36	0.44
1:B:334:LEU:HB3	1:B:415:VAL:HG23	1.99	0.44
1:A:312:ALA:O	1:A:384:PHE:HD1	2.00	0.44
1:B:108:LEU:HD11	1:B:161:ILE:HG12	1.98	0.44
1:B:326:PRO:HB2	1:B:431:LEU:CD1	2.47	0.44
1:B:353:VAL:HG21	1:B:362:VAL:HG21	1.99	0.44
1:B:269:LEU:HA	1:B:269:LEU:HD12	1.84	0.44
1:B:475:LEU:HD13	1:B:475:LEU:HA	1.74	0.44
1:A:254:ALA:HB3	1:A:275:VAL:HG22	2.00	0.44
1:A:290:ASP:O	1:A:294:THR:HG23	2.17	0.44
1:B:337:LEU:HB3	1:B:427:VAL:HG21	1.99	0.44
1:B:330:LEU:HD11	1:B:429:GLY:HA3	1.99	0.44
1:B:467:ALA:HA	1:B:518:VAL:HG12	1.99	0.44
1:A:461:TYR:CB	1:A:518:VAL:HB	2.48	0.44
1:B:57:ASP:OD2	1:B:60:VAL:HG23	2.18	0.44
1:A:214:ILE:CB	1:A:237:VAL:HG22	2.47	0.43
1:A:450:LEU:HD12	1:A:499:LEU:HD22	2.00	0.43
1:A:459:ILE:HB	1:A:498:ILE:HG22	1.99	0.43
1:A:315:VAL:HG11	1:A:320:VAL:HG11	2.00	0.43
1:B:11:ASP:OD1	1:B:53:ALA:HB3	2.18	0.43
1:B:255:GLY:HA2	1:B:276:VAL:O	2.17	0.43
1:A:145:VAL:HG21	1:A:161:ILE:HG12	1.99	0.43
1:B:440:ILE:HG13	1:B:452:ALA:HB2	2.00	0.43
1:B:161:ILE:HD13	1:B:161:ILE:HG21	1.65	0.43
1:B:463:ASP:H	1:B:495:GLY:HA2	1.83	0.43
1:A:275:VAL:O	1:A:275:VAL:HG12	2.18	0.43
1:B:463:ASP:HB2	1:B:496:ALA:HB2	2.01	0.43
1:B:4:LEU:HA	1:B:4:LEU:HD23	1.82	0.43
1:A:127:GLU:O	1:A:128:HIS:HB2	2.19	0.43
1:B:463:ASP:C	1:B:463:ASP:OD2	2.57	0.43
1:B:511:ARG:HH22	1:B:525:VAL:HB	1.74	0.43
1:A:500:LEU:HD12	1:A:500:LEU:N	2.34	0.42
1:A:11:ASP:OD1	1:A:50:VAL:HG13	2.19	0.42
1:A:174:TYR:O	1:A:394:ARG:HD3	2.19	0.42
1:A:309:VAL:O	1:A:312:ALA:CB	2.67	0.42
1:A:471:ILE:HD11	1:A:518:VAL:HG11	2.00	0.42
1:B:430:THR:CG2	1:B:431:LEU:H	2.28	0.42
1:B:483:GLN:OE1	1:B:501:ARG:NE	2.52	0.42
1:A:510:VAL:O	1:A:511:ARG:C	2.57	0.42
1:B:345:LEU:CD1	1:B:346:PRO:CD	2.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:523:LEU:HD23	1:B:524:GLU:N	2.33	0.42
1:A:317:GLY:O	1:A:319:VAL:N	2.53	0.42
1:A:119:PRO:HB3	1:B:119:PRO:HA	2.01	0.42
1:A:328:LEU:HD12	1:A:365:LEU:HD23	2.02	0.42
1:B:285:THR:HG22	1:B:287:GLU:N	2.35	0.42
1:A:183:LEU:HB3	1:A:185:ILE:HD12	2.01	0.42
1:B:32:GLY:N	1:B:33:PRO:HD2	2.35	0.42
1:B:457:LEU:HD11	1:B:459:ILE:HG12	2.01	0.42
1:B:32:GLY:HA3	1:B:54:THR:HG22	2.01	0.42
1:A:127:GLU:O	1:A:128:HIS:CB	2.68	0.42
1:A:273:ALA:C	1:A:275:VAL:H	2.23	0.42
1:A:382:VAL:HG12	1:A:384:PHE:O	2.20	0.42
1:A:487:LEU:C	1:A:487:LEU:HD12	2.39	0.42
1:A:126:ARG:NH1	1:B:275:VAL:O	2.43	0.42
1:A:121:ALA:HB1	1:B:279:PRO:HD3	2.02	0.41
1:B:523:LEU:O	1:B:524:GLU:CG	2.67	0.41
1:B:72:ARG:HD2	1:B:76:GLY:O	2.20	0.41
1:A:515:ALA:O	1:A:520:ALA:N	2.50	0.41
1:A:67:LEU:HA	1:A:67:LEU:HD23	1.84	0.41
1:B:261:THR:O	1:B:264:CYS:HB2	2.20	0.41
1:B:285:THR:HG23	1:B:287:GLU:OE1	2.20	0.41
1:B:304:LEU:C	1:B:306:GLY:H	2.23	0.41
1:A:486:GLN:O	1:A:498:ILE:HA	2.20	0.41
1:B:292:ALA:O	1:B:296:VAL:HG22	2.20	0.41
1:B:313:VAL:CG1	1:B:313:VAL:O	2.68	0.41
1:B:28:ARG:NH1	1:B:44:GLU:OE2	2.53	0.41
1:A:214:ILE:CG1	1:A:237:VAL:HG22	2.50	0.41
1:B:363:GLU:CD	1:B:366:ARG:NH1	2.74	0.41
1:B:67:LEU:HD12	1:B:67:LEU:HA	1.89	0.41
1:A:125:LEU:HD12	1:B:277:VAL:CG2	2.50	0.41
1:A:390:LEU:HA	1:A:390:LEU:HD12	1.87	0.41
1:A:462:VAL:HG13	1:A:521:TYR:OH	2.21	0.41
1:B:25:VAL:HG12	1:B:26:GLU:N	2.35	0.41
1:B:527:ASP:C	1:B:527:ASP:OD2	2.58	0.41
1:A:206:LYS:HA	1:A:210:THR:HG21	2.02	0.41
1:A:262:GLU:HA	1:A:263:PRO:C	2.41	0.41
1:A:355:GLY:HA3	1:A:410:ARG:O	2.20	0.41
1:B:378:ILE:HD11	1:B:394:ARG:HD3	2.02	0.41
1:B:239:GLU:OE1	1:B:259:PHE:HA	2.21	0.41
1:B:246:ILE:HG22	1:B:247:THR:N	2.34	0.41
1:B:450:LEU:CD1	1:B:499:LEU:HD22	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:SER:O	1:A:137:GLY:HA2	2.21	0.41
1:A:49:LEU:N	1:A:49:LEU:HD23	2.35	0.41
1:A:152:ARG:CG	1:A:152:ARG:HH21	2.31	0.41
1:B:285:THR:O	1:B:286:ALA:C	2.59	0.41
1:B:328:LEU:HD23	1:B:328:LEU:HA	1.74	0.41
1:A:366:ARG:HD2	1:A:398:ALA:O	2.20	0.40
1:B:334:LEU:CD2	1:B:427:VAL:HG12	2.51	0.40
1:B:49:LEU:HD22	1:B:71:ALA:HB3	2.03	0.40
1:A:318:GLY:C	1:A:320:VAL:H	2.23	0.40
1:B:387:ALA:HB3	1:B:388:PRO:HD3	2.04	0.40
1:A:174:TYR:O	1:A:394:ARG:CD	2.69	0.40
1:A:462:VAL:HG23	1:A:518:VAL:O	2.22	0.40
1:B:224:PRO:HG3	1:B:250:HIS:CE1	2.56	0.40
1:B:351:VAL:O	1:B:400:ILE:HA	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	524/529 (99%)	471 (90%)	47 (9%)	6 (1%)	17	40
1	B	519/529 (98%)	466 (90%)	50 (10%)	3 (1%)	28	56
All	All	1043/1058 (99%)	937 (90%)	97 (9%)	9 (1%)	20	46

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	489	GLU
1	A	491	ALA
1	A	12	LYS
1	A	22	GLY

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Mol	Chain	Res	Type
1	A	128	HIS
1	B	234	GLY
1	B	316	GLY
1	B	452	ALA
1	A	318	GLY

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	396/399 (99%)	343 (87%)	53 (13%)	4	11
1	B	394/399 (99%)	345 (88%)	49 (12%)	5	13
All	All	790/798 (99%)	688 (87%)	102 (13%)	5	12

All (102) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	LEU
1	A	12	LYS
1	A	13	LEU
1	A	21	LEU
1	A	24	GLN
1	A	28	ARG
1	A	39	LEU
1	A	49	LEU
1	A	56	VAL
1	A	57	ASP
1	A	67	LEU
1	A	69	ILE
1	A	72	ARG
1	A	90	VAL
1	A	93	VAL
1	A	102	SER
1	A	110	LEU
1	A	133	SER

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Mol	Chain	Res	Type
1	A	150	LEU
1	A	194	LEU
1	A	196	ARG
1	A	202	VAL
1	A	210	THR
1	A	213	LEU
1	A	216	LYS
1	A	219	LEU
1	A	226	VAL
1	A	242	LEU
1	A	246	ILE
1	A	261	THR
1	A	269	LEU
1	A	285	THR
1	A	296	VAL
1	A	328	LEU
1	A	333	LYS
1	A	347	VAL
1	A	371	ARG
1	A	384	PHE
1	A	385	VAL
1	A	418	VAL
1	A	430	THR
1	A	436	LEU
1	A	437	SER
1	A	442	GLN
1	A	446	ARG
1	A	462	VAL
1	A	475	LEU
1	A	497	THR
1	A	499	LEU
1	A	508	ASP
1	A	523	LEU
1	A	524	GLU
1	A	529	SER
1	B	8	LEU
1	B	18	VAL
1	B	21	LEU
1	B	39	LEU
1	B	54	THR
1	B	61	LEU
1	B	72	ARG

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Mol	Chain	Res	Type
1	B	88	ARG
1	B	94	ASN
1	B	99	ASN
1	B	102	SER
1	B	125	LEU
1	B	129	THR
1	B	134	SER
1	B	160	ARG
1	B	188	LEU
1	B	194	LEU
1	B	209	GLU
1	B	210	THR
1	B	219	LEU
1	B	226	VAL
1	B	233	ARG
1	B	269	LEU
1	B	274	GLN
1	B	285	THR
1	B	291	ARG
1	B	299	SER
1	B	315	VAL
1	B	322	GLU
1	B	330	LEU
1	B	337	LEU
1	B	343	ASP
1	B	354	ARG
1	B	363	GLU
1	B	370	LEU
1	B	371	ARG
1	B	383	THR
1	B	384	PHE
1	B	386	ASN
1	B	410	ARG
1	B	442	GLN
1	B	453	GLN
1	B	457	LEU
1	B	475	LEU
1	B	487	LEU
1	B	499	LEU
1	B	502	LEU
1	B	509	ASP
1	B	528	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	24	GLN
1	A	230	ASN
1	A	435	GLN
1	B	24	GLN
1	B	94	ASN
1	B	99	ASN
1	B	128	HIS
1	B	203	HIS
1	B	274	GLN
1	B	321	ASN
1	B	352	GLN
1	B	456	ASN
1	B	504	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no 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	SER	A	600	-	2,6,6	0.24	0	1,7,7	0.31	0
3	TLA	A	700	-	3,9,9	0.58	0	6,12,12	1.23	0
2	SER	B	600	-	2,6,6	0.38	0	1,7,7	0.72	0
3	TLA	B	700	-	3,9,9	0.24	0	6,12,12	1.30	2 (33%)
3	TLA	B	701	-	3,9,9	0.30	0	6,12,12	0.77	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	SER	A	600	-	-	0/2/6/6	0/0/0/0
3	TLA	A	700	-	-	0/4/12/12	0/0/0/0
2	SER	B	600	-	-	0/2/6/6	0/0/0/0
3	TLA	B	700	-	-	0/4/12/12	0/0/0/0
3	TLA	B	701	-	-	0/4/12/12	0/0/0/0

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	700	TLA	O2-C2-C1	-2.11	106.00	111.13
3	B	700	TLA	C1-C2-C3	-2.04	108.72	113.11

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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	526/529 (99%)	0.10	21 (3%)	39 37	50, 65, 83, 101	8 (1%)
1	B	523/529 (98%)	-0.02	13 (2%)	58 58	31, 67, 85, 114	18 (3%)
All	All	1049/1058 (99%)	0.04	34 (3%)	48 48	31, 66, 84, 114	26 (2%)

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	379	GLU	4.6
1	A	125	LEU	4.5
1	A	319	VAL	4.2
1	A	308	PHE	4.0
1	A	521	TYR	3.8
1	A	4	LEU	3.6
1	B	526	VAL	3.3
1	B	374	PHE	3.3
1	B	491	ALA	3.2
1	A	318	GLY	3.1
1	A	129	THR	3.0
1	B	482	ILE	3.0
1	A	42	VAL	3.0
1	A	20	ALA	2.9
1	B	492	GLU	2.9
1	B	417	ALA	2.7
1	A	270	PHE	2.7
1	B	376	ALA	2.6
1	A	496	ALA	2.5
1	A	90	VAL	2.5
1	A	130	TRP	2.5
1	A	23	ASP	2.4
1	B	4	LEU	2.3
1	B	349	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	462	VAL	2.3
1	B	319	VAL	2.3
1	A	265	THR	2.2
1	A	268	PRO	2.2
1	A	242	LEU	2.2
1	A	446	ARG	2.1
1	B	338	ALA	2.1
1	A	514	ILE	2.1
1	A	306	GLY	2.1
1	B	213	LEU	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
3	TLA	B	700	10/10	0.94	0.44	8.31	81,93,100,100	0
3	TLA	B	701	10/10	0.95	0.23	3.61	63,79,81,81	10
2	SER	B	600	7/7	0.95	0.34	2.24	72,82,90,90	0
2	SER	A	600	7/7	0.95	0.33	0.93	80,80,84,85	0
3	TLA	A	700	10/10	0.90	0.18	-0.08	82,94,101,102	0

6.5 Other polymers [i](#)

There are no such residues in this entry.