



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 09:10 AM UTC

PDB ID : 2YQ4 / pdb_00002yq4
Title : Crystal Structure of D-isomer specific 2-hydroxyacid dehydrogenase from *Lactobacillus delbrueckii* ssp. *bulgaricus*
Authors : Holton, S.J.; Anandhakrishnan, M.; Geerlof, A.; Wilmanns, M.
Deposited on : 2012-11-05
Resolution : 3.45 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

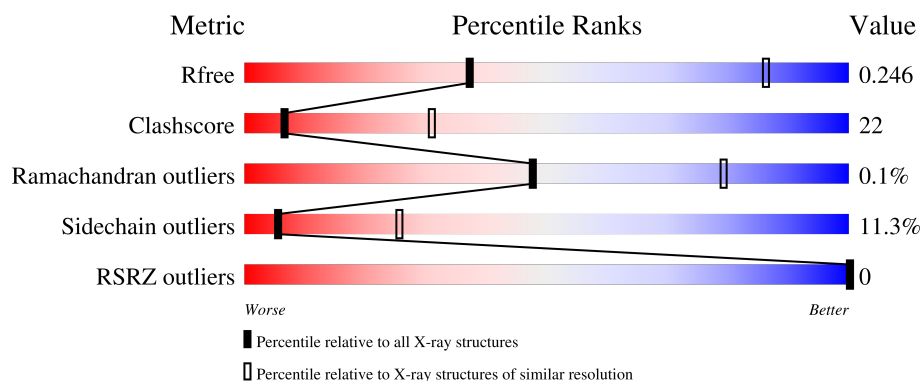
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.45 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}	180053	1070 (3.50-3.42)
Clashscore	190562	1128 (3.50-3.42)
Ramachandran outliers	187476	1101 (3.50-3.42)
Sidechain outliers	187428	1102 (3.50-3.42)
RSRZ outliers	180081	1070 (3.50-3.42)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	343	
1	B	343	
1	C	343	
1	D	343	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 10188 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-ISOMER SPECIFIC 2-HYDROXYACID DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	328	Total	C	N	O	S	0	0	0
			2545	1628	410	494	13			
1	B	328	Total	C	N	O	S	0	0	0
			2544	1626	410	495	13			
1	C	331	Total	C	N	O	S	0	0	0
			2573	1645	415	500	13			
1	D	321	Total	C	N	O	S	0	0	0
			2492	1593	399	487	13			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	334	THR	-	expression tag	UNP Q1GAA2
A	335	ALA	-	expression tag	UNP Q1GAA2
A	336	SER	-	expression tag	UNP Q1GAA2
A	337	GLY	-	expression tag	UNP Q1GAA2
A	338	HIS	-	expression tag	UNP Q1GAA2
A	339	HIS	-	expression tag	UNP Q1GAA2
A	340	HIS	-	expression tag	UNP Q1GAA2
A	341	HIS	-	expression tag	UNP Q1GAA2
A	342	HIS	-	expression tag	UNP Q1GAA2
A	343	HIS	-	expression tag	UNP Q1GAA2
B	334	THR	-	expression tag	UNP Q1GAA2
B	335	ALA	-	expression tag	UNP Q1GAA2
B	336	SER	-	expression tag	UNP Q1GAA2
B	337	GLY	-	expression tag	UNP Q1GAA2
B	338	HIS	-	expression tag	UNP Q1GAA2
B	339	HIS	-	expression tag	UNP Q1GAA2
B	340	HIS	-	expression tag	UNP Q1GAA2
B	341	HIS	-	expression tag	UNP Q1GAA2
B	342	HIS	-	expression tag	UNP Q1GAA2
B	343	HIS	-	expression tag	UNP Q1GAA2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	334	THR	-	expression tag	UNP Q1GAA2
C	335	ALA	-	expression tag	UNP Q1GAA2
C	336	SER	-	expression tag	UNP Q1GAA2
C	337	GLY	-	expression tag	UNP Q1GAA2
C	338	HIS	-	expression tag	UNP Q1GAA2
C	339	HIS	-	expression tag	UNP Q1GAA2
C	340	HIS	-	expression tag	UNP Q1GAA2
C	341	HIS	-	expression tag	UNP Q1GAA2
C	342	HIS	-	expression tag	UNP Q1GAA2
C	343	HIS	-	expression tag	UNP Q1GAA2
D	334	THR	-	expression tag	UNP Q1GAA2
D	335	ALA	-	expression tag	UNP Q1GAA2
D	336	SER	-	expression tag	UNP Q1GAA2
D	337	GLY	-	expression tag	UNP Q1GAA2
D	338	HIS	-	expression tag	UNP Q1GAA2
D	339	HIS	-	expression tag	UNP Q1GAA2
D	340	HIS	-	expression tag	UNP Q1GAA2
D	341	HIS	-	expression tag	UNP Q1GAA2
D	342	HIS	-	expression tag	UNP Q1GAA2
D	343	HIS	-	expression tag	UNP Q1GAA2

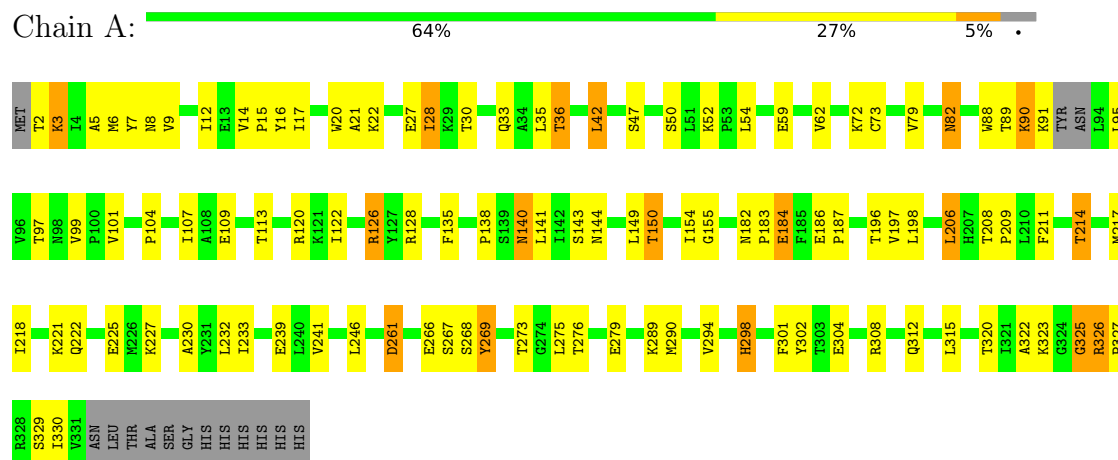
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	7	Total O 7 7	0	0
2	B	13	Total O 13 13	0	0
2	C	7	Total O 7 7	0	0
2	D	7	Total O 7 7	0	0

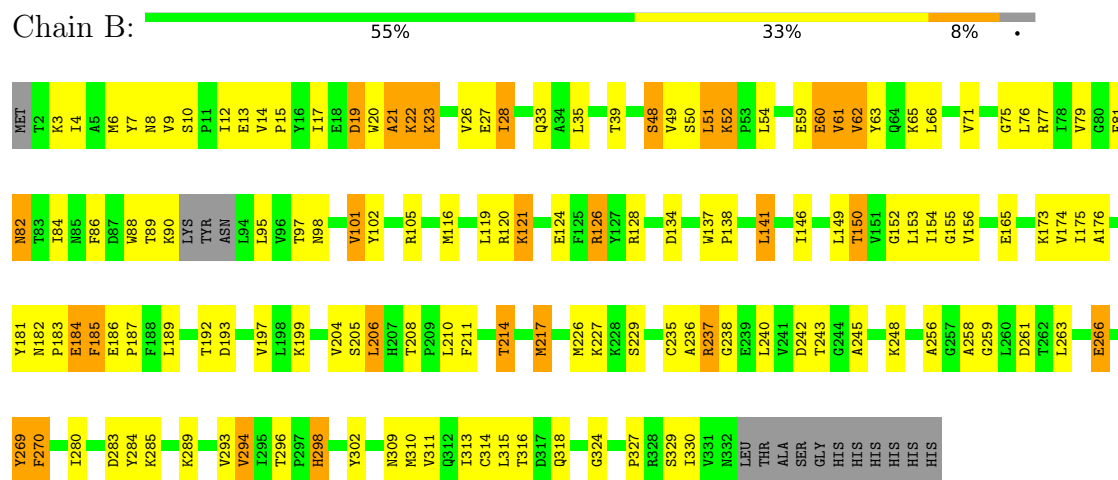
3 Residue-property plots

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.

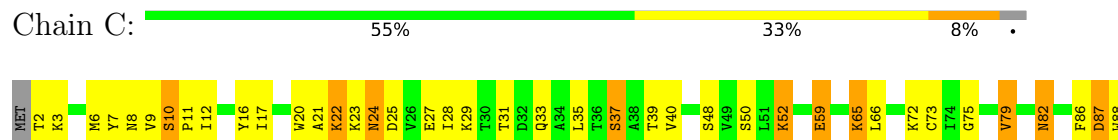
• Molecule 1: D-ISOMER SPECIFIC 2-HYDROXYACID DEHYDROGENASE

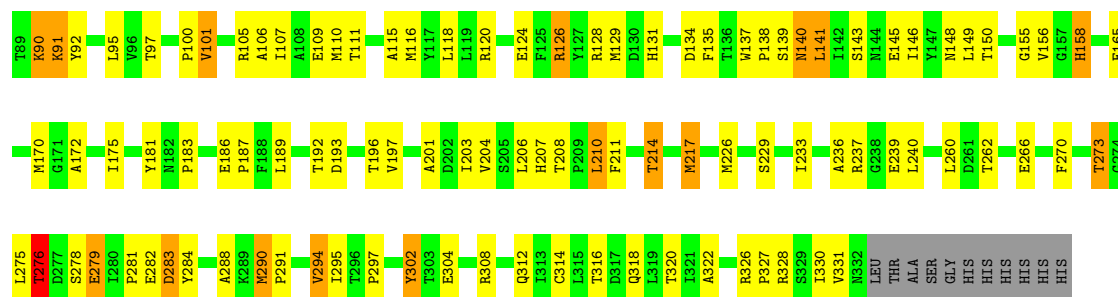


• Molecule 1: D-ISOMER SPECIFIC 2-HYDROXYACID DEHYDROGENASE



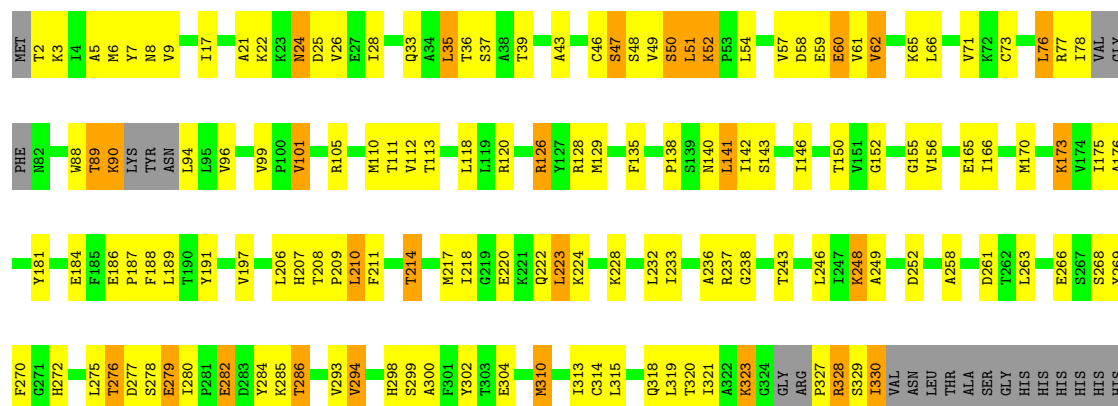
• Molecule 1: D-ISOMER SPECIFIC 2-HYDROXYACID DEHYDROGENASE





● Molecule 1: D-ISOMER SPECIFIC 2-HYDROXYACID DEHYDROGENASE

Chain D: 51% 34% 8% 6%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	92.21Å 108.37Å 147.18Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.00 – 3.45 44.00 – 3.45	Depositor EDS
% Data completeness (in resolution range)	92.2 (44.00-3.45) 98.0 (44.00-3.45)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.30 (at 3.48Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.179 , 0.250 0.185 , 0.246	Depositor DCC
R_{free} test set	998 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	64.5	Xtriage
Anisotropy	0.407	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 40.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	10188	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.81% 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

5.1 Standard geometry

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	0.77	0/2596	1.24	15/3528 (0.4%)
1	B	0.79	0/2595	1.22	14/3528 (0.4%)
1	C	0.82	1/2626 (0.0%)	1.31	23/3571 (0.6%)
1	D	0.78	0/2540	1.20	12/3450 (0.3%)
All	All	0.79	1/10357 (0.0%)	1.24	64/14077 (0.5%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	294	VAL	CA-CB	5.18	1.61	1.54

All (64) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	52	LYS	CA-C-N	11.04	131.15	119.78
1	C	52	LYS	C-N-CA	11.04	131.15	119.78
1	C	137	TRP	CA-C-N	-9.07	110.53	120.14
1	C	137	TRP	C-N-CA	-9.07	110.53	120.14
1	D	99	VAL	CA-C-N	8.45	128.15	119.19
1	D	99	VAL	C-N-CA	8.45	128.15	119.19
1	C	87	ASP	N-CA-C	-8.36	100.83	111.02
1	B	52	LYS	CA-C-N	8.00	128.02	119.78
1	B	52	LYS	C-N-CA	8.00	128.02	119.78
1	A	302	TYR	N-CA-C	7.71	121.93	108.52
1	C	210	LEU	N-CA-C	7.29	120.15	108.41
1	B	235	CYS	N-CA-C	-7.17	104.55	112.72
1	A	267	SER	N-CA-C	7.14	119.93	111.71
1	A	99	VAL	CA-C-N	7.03	128.63	119.84
1	A	99	VAL	C-N-CA	7.03	128.63	119.84
1	B	266	GLU	N-CA-C	6.98	119.73	111.71
1	B	174	VAL	N-CA-C	6.61	117.43	108.17
1	A	289	LYS	N-CA-C	-6.59	105.40	113.50
1	A	30	THR	N-CA-C	6.56	120.22	109.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	302	TYR	N-CA-C	6.56	119.45	109.62
1	B	21	ALA	N-CA-C	-6.39	104.31	111.28
1	D	223	LEU	N-CA-C	6.17	118.09	111.36
1	A	290	MET	CA-C-N	6.17	126.06	119.28
1	A	290	MET	C-N-CA	6.17	126.06	119.28
1	C	10	SER	N-CA-C	-6.16	102.33	110.40
1	A	52	LYS	CA-C-N	6.03	125.94	119.85
1	A	52	LYS	C-N-CA	6.03	125.94	119.85
1	C	281	PRO	N-CA-C	6.01	120.42	111.41
1	A	17	ILE	CB-CA-C	-5.99	104.06	112.14
1	D	328	ARG	N-CA-C	5.89	120.07	113.01
1	C	276	THR	N-CA-C	-5.80	100.69	109.85
1	C	290	MET	CA-C-N	5.70	125.37	119.56
1	C	290	MET	C-N-CA	5.70	125.37	119.56
1	B	324	GLY	N-CA-C	5.68	123.44	115.43
1	C	283	ASP	CB-CA-C	-5.65	102.00	110.88
1	D	173	LYS	CA-C-N	-5.65	115.81	123.10
1	D	173	LYS	C-N-CA	-5.65	115.81	123.10
1	B	61	VAL	N-CA-C	-5.65	104.36	110.23
1	C	331	VAL	N-CA-C	5.65	116.87	108.23
1	B	311	VAL	N-CA-C	5.63	115.82	110.53
1	C	201	ALA	N-CA-C	5.61	119.38	109.96
1	B	302	TYR	N-CA-C	5.60	118.29	109.39
1	A	325	GLY	N-CA-C	-5.58	104.08	112.89
1	B	199	LYS	N-CA-C	5.54	117.40	111.36
1	D	140	ASN	N-CA-C	5.51	119.62	113.01
1	C	156	VAL	CA-C-N	-5.45	110.73	121.41
1	C	156	VAL	C-N-CA	-5.45	110.73	121.41
1	C	273	THR	CB-CA-C	-5.43	100.03	110.24
1	A	261	ASP	N-CA-C	-5.42	106.04	113.30
1	C	302	TYR	N-CA-C	5.40	117.98	109.39
1	B	185	PHE	N-CA-C	5.36	119.97	113.38
1	C	16	TYR	N-CA-C	-5.35	106.26	112.89
1	A	12	ILE	N-CA-C	5.32	117.70	111.05
1	A	290	MET	N-CA-C	5.31	116.34	109.65
1	D	35	LEU	N-CA-C	5.28	117.35	109.59
1	D	228	LYS	N-CA-C	-5.23	106.16	112.54
1	C	158	HIS	N-CA-C	-5.21	105.50	111.07
1	C	288	ALA	N-CA-C	5.19	117.84	111.82
1	C	88	TRP	N-CA-C	5.15	117.79	111.82
1	D	210	LEU	N-CA-C	5.13	116.98	108.20
1	D	50	SER	N-CA-C	5.11	117.23	108.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	270	PHE	N-CA-C	-5.10	101.65	109.76
1	C	131	HIS	N-CA-C	5.02	120.06	113.88
1	B	81	PHE	N-CA-C	5.02	120.02	113.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2545	0	2543	90	0
1	B	2544	0	2536	132	0
1	C	2573	0	2565	118	0
1	D	2492	0	2483	126	0
2	A	7	0	0	2	0
2	B	13	0	0	0	0
2	C	7	0	0	1	0
2	D	7	0	0	3	0
All	All	10188	0	10127	437	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 22.

All (437) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:ARG:HG2	1:A:126:ARG:HH11	1.05	1.16
1:B:237:ARG:HH11	1:B:237:ARG:HG2	1.02	1.10
1:B:6:MET:HE2	1:B:28:ILE:HG21	1.27	1.09
1:D:314:CYS:O	1:D:318:GLN:HG2	1.54	1.06
1:D:126:ARG:HH11	1:D:126:ARG:HG2	0.87	1.04
1:B:126:ARG:HG3	1:B:126:ARG:HH11	1.20	1.03
1:C:79:VAL:HG13	1:C:100:PRO:HA	1.41	1.02
1:B:126:ARG:HH11	1:B:126:ARG:CG	1.76	0.99
1:B:237:ARG:HG2	1:B:237:ARG:NH1	1.66	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:ARG:HH11	1:A:126:ARG:CG	1.80	0.94
1:D:211:PHE:H	1:D:214:THR:HG22	1.31	0.94
1:D:126:ARG:HG2	1:D:126:ARG:NH1	1.64	0.94
1:B:237:ARG:HH11	1:B:237:ARG:CG	1.81	0.92
1:C:6:MET:HE1	1:C:17:ILE:HG12	1.50	0.92
1:A:126:ARG:HG2	1:A:126:ARG:NH1	1.77	0.90
1:B:6:MET:CE	1:B:28:ILE:HG21	2.02	0.89
1:A:211:PHE:H	1:A:214:THR:HG22	1.37	0.89
1:C:20:TRP:HE1	1:C:316:THR:CG2	1.89	0.86
1:D:276:THR:H	1:D:279:GLU:HG3	1.41	0.84
1:A:6:MET:HE1	1:A:315:LEU:HD11	1.58	0.84
1:D:155:GLY:O	1:D:207:HIS:HB2	1.78	0.84
1:C:3:LYS:HE3	1:C:29:LYS:HE2	1.60	0.84
1:A:211:PHE:H	1:A:214:THR:CG2	1.90	0.83
1:A:6:MET:HE2	1:A:315:LEU:HD21	1.61	0.83
1:B:20:TRP:HE1	1:B:316:THR:HG23	1.43	0.82
1:C:140:ASN:H	1:C:140:ASN:HD22	1.24	0.81
1:D:128:ARG:HD3	2:D:2003:HOH:O	1.79	0.81
1:C:79:VAL:CG1	1:C:100:PRO:HA	2.11	0.80
1:C:170:MET:HE3	1:D:170:MET:HE2	1.67	0.77
1:A:183:PRO:HG2	1:D:101:VAL:HG22	1.67	0.77
1:D:211:PHE:H	1:D:214:THR:CG2	1.98	0.76
1:C:20:TRP:HE1	1:C:316:THR:HG23	1.50	0.75
1:C:90:LYS:HA	1:C:90:LYS:HE3	1.67	0.75
1:B:59:GLU:O	1:B:62:VAL:HG22	1.87	0.74
1:C:210:LEU:HA	1:C:214:THR:HG21	1.68	0.74
1:D:3:LYS:O	1:D:46:CYS:HA	1.88	0.74
1:C:211:PHE:H	1:C:214:THR:CG2	2.01	0.73
1:C:72:LYS:HE2	1:C:322:ALA:HA	1.69	0.73
1:B:60:GLU:HG3	1:B:88:TRP:CZ3	2.23	0.73
1:B:211:PHE:H	1:B:214:THR:CG2	2.02	0.73
1:C:37:SER:OG	1:C:59:GLU:OE1	2.05	0.73
1:D:138:PRO:HG2	1:D:141:LEU:HB2	1.71	0.71
1:B:211:PHE:H	1:B:214:THR:HG22	1.53	0.71
1:D:57:VAL:HG12	1:D:57:VAL:O	1.91	0.71
1:B:126:ARG:HG3	1:B:126:ARG:NH1	1.99	0.71
1:D:126:ARG:HH11	1:D:126:ARG:CG	1.83	0.70
1:C:6:MET:CE	1:C:17:ILE:HG23	2.21	0.70
1:B:66:LEU:HB3	1:B:71:VAL:CG2	2.21	0.70
1:A:104:PRO:HG2	1:D:184:GLU:HB3	1.72	0.69
1:B:14:VAL:HB	1:B:15:PRO:HD3	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:211:PHE:H	1:C:214:THR:HG22	1.55	0.68
1:D:280:ILE:O	1:D:285:LYS:HE3	1.94	0.68
1:C:276:THR:H	1:C:279:GLU:HG3	1.59	0.67
1:D:155:GLY:HA3	1:D:208:THR:HG22	1.76	0.67
1:D:77:ARG:O	1:D:310:MET:HG2	1.93	0.67
1:D:208:THR:HG21	1:D:217:MET:HE1	1.76	0.67
1:D:6:MET:HE3	1:D:28:ILE:HG21	1.77	0.67
1:C:21:ALA:HB2	1:C:28:ILE:HD12	1.75	0.67
1:D:52:LYS:HB3	1:D:77:ARG:NH2	2.09	0.67
1:B:20:TRP:HE1	1:B:316:THR:CG2	2.08	0.67
1:C:129:MET:HG2	1:C:135:PHE:CE2	2.30	0.66
1:C:20:TRP:HE1	1:C:316:THR:HG22	1.61	0.66
1:D:76:LEU:N	1:D:76:LEU:CD2	2.58	0.66
1:D:209:PRO:O	1:D:214:THR:HG21	1.95	0.66
1:A:20:TRP:CE3	1:A:315:LEU:HD13	2.31	0.66
1:C:140:ASN:HD22	1:C:140:ASN:N	1.94	0.66
1:D:89:THR:HG21	1:D:96:VAL:HG23	1.78	0.66
1:D:7:TYR:CE2	1:D:35:LEU:HD13	2.31	0.66
1:D:282:GLU:O	1:D:286:THR:OG1	2.12	0.66
1:C:126:ARG:HH11	1:C:126:ARG:CG	2.08	0.66
1:A:82:ASN:HD22	1:A:82:ASN:H	1.43	0.65
1:A:150:THR:CG2	2:A:2004:HOH:O	2.44	0.65
1:B:6:MET:HE1	1:B:17:ILE:HG23	1.78	0.65
1:B:126:ARG:CG	1:B:126:ARG:NH1	2.43	0.65
1:C:314:CYS:O	1:C:318:GLN:HG2	1.95	0.65
1:A:327:PRO:O	1:A:330:ILE:HG12	1.97	0.65
1:A:150:THR:HG23	2:A:2004:HOH:O	1.97	0.65
1:D:2:THR:O	1:D:26:VAL:HG13	1.96	0.65
1:B:20:TRP:NE1	1:B:316:THR:HG23	2.11	0.65
1:B:181:TYR:CE2	1:B:183:PRO:HD3	2.32	0.64
1:D:48:SER:HA	1:D:71:VAL:HG13	1.79	0.64
1:D:7:TYR:CZ	1:D:35:LEU:HD13	2.31	0.64
1:A:113:THR:OG1	1:B:116:MET:HB3	1.98	0.64
1:D:6:MET:HE1	1:D:315:LEU:HD11	1.80	0.64
1:D:76:LEU:HD23	1:D:76:LEU:H	1.63	0.64
1:A:275:LEU:HA	1:A:279:GLU:OE1	1.99	0.63
1:D:89:THR:HG22	1:D:94:LEU:O	1.98	0.63
1:B:210:LEU:HA	1:B:214:THR:HG21	1.81	0.63
1:B:6:MET:HE1	1:B:17:ILE:CG2	2.29	0.62
1:D:50:SER:C	1:D:51:LEU:HD23	2.25	0.62
1:A:208:THR:HG21	1:A:217:MET:HE1	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:21:ALA:HB2	1:B:28:ILE:HG13	1.82	0.62
1:A:97:THR:HA	1:A:329:SER:O	1.99	0.61
1:B:6:MET:HG2	1:B:50:SER:HB3	1.81	0.61
1:B:280:ILE:O	1:B:285:LYS:HE3	2.01	0.61
1:D:261:ASP:O	1:D:298:HIS:HA	2.00	0.61
1:A:128:ARG:CZ	1:A:138:PRO:HG3	2.31	0.61
1:D:112:VAL:HG11	1:D:170:MET:HE1	1.81	0.61
1:B:186:GLU:N	1:B:187:PRO:CD	2.64	0.61
1:B:211:PHE:O	1:B:214:THR:HG22	2.01	0.61
1:D:220:GLU:HG2	1:D:224:LYS:HE2	1.83	0.60
1:D:33:GLN:HE21	1:D:39:THR:HG21	1.67	0.60
1:C:82:ASN:H	1:C:82:ASN:HD22	1.50	0.60
1:C:6:MET:HE3	1:C:17:ILE:HG23	1.84	0.60
1:C:3:LYS:CE	1:C:29:LYS:HE2	2.32	0.60
1:D:284:TYR:CD1	1:D:284:TYR:C	2.79	0.60
1:B:204:VAL:CG2	1:B:226:MET:HE3	2.32	0.59
1:C:107:ILE:HD12	1:C:107:ILE:H	1.67	0.59
1:C:107:ILE:HD12	1:C:107:ILE:N	2.17	0.59
1:C:304:GLU:HG2	1:D:142:ILE:HD13	1.84	0.59
1:A:209:PRO:O	1:A:214:THR:HG21	2.02	0.59
1:B:102:TYR:CE2	1:B:310:MET:HE3	2.37	0.59
1:C:155:GLY:O	1:C:207:HIS:HB2	2.03	0.58
1:B:102:TYR:CZ	1:B:310:MET:HE3	2.38	0.58
1:C:3:LYS:HG3	1:C:27:GLU:HB3	1.84	0.58
1:C:210:LEU:HA	1:C:214:THR:CG2	2.33	0.58
1:D:211:PHE:O	1:D:214:THR:N	2.34	0.58
1:B:60:GLU:HB2	1:B:88:TRP:CD2	2.38	0.58
1:C:126:ARG:HH11	1:C:126:ARG:CB	2.17	0.58
1:C:82:ASN:H	1:C:82:ASN:ND2	2.01	0.58
1:D:276:THR:N	1:D:279:GLU:HG3	2.15	0.58
1:C:129:MET:HG2	1:C:135:PHE:CD2	2.39	0.58
1:C:149:LEU:HD12	1:C:149:LEU:N	2.19	0.58
1:B:50:SER:HA	1:B:75:GLY:O	2.04	0.57
1:C:126:ARG:NH1	1:C:126:ARG:HG2	2.18	0.57
1:B:138:PRO:HG2	1:B:141:LEU:HB2	1.86	0.57
1:D:59:GLU:O	1:D:62:VAL:CG2	2.53	0.57
1:A:325:GLY:O	1:A:326:ARG:HG2	2.04	0.57
1:A:261:ASP:CG	1:A:298:HIS:HA	2.29	0.56
1:C:7:TYR:CZ	1:C:35:LEU:HD13	2.39	0.56
1:A:6:MET:CE	1:A:315:LEU:HD11	2.31	0.56
1:B:66:LEU:HB3	1:B:71:VAL:HG21	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:6:MET:HE3	1:C:17:ILE:CG2	2.35	0.56
1:D:25:ASP:CG	1:D:25:ASP:O	2.48	0.56
1:C:211:PHE:O	1:C:214:THR:HG22	2.06	0.56
1:A:140:ASN:H	1:A:140:ASN:HD22	1.53	0.55
1:A:206:LEU:HD21	1:A:218:ILE:HG13	1.87	0.55
1:B:84:ILE:HD12	1:B:84:ILE:N	2.22	0.55
1:B:128:ARG:HD2	1:B:141:LEU:CD2	2.35	0.55
1:D:210:LEU:HA	1:D:214:THR:HG21	1.87	0.55
1:A:154:ILE:O	1:A:208:THR:HG23	2.06	0.55
1:D:8:ASN:HD22	1:D:52:LYS:H	1.55	0.55
1:B:66:LEU:HB3	1:B:71:VAL:HG22	1.88	0.55
1:C:126:ARG:CG	1:C:126:ARG:NH1	2.69	0.55
1:D:232:LEU:O	1:D:258:ALA:HA	2.06	0.55
1:A:6:MET:HE3	1:A:28:ILE:HG12	1.87	0.54
1:B:8:ASN:HB2	1:B:52:LYS:H	1.72	0.54
1:B:33:GLN:HE21	1:B:39:THR:CG2	2.20	0.54
1:B:76:LEU:HD21	1:B:84:ILE:HD11	1.89	0.54
1:B:101:VAL:O	1:B:101:VAL:HG22	2.06	0.54
1:B:12:ILE:O	1:B:15:PRO:HD2	2.06	0.54
1:A:155:GLY:HA3	1:A:208:THR:HG22	1.89	0.54
1:D:21:ALA:HB2	1:D:28:ILE:HD12	1.90	0.54
1:D:318:GLN:OE1	1:D:318:GLN:HA	2.08	0.54
1:A:276:THR:N	1:A:279:GLU:OE1	2.35	0.54
1:B:284:TYR:CD1	1:B:284:TYR:C	2.85	0.54
1:B:318:GLN:HA	1:B:318:GLN:NE2	2.21	0.54
1:B:82:ASN:H	1:B:82:ASN:HD22	1.54	0.54
1:B:192:THR:OG1	1:B:193:ASP:N	2.39	0.54
1:C:134:ASP:C	1:C:134:ASP:OD1	2.51	0.54
1:B:126:ARG:NH1	1:B:126:ARG:HG2	2.22	0.54
1:C:189:LEU:C	1:C:189:LEU:HD12	2.33	0.53
1:C:211:PHE:N	1:C:214:THR:HG22	2.22	0.53
1:A:47:SER:OG	1:A:72:LYS:HE2	2.07	0.53
1:A:308:ARG:O	1:A:312:GLN:HG3	2.07	0.53
1:B:184:GLU:HG2	1:C:158:HIS:CD2	2.43	0.53
1:B:60:GLU:HB2	1:B:88:TRP:CE2	2.43	0.53
1:C:126:ARG:HH11	1:C:126:ARG:HB3	1.74	0.53
1:B:82:ASN:H	1:B:82:ASN:ND2	2.06	0.53
1:D:24:ASN:N	1:D:24:ASN:HD22	2.07	0.53
1:A:88:TRP:O	1:A:91:LYS:HG2	2.09	0.53
1:B:3:LYS:HD2	1:B:27:GLU:CD	2.34	0.53
1:D:49:VAL:HG11	1:D:66:LEU:HD21	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:8:ASN:HD22	1:B:51:LEU:HB3	1.74	0.52
1:A:14:VAL:HB	1:A:15:PRO:HD3	1.92	0.52
1:B:89:THR:C	1:B:90:LYS:HD2	2.35	0.52
1:B:152:GLY:HA2	1:B:175:ILE:O	2.10	0.52
1:A:36:THR:HG22	1:A:59:GLU:OE1	2.09	0.52
1:A:187:PRO:HG3	1:D:105:ARG:HG3	1.90	0.52
1:D:320:THR:OG1	1:D:327:PRO:HG3	2.09	0.52
1:A:320:THR:HG22	1:A:325:GLY:HA3	1.90	0.52
1:B:184:GLU:HG2	1:C:158:HIS:HD2	1.73	0.52
1:B:124:GLU:O	1:B:128:ARG:HG3	2.09	0.52
1:D:155:GLY:CA	1:D:208:THR:HG22	2.39	0.52
1:B:119:LEU:HD13	1:B:149:LEU:HD21	1.92	0.52
1:D:5:ALA:HB2	1:D:46:CYS:SG	2.49	0.52
1:D:165:GLU:HG2	1:D:188:PHE:CE1	2.45	0.52
1:A:155:GLY:CA	1:A:208:THR:HG22	2.40	0.52
1:C:270:PHE:CE2	1:C:297:PRO:HA	2.45	0.52
1:C:302:TYR:CE2	1:D:142:ILE:HA	2.45	0.52
1:A:126:ARG:CG	1:A:126:ARG:NH1	2.50	0.51
1:A:182:ASN:HB3	1:A:184:GLU:OE2	2.10	0.51
1:C:90:LYS:HA	1:C:90:LYS:CE	2.38	0.51
1:B:150:THR:HB	1:B:173:LYS:HB3	1.92	0.51
1:C:110:MET:HE2	1:D:120:ARG:NH2	2.26	0.51
1:B:119:LEU:CD1	1:B:149:LEU:HD21	2.41	0.51
1:D:73:CYS:SG	1:D:321:ILE:HD12	2.50	0.51
1:A:104:PRO:HG2	1:D:184:GLU:CB	2.41	0.51
1:B:206:LEU:O	1:B:236:ALA:HB2	2.10	0.51
1:D:266:GLU:O	1:D:270:PHE:HB2	2.10	0.51
1:C:320:THR:OG1	1:C:327:PRO:HG3	2.11	0.51
1:C:148:ASN:C	1:C:149:LEU:HD12	2.36	0.51
1:B:22:LYS:HB2	1:B:22:LYS:NZ	2.26	0.50
1:C:20:TRP:O	1:C:24:ASN:ND2	2.33	0.50
1:D:152:GLY:HA2	1:D:175:ILE:O	2.10	0.50
1:D:176:ALA:HB3	1:D:189:LEU:HD13	1.92	0.50
1:B:61:VAL:HG12	1:B:65:LYS:HG3	1.94	0.50
1:C:126:ARG:HH11	1:C:126:ARG:HG2	1.72	0.50
1:D:76:LEU:N	1:D:76:LEU:HD23	2.21	0.50
1:D:126:ARG:NH1	1:D:126:ARG:CG	2.52	0.50
1:D:181:TYR:HD1	1:D:191:TYR:CE2	2.30	0.50
1:C:308:ARG:O	1:C:312:GLN:HG3	2.12	0.50
1:D:218:ILE:HD13	1:D:222:GLN:HG2	1.93	0.50
1:B:269:TYR:CD1	1:B:269:TYR:N	2.79	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:187:PRO:HG3	1:C:105:ARG:HG3	1.92	0.50
1:B:8:ASN:ND2	1:B:51:LEU:HB3	2.27	0.50
1:B:261:ASP:OD2	1:B:298:HIS:HA	2.12	0.50
1:C:120:ARG:HD2	1:C:143:SER:OG	2.11	0.50
1:A:6:MET:HE3	1:A:28:ILE:HG21	1.93	0.49
1:B:204:VAL:HG23	1:B:226:MET:HE3	1.93	0.49
1:D:8:ASN:ND2	1:D:52:LYS:H	2.10	0.49
1:A:5:ALA:HB1	1:A:42:LEU:CD1	2.43	0.49
1:A:140:ASN:HD22	1:A:140:ASN:N	2.10	0.49
1:D:96:VAL:O	1:D:330:ILE:HA	2.13	0.49
1:D:277:ASP:O	1:D:285:LYS:NZ	2.36	0.49
1:B:27:GLU:C	1:B:28:ILE:HG12	2.38	0.49
1:C:111:THR:HG23	1:C:233:ILE:HG21	1.95	0.49
1:D:211:PHE:N	1:D:214:THR:HG22	2.13	0.48
1:B:181:TYR:CD2	1:B:183:PRO:HD3	2.47	0.48
1:C:181:TYR:CE2	1:C:183:PRO:HD3	2.49	0.48
1:D:52:LYS:O	1:D:52:LYS:HG3	2.12	0.48
1:B:86:PHE:HA	1:B:89:THR:OG1	2.12	0.48
1:C:109:GLU:CD	1:D:146:ILE:HG22	2.39	0.48
1:D:59:GLU:O	1:D:62:VAL:HG23	2.13	0.48
1:C:50:SER:HA	1:C:75:GLY:O	2.14	0.48
1:C:328:ARG:CZ	1:C:328:ARG:HB3	2.42	0.48
1:B:84:ILE:N	1:B:84:ILE:CD1	2.77	0.48
1:D:90:LYS:HA	1:D:90:LYS:CE	2.44	0.48
1:D:186:GLU:N	1:D:187:PRO:CD	2.77	0.48
1:A:72:LYS:HE3	1:A:322:ALA:HA	1.96	0.47
1:B:126:ARG:HH11	1:B:126:ARG:HG2	1.70	0.47
1:B:4:ILE:HD13	1:B:315:LEU:HD22	1.96	0.47
1:C:146:ILE:HG13	1:C:172:ALA:HB2	1.94	0.47
1:A:6:MET:HG2	1:A:50:SER:HB3	1.96	0.47
1:D:111:THR:HG23	1:D:233:ILE:HG21	1.95	0.47
1:B:101:VAL:HG22	1:C:183:PRO:HG2	1.97	0.47
1:B:259:GLY:HA2	1:B:294:VAL:HG13	1.95	0.47
1:A:221:LYS:HE3	1:A:222:GLN:HE21	1.78	0.47
1:D:166:ILE:HG22	1:D:170:MET:HE3	1.96	0.47
1:D:243:THR:O	1:D:246:LEU:HB3	2.14	0.47
1:A:261:ASP:OD2	1:A:298:HIS:HA	2.15	0.47
1:D:60:GLU:HB3	1:D:88:TRP:CD2	2.49	0.47
1:A:90:LYS:HA	1:A:90:LYS:CE	2.44	0.47
1:A:221:LYS:HB3	1:A:222:GLN:NE2	2.30	0.47
1:A:221:LYS:O	1:A:225:GLU:HG3	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:105:ARG:O	1:C:106:ALA:C	2.55	0.47
1:C:124:GLU:O	1:C:128:ARG:HG3	2.15	0.47
1:D:210:LEU:HA	1:D:214:THR:CG2	2.45	0.47
1:D:261:ASP:OD2	1:D:300:ALA:CB	2.62	0.47
1:B:88:TRP:C	1:B:90:LYS:H	2.21	0.47
1:D:236:ALA:C	1:D:237:ARG:HG2	2.40	0.47
1:A:269:TYR:CD1	1:A:269:TYR:N	2.81	0.47
1:B:13:GLU:O	1:B:14:VAL:C	2.58	0.47
1:B:208:THR:HG21	1:B:217:MET:HE1	1.96	0.47
1:C:24:ASN:O	1:C:25:ASP:CB	2.63	0.46
1:B:21:ALA:CB	1:B:28:ILE:HG13	2.46	0.46
1:B:48:SER:OG	1:B:318:GLN:NE2	2.48	0.46
1:A:211:PHE:O	1:A:214:THR:HG22	2.16	0.46
1:D:6:MET:CE	1:D:17:ILE:HG23	2.45	0.46
1:D:319:LEU:O	1:D:323:LYS:HE2	2.15	0.46
1:B:309:ASN:HB3	1:B:313:ILE:HD12	1.97	0.46
1:D:293:VAL:CG1	1:D:294:VAL:N	2.79	0.46
1:C:52:LYS:HE2	2:C:2001:HOH:O	2.14	0.46
1:B:183:PRO:HG2	1:C:101:VAL:HG22	1.98	0.46
1:C:204:VAL:CG2	1:C:226:MET:HE3	2.46	0.46
1:D:272:HIS:HB2	1:D:275:LEU:HD11	1.97	0.46
1:C:210:LEU:HD22	1:C:239:GLU:HB2	1.97	0.46
1:C:284:TYR:CD1	1:C:284:TYR:C	2.94	0.46
1:D:52:LYS:HB3	1:D:77:ARG:CZ	2.45	0.46
1:A:109:GLU:CD	1:B:146:ILE:HG22	2.41	0.46
1:B:77:ARG:O	1:B:310:MET:HG2	2.15	0.46
1:A:241:VAL:HG11	1:A:246:LEU:HD22	1.97	0.45
1:B:189:LEU:HD12	1:B:189:LEU:C	2.41	0.45
1:D:166:ILE:CG2	1:D:170:MET:HE2	2.47	0.45
1:C:140:ASN:H	1:C:140:ASN:ND2	2.03	0.45
1:D:223:LEU:HD13	1:D:249:ALA:HB2	1.98	0.45
1:D:248:LYS:HD3	1:D:252:ASP:OD2	2.15	0.45
1:C:204:VAL:HG23	1:C:226:MET:HE3	1.99	0.45
1:C:275:LEU:HD22	1:C:279:GLU:HB2	1.97	0.45
1:D:118:LEU:HA	1:D:118:LEU:HD23	1.65	0.45
1:B:238:GLY:C	1:B:240:LEU:H	2.23	0.45
1:D:52:LYS:O	1:D:52:LYS:CG	2.65	0.45
1:D:60:GLU:HB3	1:D:88:TRP:CE2	2.51	0.45
1:C:33:GLN:HE21	1:C:39:THR:HG21	1.82	0.45
1:A:7:TYR:O	1:A:8:ASN:HB2	2.17	0.45
1:C:236:ALA:C	1:C:237:ARG:HG2	2.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:316:THR:O	1:C:320:THR:HG23	2.17	0.45
1:A:6:MET:HE3	1:A:28:ILE:CG2	2.46	0.45
1:D:7:TYR:CD2	1:D:35:LEU:HB2	2.51	0.45
1:C:72:LYS:CE	1:C:322:ALA:HA	2.44	0.45
1:D:261:ASP:OD1	1:D:299:SER:N	2.44	0.45
1:A:82:ASN:H	1:A:82:ASN:ND2	2.14	0.44
1:A:122:ILE:HG12	1:B:296:THR:HG21	1.99	0.44
1:A:325:GLY:C	1:A:326:ARG:HG2	2.41	0.44
1:B:62:VAL:O	1:B:66:LEU:HD12	2.17	0.44
1:D:120:ARG:HD2	1:D:143:SER:OG	2.17	0.44
1:A:21:ALA:HB2	1:A:28:ILE:HD13	1.99	0.44
1:D:6:MET:HE1	1:D:17:ILE:HG23	1.99	0.44
1:C:10:SER:O	1:C:11:PRO:C	2.60	0.44
1:C:208:THR:HG21	1:C:217:MET:HE1	2.00	0.44
1:D:90:LYS:HA	1:D:90:LYS:HE3	1.98	0.44
1:D:189:LEU:C	1:D:189:LEU:HD12	2.43	0.44
1:A:5:ALA:HB1	1:A:42:LEU:HD12	1.99	0.44
1:A:143:SER:OG	1:A:144:ASN:N	2.51	0.44
1:B:63:TYR:CG	1:B:88:TRP:HB3	2.53	0.44
1:B:155:GLY:CA	1:B:208:THR:HG22	2.48	0.44
1:C:6:MET:CE	1:C:17:ILE:HG12	2.35	0.44
1:C:31:THR:OG1	1:C:33:GLN:HG3	2.17	0.44
1:A:232:LEU:O	1:A:233:ILE:HD13	2.17	0.44
1:B:165:GLU:OE2	1:C:165:GLU:OE2	2.35	0.44
1:C:302:TYR:CD2	1:D:142:ILE:HA	2.53	0.44
1:D:112:VAL:CG1	1:D:170:MET:HE1	2.48	0.44
1:D:166:ILE:HG22	1:D:170:MET:CE	2.47	0.44
1:B:19:ASP:O	1:B:23:LYS:HB2	2.17	0.44
1:D:268:SER:HB2	1:D:269:TYR:HD1	1.83	0.44
1:A:227:LYS:HB2	1:A:230:ALA:HB2	2.00	0.44
1:B:238:GLY:C	1:B:240:LEU:N	2.74	0.44
1:C:297:PRO:HG3	1:D:129:MET:SD	2.58	0.44
1:D:173:LYS:HE2	1:D:175:ILE:CG2	2.47	0.44
1:D:33:GLN:HE21	1:D:39:THR:CG2	2.31	0.43
1:D:43:ALA:HA	1:D:46:CYS:SG	2.58	0.43
1:D:330:ILE:H	1:D:330:ILE:HG12	1.31	0.43
1:A:89:THR:C	1:A:90:LYS:HE3	2.43	0.43
1:C:24:ASN:O	1:C:25:ASP:HB3	2.16	0.43
1:C:145:GLU:O	1:C:149:LEU:HD13	2.18	0.43
1:A:88:TRP:C	1:A:90:LYS:H	2.26	0.43
1:C:6:MET:CE	1:C:17:ILE:CG2	2.91	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:GLN:H	1:A:33:GLN:HG2	1.67	0.43
1:A:320:THR:HB	1:A:327:PRO:HG3	1.99	0.43
1:B:3:LYS:HG3	1:B:27:GLU:HB3	2.00	0.43
1:B:238:GLY:HA3	1:B:263:LEU:C	2.43	0.43
1:C:196:THR:O	1:C:197:VAL:C	2.58	0.43
1:C:115:ALA:HB1	1:C:203:ILE:HD13	2.00	0.43
1:C:149:LEU:N	1:C:149:LEU:CD1	2.81	0.43
1:B:153:LEU:HD22	1:B:205:SER:HB3	2.01	0.43
1:C:7:TYR:O	1:C:8:ASN:HB2	2.19	0.43
1:B:154:ILE:HD13	1:B:197:VAL:HG11	2.01	0.43
1:B:242:ASP:HB3	1:B:245:ALA:HB3	2.00	0.43
1:C:73:CYS:HB2	1:C:95:LEU:HB2	2.01	0.43
1:B:79:VAL:HA	1:B:98:ASN:HD22	1.84	0.43
1:C:6:MET:HE1	1:C:17:ILE:HG23	1.98	0.43
1:C:86:PHE:O	1:C:87:ASP:C	2.60	0.43
1:C:120:ARG:NH2	1:D:110:MET:HE2	2.34	0.43
1:D:272:HIS:CB	1:D:275:LEU:HD11	2.49	0.43
1:A:266:GLU:OE2	1:A:298:HIS:ND1	2.49	0.43
1:B:229:SER:HA	1:B:256:ALA:HB2	2.00	0.43
1:D:211:PHE:O	1:D:214:THR:HG22	2.19	0.43
1:C:75:GLY:HA2	1:C:97:THR:OG1	2.19	0.43
1:D:128:ARG:HB2	2:D:2003:HOH:O	2.18	0.43
1:A:120:ARG:HD2	1:A:120:ARG:HA	1.73	0.42
1:A:211:PHE:H	1:A:214:THR:HG21	1.79	0.42
1:C:40:VAL:HG11	1:C:65:LYS:HD2	2.01	0.42
1:B:121:LYS:HD2	1:B:141:LEU:HA	2.01	0.42
1:D:60:GLU:CB	1:D:88:TRP:CE2	3.01	0.42
1:A:35:LEU:HG	1:A:62:VAL:HG11	2.01	0.42
1:A:268:SER:HB2	1:A:269:TYR:HD1	1.84	0.42
1:B:7:TYR:O	1:B:8:ASN:HB2	2.19	0.42
1:C:262:THR:OG1	1:C:266:GLU:OE1	2.34	0.42
1:C:290:MET:HA	1:C:291:PRO:HD3	1.83	0.42
1:D:66:LEU:HD22	1:D:71:VAL:HG11	2.01	0.42
1:A:73:CYS:HB2	1:A:95:LEU:HB2	2.02	0.42
1:A:239:GLU:OE1	1:A:239:GLU:N	2.49	0.42
1:B:266:GLU:HB2	1:B:270:PHE:CD2	2.54	0.42
1:C:240:LEU:HD23	1:C:240:LEU:HA	1.81	0.42
1:B:6:MET:HE1	1:B:17:ILE:HG12	2.00	0.42
1:D:152:GLY:HA3	1:D:197:VAL:HG13	2.01	0.42
1:B:7:TYR:CZ	1:B:35:LEU:CD1	3.03	0.42
1:B:182:ASN:HB2	1:B:185:PHE:CD2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:327:PRO:C	1:B:329:SER:H	2.27	0.42
1:D:3:LYS:O	1:D:47:SER:N	2.48	0.42
1:B:33:GLN:HG3	1:B:39:THR:HG21	2.02	0.42
1:B:66:LEU:HD22	1:B:71:VAL:HG21	2.01	0.42
1:B:7:TYR:CE1	1:B:35:LEU:HD13	2.54	0.42
1:A:109:GLU:OE2	1:B:146:ILE:HG22	2.20	0.42
1:B:60:GLU:O	1:B:61:VAL:C	2.61	0.42
1:A:186:GLU:N	1:A:187:PRO:CD	2.83	0.42
1:B:60:GLU:HB2	1:B:88:TRP:CE3	2.54	0.42
1:D:238:GLY:HA3	1:D:263:LEU:C	2.45	0.42
1:B:134:ASP:C	1:B:134:ASP:OD1	2.61	0.41
1:B:156:VAL:HG21	1:B:176:ALA:HB1	2.01	0.41
1:C:118:LEU:HD23	1:C:118:LEU:HA	1.82	0.41
1:A:198:LEU:HA	1:A:198:LEU:HD23	1.66	0.41
1:A:320:THR:HG21	1:A:327:PRO:HG3	2.02	0.41
1:C:138:PRO:HG2	1:C:141:LEU:HB2	2.01	0.41
1:C:186:GLU:N	1:C:187:PRO:CD	2.83	0.41
1:A:20:TRP:CZ2	1:A:315:LEU:HB3	2.55	0.41
1:A:187:PRO:CG	1:D:105:ARG:HG3	2.51	0.41
1:A:301:PHE:HE1	1:B:137:TRP:CZ2	2.38	0.41
1:C:66:LEU:HA	1:C:66:LEU:HD23	1.79	0.41
1:A:315:LEU:HA	1:A:315:LEU:HD23	1.85	0.41
1:B:314:CYS:O	1:B:318:GLN:HG2	2.21	0.41
1:C:120:ARG:HH11	1:C:120:ARG:HD3	1.69	0.41
1:A:16:TYR:OH	1:A:304:GLU:HB3	2.20	0.41
1:B:26:VAL:HG12	1:B:27:GLU:O	2.20	0.41
1:B:120:ARG:HH11	1:B:120:ARG:HD3	1.70	0.41
1:A:3:LYS:HG3	1:A:27:GLU:HB3	2.02	0.41
1:B:183:PRO:C	1:B:185:PHE:N	2.78	0.41
1:C:106:ALA:HB3	1:C:107:ILE:HD12	2.03	0.41
1:D:129:MET:HG2	1:D:135:PHE:CD2	2.56	0.41
1:A:155:GLY:HA3	1:A:208:THR:CG2	2.51	0.41
1:C:260:LEU:O	1:C:295:ILE:HA	2.21	0.41
1:D:128:ARG:CB	2:D:2003:HOH:O	2.68	0.41
1:B:6:MET:HE2	1:B:28:ILE:CG2	2.20	0.41
1:B:33:GLN:CG	1:B:39:THR:HG21	2.50	0.41
1:B:88:TRP:C	1:B:90:LYS:N	2.79	0.41
1:B:97:THR:HA	1:B:329:SER:O	2.20	0.41
1:B:105:ARG:HG3	1:C:187:PRO:HG3	2.02	0.41
1:D:60:GLU:HG2	1:D:88:TRP:CE2	2.55	0.41
1:D:120:ARG:HD2	1:D:120:ARG:HA	1.74	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:ILE:N	1:A:107:ILE:HD12	2.36	0.41
1:C:192:THR:OG1	1:C:193:ASP:N	2.54	0.41
1:B:185:PHE:C	1:B:187:PRO:HD2	2.46	0.40
1:C:22:LYS:HG3	1:C:23:LYS:N	2.33	0.40
1:C:116:MET:HB3	1:D:113:THR:OG1	2.21	0.40
1:C:120:ARG:HH21	1:D:110:MET:HE2	1.85	0.40
1:A:196:THR:O	1:A:197:VAL:C	2.62	0.40
1:B:211:PHE:H	1:B:214:THR:HG21	1.82	0.40
1:C:210:LEU:CD2	1:C:239:GLU:HB2	2.51	0.40
1:C:100:PRO:HG2	1:C:101:VAL:HG12	2.03	0.40
1:A:89:THR:O	1:A:90:LYS:HE3	2.22	0.40
1:A:135:PHE:HB2	1:B:269:TYR:O	2.21	0.40
1:B:283:ASP:OD1	1:B:284:TYR:N	2.55	0.40
1:C:91:LYS:HE2	1:C:92:TYR:CZ	2.57	0.40
1:C:170:MET:HE3	1:D:170:MET:CE	2.45	0.40
1:B:95:LEU:HD22	1:B:330:ILE:HG21	2.03	0.40
1:B:258:ALA:O	1:B:293:VAL:HA	2.21	0.40
1:D:128:ARG:HD2	1:D:141:LEU:CD2	2.51	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	324/343 (94%)	309 (95%)	15 (5%)	0	100	100
1	B	324/343 (94%)	309 (95%)	14 (4%)	1 (0%)	36	67
1	C	329/343 (96%)	316 (96%)	13 (4%)	0	100	100
1	D	313/343 (91%)	296 (95%)	17 (5%)	0	100	100
All	All	1290/1372 (94%)	1230 (95%)	59 (5%)	1 (0%)	48	79

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	184	GLU

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	281/294 (96%)	255 (91%)	26 (9%)	8	32
1	B	281/294 (96%)	252 (90%)	29 (10%)	7	28
1	C	284/294 (97%)	251 (88%)	33 (12%)	5	25
1	D	276/294 (94%)	237 (86%)	39 (14%)	3	19
All	All	1122/1176 (95%)	995 (89%)	127 (11%)	5	25

All (127) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	THR
1	A	3	LYS
1	A	9	VAL
1	A	22	LYS
1	A	28	ILE
1	A	36	THR
1	A	42	LEU
1	A	54	LEU
1	A	79	VAL
1	A	82	ASN
1	A	90	LYS
1	A	101	VAL
1	A	126	ARG
1	A	140	ASN
1	A	141	LEU
1	A	149	LEU
1	A	150	THR
1	A	184	GLU
1	A	206	LEU
1	A	214	THR
1	A	269	TYR

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Mol	Chain	Res	Type
1	A	273	THR
1	A	294	VAL
1	A	298	HIS
1	A	323	LYS
1	A	326	ARG
1	B	9	VAL
1	B	10	SER
1	B	19	ASP
1	B	22	LYS
1	B	23	LYS
1	B	28	ILE
1	B	48	SER
1	B	49	VAL
1	B	51	LEU
1	B	54	LEU
1	B	60	GLU
1	B	62	VAL
1	B	82	ASN
1	B	101	VAL
1	B	121	LYS
1	B	126	ARG
1	B	141	LEU
1	B	150	THR
1	B	206	LEU
1	B	214	THR
1	B	217	MET
1	B	227	LYS
1	B	237	ARG
1	B	243	THR
1	B	248	LYS
1	B	269	TYR
1	B	289	LYS
1	B	294	VAL
1	B	298	HIS
1	C	2	THR
1	C	9	VAL
1	C	12	ILE
1	C	22	LYS
1	C	24	ASN
1	C	37	SER
1	C	48	SER
1	C	59	GLU

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Mol	Chain	Res	Type
1	C	65	LYS
1	C	79	VAL
1	C	82	ASN
1	C	90	LYS
1	C	91	LYS
1	C	101	VAL
1	C	126	ARG
1	C	139	SER
1	C	140	ASN
1	C	141	LEU
1	C	150	THR
1	C	175	ILE
1	C	206	LEU
1	C	214	THR
1	C	217	MET
1	C	229	SER
1	C	273	THR
1	C	276	THR
1	C	278	SER
1	C	279	GLU
1	C	282	GLU
1	C	283	ASP
1	C	294	VAL
1	C	326	ARG
1	C	330	ILE
1	D	9	VAL
1	D	22	LYS
1	D	24	ASN
1	D	36	THR
1	D	37	SER
1	D	47	SER
1	D	51	LEU
1	D	52	LYS
1	D	54	LEU
1	D	58	ASP
1	D	60	GLU
1	D	61	VAL
1	D	62	VAL
1	D	65	LYS
1	D	76	LEU
1	D	78	ILE
1	D	89	THR

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Mol	Chain	Res	Type
1	D	90	LYS
1	D	101	VAL
1	D	126	ARG
1	D	141	LEU
1	D	150	THR
1	D	156	VAL
1	D	206	LEU
1	D	214	THR
1	D	248	LYS
1	D	276	THR
1	D	278	SER
1	D	279	GLU
1	D	282	GLU
1	D	286	THR
1	D	294	VAL
1	D	304	GLU
1	D	310	MET
1	D	313	ILE
1	D	323	LYS
1	D	328	ARG
1	D	329	SER
1	D	330	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	64	GLN
1	A	82	ASN
1	A	131	HIS
1	A	140	ASN
1	A	158	HIS
1	A	312	GLN
1	B	8	ASN
1	B	33	GLN
1	B	82	ASN
1	B	133	HIS
1	B	158	HIS
1	B	272	HIS
1	B	318	GLN
1	C	8	ASN
1	C	33	GLN
1	C	82	ASN

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Mol	Chain	Res	Type
1	C	140	ASN
1	C	158	HIS
1	C	272	HIS
1	C	332	ASN
1	D	8	ASN
1	D	24	ASN
1	D	33	GLN
1	D	85	ASN
1	D	98	ASN
1	D	140	ASN
1	D	272	HIS
1	D	318	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	328/343 (95%)	-0.50	0 100 100	25, 50, 88, 104	0
1	B	328/343 (95%)	-0.47	0 100 100	22, 45, 98, 114	0
1	C	331/343 (96%)	-0.62	0 100 100	24, 43, 64, 73	0
1	D	321/343 (93%)	-0.37	0 100 100	28, 56, 94, 111	0
All	All	1308/1372 (95%)	-0.49	0 100 100	22, 48, 92, 114	0

There are no RSRZ outliers to report.

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.