



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 01:43 PM UTC

PDB ID : 1XDL / pdb_00001xdl
Title : Structure of human aldolase B associated with hereditary fructose intolerance (A149P), at 277K
Authors : Malay, A.D.; Allen, K.N.; Tolan, D.R.
Deposited on : 2004-09-07
Resolution : 3.00 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

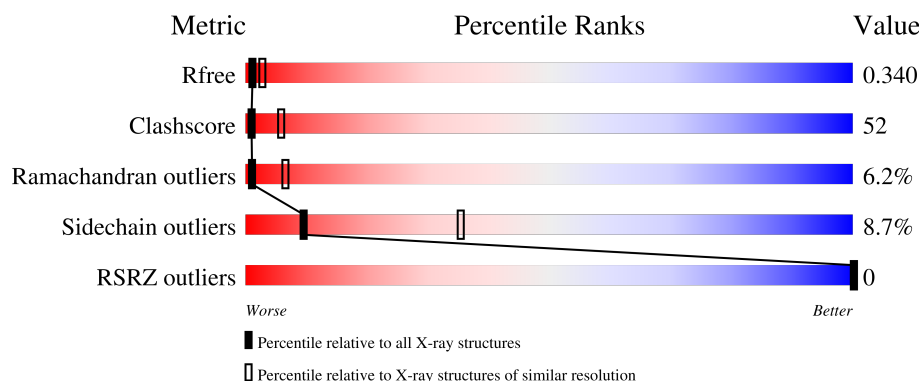
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	365	 29% 43% 11% 17%
1	B	365	 24% 46% 11% • 18%
1	C	365	 24% 54% 12% • 10%
1	D	365	 28% 43% 10% • 19%
1	W	365	 27% 43% 10% • 19%

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Mol	Chain	Length	Quality of chain
1	X	365	25%50%14%•10%
1	Y	365	23%50%9%•17%
1	Z	365	26%45%10%•18%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 18932 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 Fructose-bisphosphate aldolase B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	303	Total	C	N	O	S	0	0	0
			2331	1469	411	439	12			
1	B	299	Total	C	N	O	S	0	0	0
			2298	1448	405	433	12			
1	C	329	Total	C	N	O	S	0	0	0
			2527	1589	446	479	13			
1	D	297	Total	C	N	O	S	0	0	0
			2282	1436	403	431	12			
1	W	296	Total	C	N	O	S	0	0	0
			2274	1431	400	431	12			
1	X	329	Total	C	N	O	S	0	0	0
			2523	1584	445	481	13			
1	Y	302	Total	C	N	O	S	0	0	0
			2318	1460	408	438	12			
1	Z	301	Total	C	N	O	S	0	0	0
			2318	1461	408	437	12			

There are 24 discrepancies between the modelled and reference sequences:

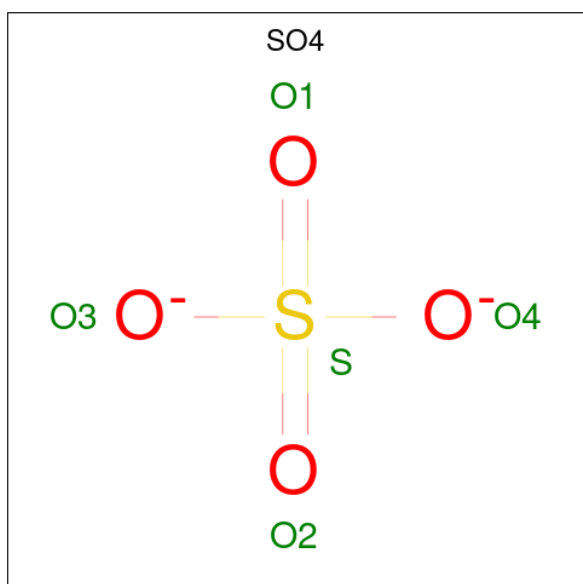
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	cloning artifact	UNP P05062
A	0	SER	-	cloning artifact	UNP P05062
A	149	PRO	ALA	engineered mutation	UNP P05062
B	-1	GLY	-	cloning artifact	UNP P05062
B	0	SER	-	cloning artifact	UNP P05062
B	149	PRO	ALA	engineered mutation	UNP P05062
C	-1	GLY	-	cloning artifact	UNP P05062
C	0	SER	-	cloning artifact	UNP P05062
C	149	PRO	ALA	engineered mutation	UNP P05062
D	-1	GLY	-	cloning artifact	UNP P05062
D	0	SER	-	cloning artifact	UNP P05062
D	149	PRO	ALA	engineered mutation	UNP P05062
W	-1	GLY	-	cloning artifact	UNP P05062

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Chain	Residue	Modelled	Actual	Comment	Reference
W	0	SER	-	cloning artifact	UNP P05062
W	149	PRO	ALA	engineered mutation	UNP P05062
X	-1	GLY	-	cloning artifact	UNP P05062
X	0	SER	-	cloning artifact	UNP P05062
X	149	PRO	ALA	engineered mutation	UNP P05062
Y	-1	GLY	-	cloning artifact	UNP P05062
Y	0	SER	-	cloning artifact	UNP P05062
Y	149	PRO	ALA	engineered mutation	UNP P05062
Z	-1	GLY	-	cloning artifact	UNP P05062
Z	0	SER	-	cloning artifact	UNP P05062
Z	149	PRO	ALA	engineered mutation	UNP P05062

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	Y	1	Total	O	S	0	0
			5	4	1		
2	Y	1	Total	O	S	0	0
			5	4	1		

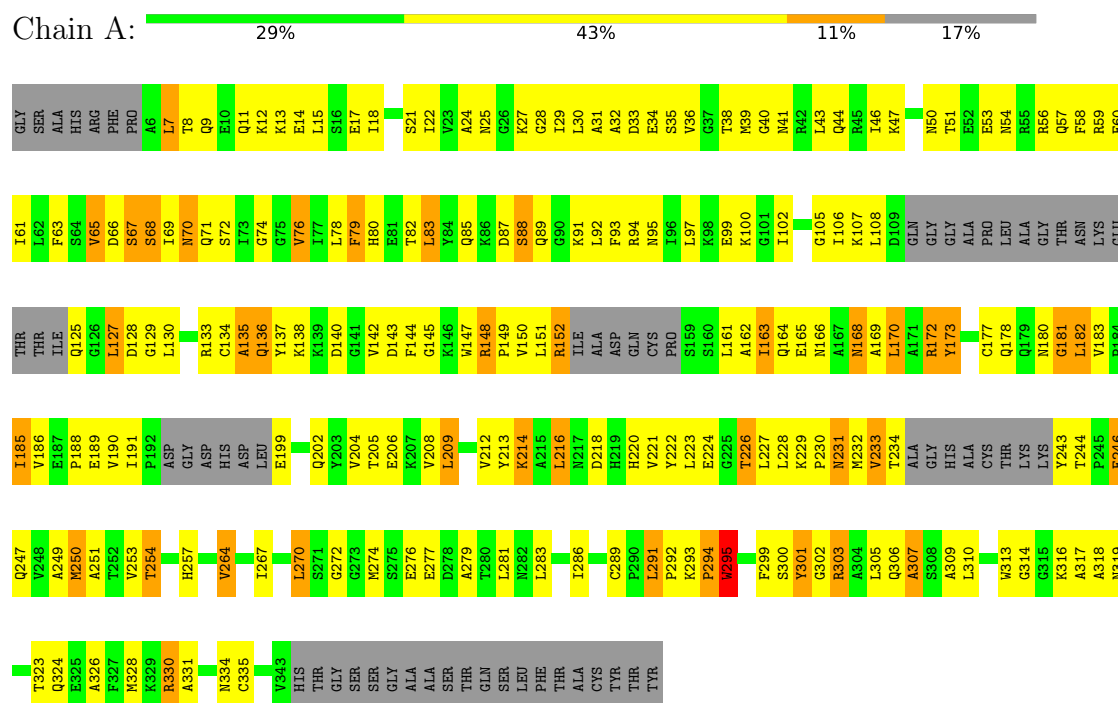
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	4	Total	O	0	0
			4	4		
3	B	4	Total	O	0	0
			4	4		
3	C	3	Total	O	0	0
			3	3		
3	D	2	Total	O	0	0
			2	2		
3	W	2	Total	O	0	0
			2	2		
3	X	1	Total	O	0	0
			1	1		
3	Y	2	Total	O	0	0
			2	2		
3	Z	3	Total	O	0	0
			3	3		

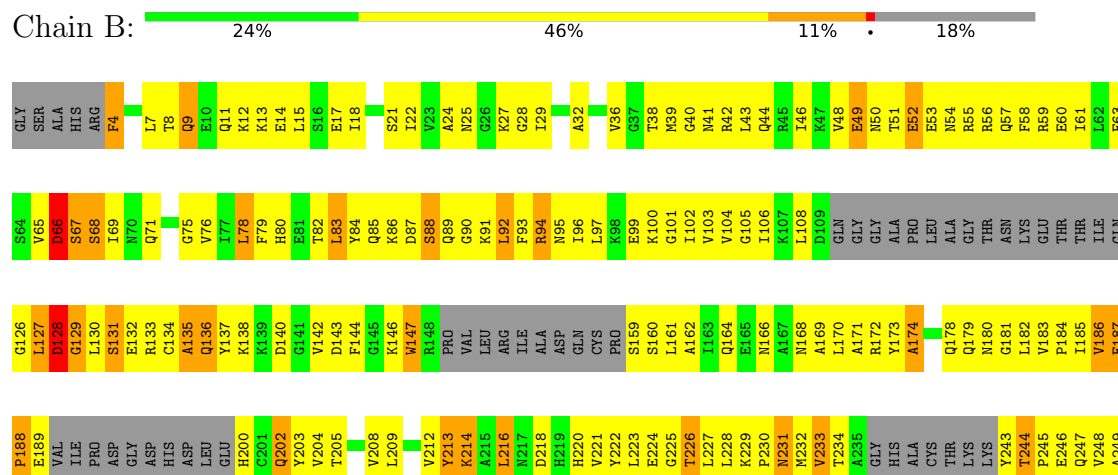
3 Residue-property plots

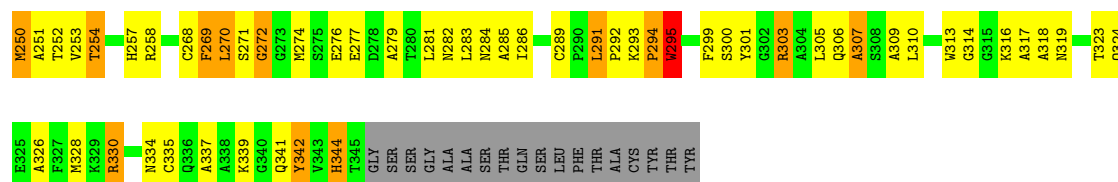
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Fructose-bisphosphate aldolase B



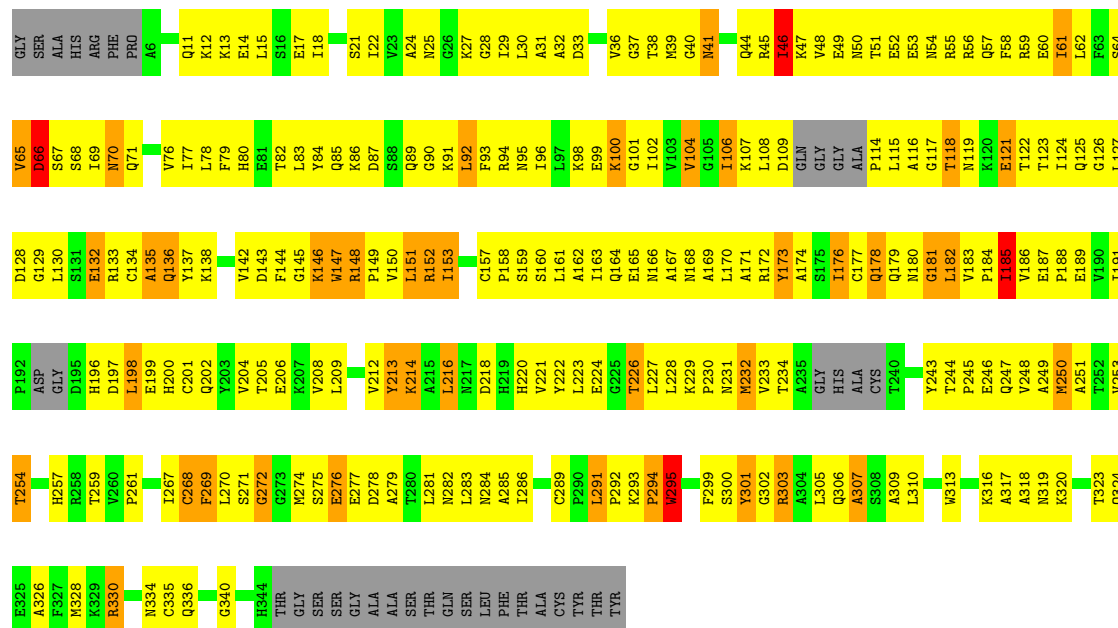
• Molecule 1: Fructose-bisphosphate aldolase B





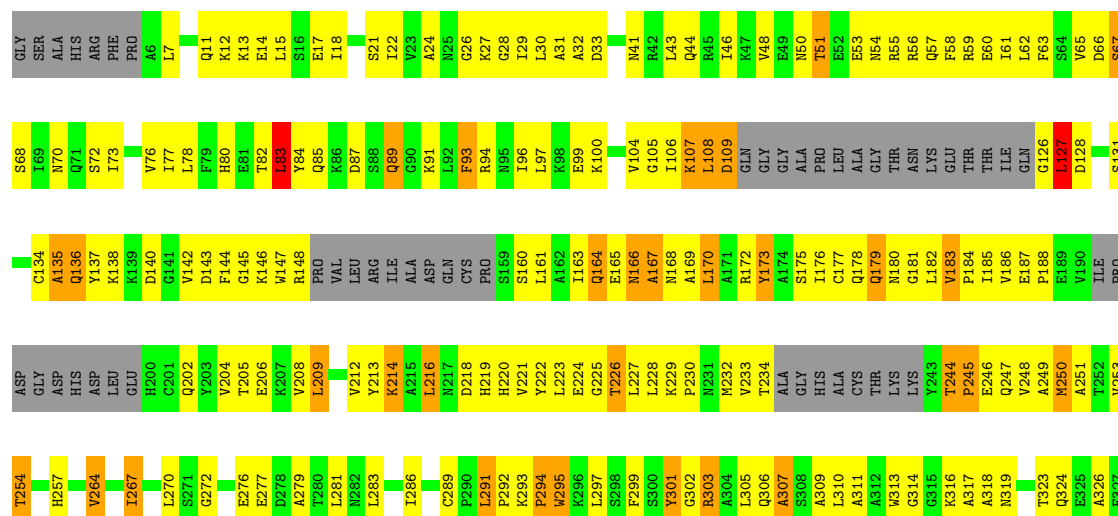
• Molecule 1: Fructose-bisphosphate aldolase B

Chain C: 24% 54% 12% 10%



• Molecule 1: Fructose-bisphosphate aldolase B

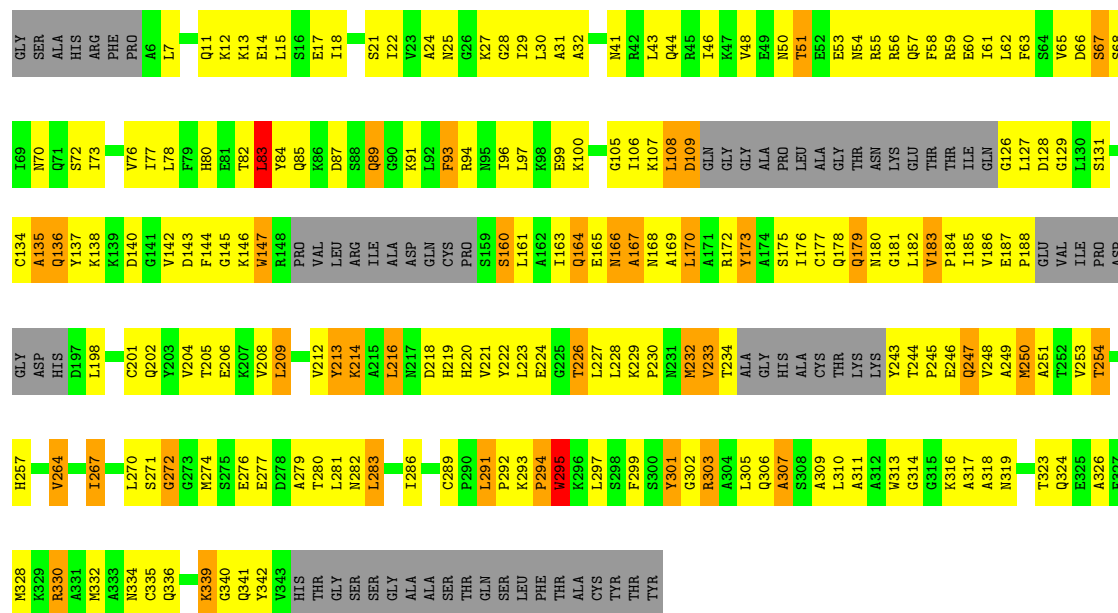
Chain D: 28% 43% 10% 19%





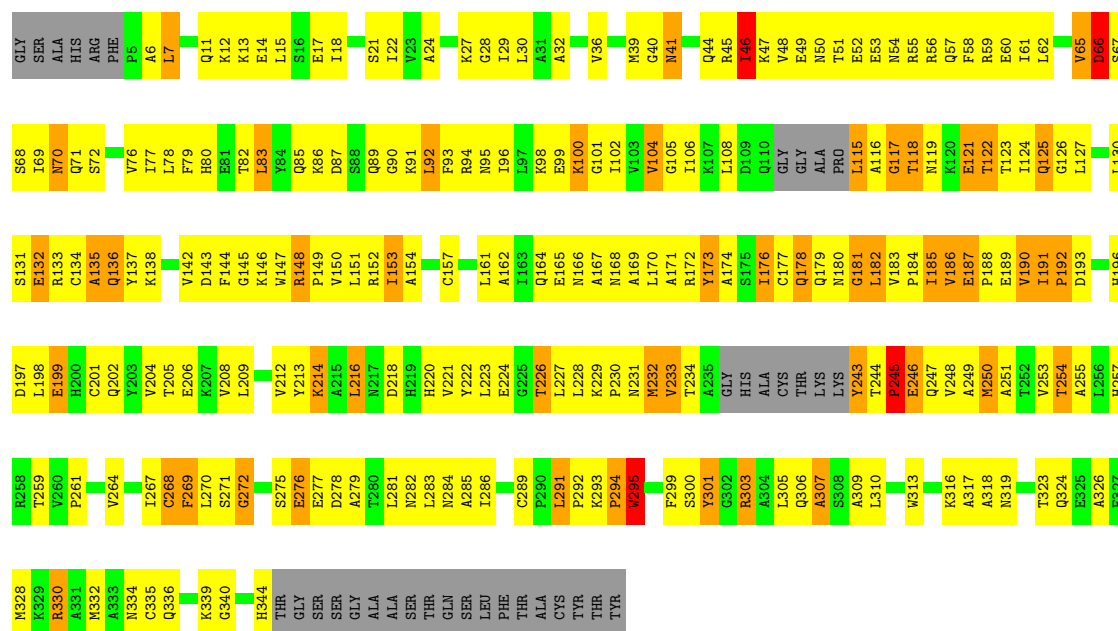
• Molecule 1: Fructose-bisphosphate aldolase B

Chain W: 27% 43% 10% 19%

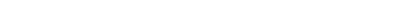


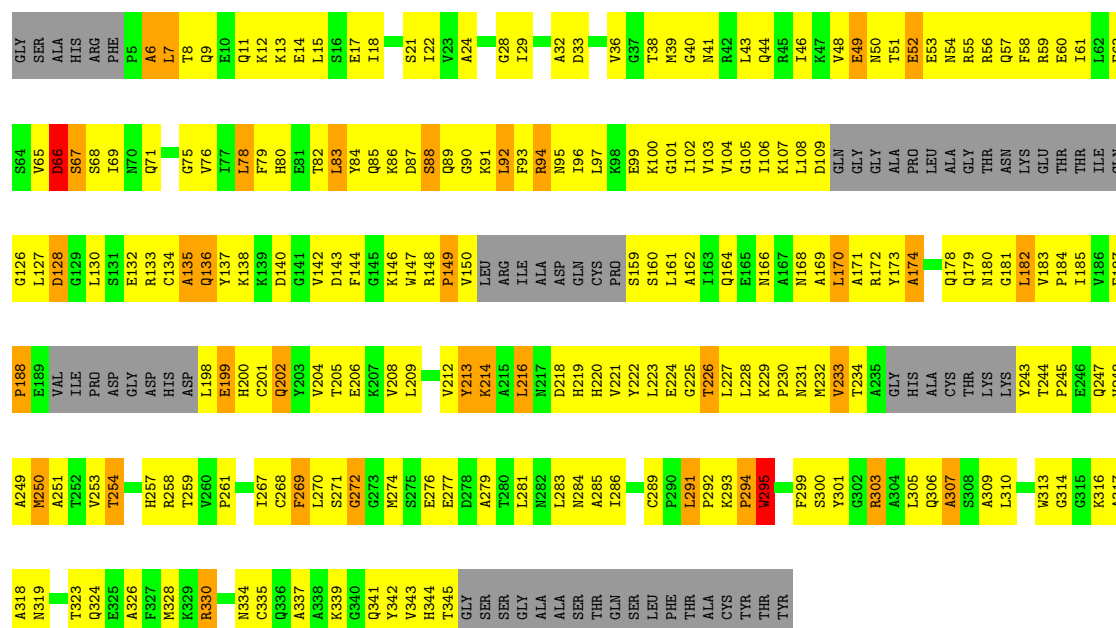
• Molecule 1: Fructose-bisphosphate aldolase B

Chain X: 25% 50% 14% 10%



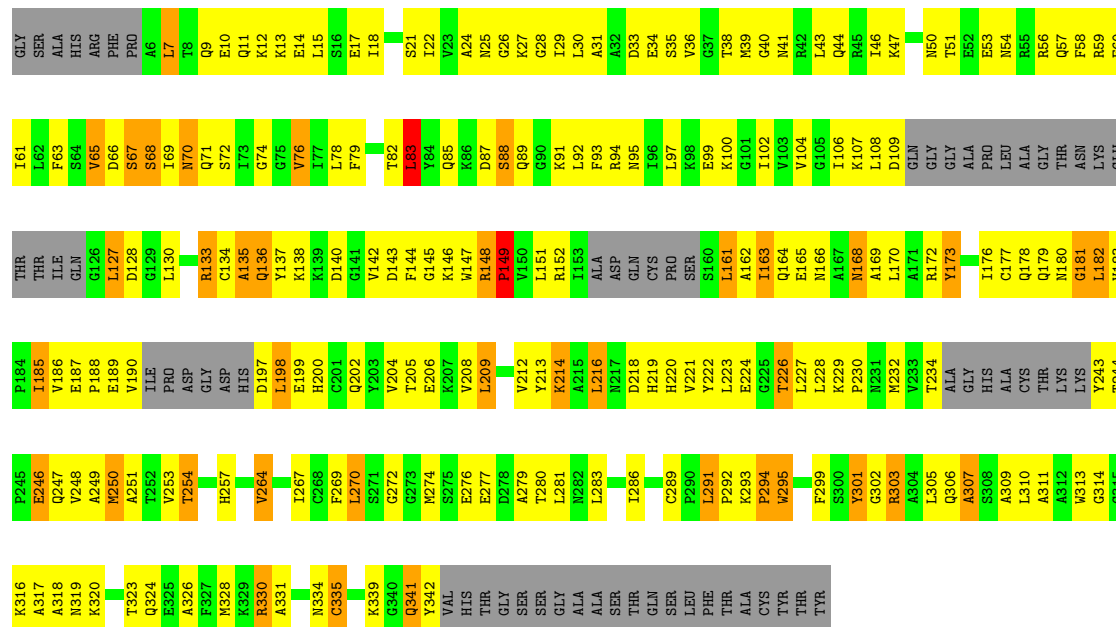
• Molecule 1: Fructose-bisphosphate aldolase B

Chain Y:  23% 50% 9% • 17%



- Molecule 1: Fructose-bisphosphate aldolase B

Chain Z: 26% 45% 10% 1% 18%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	153.48Å 153.51Å 186.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.15 – 3.00 20.15 – 3.00	Depositor EDS
% Data completeness (in resolution range)	78.1 (20.15-3.00) 84.8 (20.15-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.16 (at 2.50Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.304 , 0.349 0.299 , 0.340	Depositor DCC
R_{free} test set	7001 reflections (5.21%)	wwPDB-VP
Wilson B-factor (Å ²)	44.5	Xtriage
Anisotropy	0.708	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 68.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.458 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	18932	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.09% 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

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.49	0/2365	1.04	14/3190 (0.4%)
1	B	0.60	0/2333	1.09	17/3146 (0.5%)
1	C	0.58	1/2566 (0.0%)	1.11	20/3465 (0.6%)
1	D	0.50	0/2315	1.09	16/3121 (0.5%)
1	W	0.50	0/2306	1.07	17/3108 (0.5%)
1	X	0.58	1/2563 (0.0%)	1.12	24/3464 (0.7%)
1	Y	0.59	0/2353	1.07	15/3174 (0.5%)
1	Z	0.48	0/2351	1.02	16/3170 (0.5%)
All	All	0.54	2/19152 (0.0%)	1.08	139/25838 (0.5%)

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
1	C	0	2
1	W	0	1
1	Y	0	1
All	All	0	5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	185	ILE	CA-CB	5.31	1.60	1.53
1	X	70	ASN	CB-CG	-5.18	1.39	1.52

All (139) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	W	170	LEU	N-CA-C	-12.13	98.09	111.07
1	D	170	LEU	N-CA-C	-12.08	98.14	111.07
1	X	66	ASP	N-CA-C	11.70	126.26	110.35
1	C	66	ASP	N-CA-C	11.25	125.65	110.35
1	X	70	ASN	CB-CA-C	-10.79	88.96	110.42
1	C	132	GLU	N-CA-C	-9.80	100.88	113.12
1	X	117	GLY	N-CA-C	-9.17	103.78	115.42
1	A	148	ARG	CA-C-N	8.98	131.07	119.84
1	A	148	ARG	C-N-CA	8.98	131.07	119.84
1	W	166	ASN	N-CA-C	-8.97	101.45	111.14
1	C	117	GLY	N-CA-C	-8.40	104.47	115.47
1	C	70	ASN	CA-CB-CG	8.20	120.80	112.60
1	D	339	LYS	N-CA-C	-8.10	103.19	113.23
1	D	166	ASN	N-CA-C	-8.02	101.61	111.40
1	W	183	VAL	CA-C-N	7.98	129.82	119.84
1	W	183	VAL	C-N-CA	7.98	129.82	119.84
1	D	183	VAL	CA-C-N	7.89	129.70	119.84
1	D	183	VAL	C-N-CA	7.89	129.70	119.84
1	D	270	LEU	N-CA-C	-7.86	98.25	110.42
1	W	270	LEU	N-CA-C	-7.74	98.42	110.42
1	B	179	GLN	N-CA-C	-7.42	102.57	111.69
1	X	70	ASN	CA-CB-CG	7.36	119.96	112.60
1	W	264	VAL	CA-C-N	7.20	126.84	119.56
1	W	264	VAL	C-N-CA	7.20	126.84	119.56
1	Y	132	GLU	N-CA-C	-7.20	103.46	112.90
1	C	214	LYS	N-CA-C	-7.16	103.41	111.14
1	Y	214	LYS	N-CA-C	-7.15	103.42	111.14
1	Y	7	LEU	N-CA-C	7.14	121.15	109.94
1	Y	179	GLN	N-CA-C	-7.12	102.93	111.69
1	B	128	ASP	N-CA-C	7.11	120.31	110.35
1	D	264	VAL	CA-C-N	6.90	126.53	119.56
1	D	264	VAL	C-N-CA	6.90	126.53	119.56
1	A	47	LYS	N-CA-C	6.88	120.87	111.17
1	D	233	VAL	N-CA-C	6.88	118.72	108.54
1	B	231	ASN	N-CA-C	-6.86	101.69	110.19
1	B	214	LYS	N-CA-C	-6.83	103.76	111.14
1	D	214	LYS	N-CA-C	-6.80	103.79	111.14
1	X	214	LYS	N-CA-C	-6.78	103.82	111.14
1	Z	47	LYS	N-CA-C	6.76	120.71	111.17
1	B	188	PRO	N-CA-C	6.73	121.25	110.21
1	X	132	GLU	N-CA-C	-6.69	104.82	114.12
1	W	214	LYS	N-CA-C	-6.69	103.92	111.14
1	C	104	VAL	N-CA-C	6.56	117.55	108.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	214	LYS	N-CA-C	-6.53	104.09	111.14
1	Z	214	LYS	N-CA-C	-6.52	104.10	111.14
1	B	92	LEU	N-CA-C	6.47	119.28	108.73
1	Y	52	GLU	N-CA-C	-6.43	102.78	112.04
1	B	52	GLU	N-CA-C	-6.42	102.80	112.04
1	Y	92	LEU	N-CA-C	6.41	119.19	108.73
1	Z	270	LEU	N-CA-C	-6.37	99.92	110.17
1	X	7	LEU	N-CA-C	6.37	119.58	109.65
1	X	104	VAL	N-CA-C	6.36	117.29	108.89
1	Z	68	SER	N-CA-C	-6.31	105.22	113.17
1	Z	264	VAL	CA-C-N	6.26	125.88	119.56
1	Z	264	VAL	C-N-CA	6.26	125.88	119.56
1	Y	335	CYS	N-CA-C	-6.18	105.00	112.54
1	A	270	LEU	N-CA-C	-6.17	100.23	110.17
1	C	233	VAL	N-CA-C	6.14	116.96	107.99
1	A	68	SER	N-CA-C	-6.14	105.44	113.17
1	B	295	TRP	N-CA-C	6.06	119.37	109.06
1	X	191	ILE	CA-C-N	6.04	127.40	119.84
1	X	191	ILE	C-N-CA	6.04	127.40	119.84
1	Y	295	TRP	N-CA-C	6.01	119.28	109.06
1	Z	148	ARG	CA-C-N	5.97	127.30	119.84
1	Z	148	ARG	C-N-CA	5.97	127.30	119.84
1	W	232	MET	N-CA-C	-5.96	102.10	110.50
1	X	335	CYS	N-CA-C	-5.95	105.28	112.54
1	A	79	PHE	N-CA-C	-5.95	100.86	110.32
1	Y	128	ASP	N-CA-C	5.95	118.97	110.10
1	X	6	ALA	N-CA-C	5.94	120.33	112.72
1	B	335	CYS	N-CA-C	-5.92	105.32	112.54
1	C	335	CYS	N-CA-C	-5.85	105.41	112.54
1	X	92	LEU	N-CA-C	5.79	118.10	108.20
1	X	233	VAL	N-CA-C	5.79	116.48	108.84
1	W	339	LYS	N-CA-C	-5.79	106.26	113.38
1	D	343	VAL	CA-C-N	5.75	129.04	120.87
1	D	343	VAL	C-N-CA	5.75	129.04	120.87
1	W	233	VAL	N-CA-C	5.75	116.87	108.58
1	B	268	CYS	N-CA-C	5.75	118.53	109.39
1	W	93	PHE	N-CA-C	-5.75	105.10	111.71
1	W	247	GLN	N-CA-C	-5.71	104.69	111.03
1	D	335	CYS	N-CA-C	-5.71	105.58	112.54
1	Z	152	ARG	N-CA-C	5.70	115.63	108.45
1	B	270	LEU	N-CA-C	-5.69	101.33	110.14
1	A	150	VAL	N-CA-C	5.64	118.70	109.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	335	CYS	N-CA-C	-5.64	105.66	112.54
1	C	153	ILE	N-CA-C	5.64	114.48	106.53
1	D	93	PHE	N-CA-C	-5.63	105.23	111.71
1	C	106	ILE	N-CA-C	5.63	116.70	107.24
1	A	264	VAL	CA-C-N	5.62	125.24	119.56
1	A	264	VAL	C-N-CA	5.62	125.24	119.56
1	W	335	CYS	N-CA-C	-5.61	105.70	112.54
1	C	92	LEU	N-CA-C	5.60	117.86	108.73
1	C	295	TRP	N-CA-C	5.57	118.53	109.06
1	Y	270	LEU	N-CA-C	-5.56	101.52	110.14
1	C	121	GLU	N-CA-C	-5.54	101.20	109.96
1	X	295	TRP	N-CA-C	5.54	118.47	109.06
1	C	41	ASN	N-CA-C	-5.53	104.47	111.11
1	X	191	ILE	N-CA-C	5.53	114.37	108.95
1	X	148	ARG	N-CA-C	5.52	122.00	109.81
1	X	264	VAL	CA-C-N	5.48	125.09	119.56
1	X	264	VAL	C-N-CA	5.48	125.09	119.56
1	Z	335	CYS	N-CA-C	-5.43	105.92	112.54
1	B	342	TYR	N-CA-C	5.42	117.06	108.67
1	C	232	MET	N-CA-C	-5.41	102.99	110.35
1	X	41	ASN	N-CA-C	-5.41	104.62	111.11
1	Y	268	CYS	N-CA-C	5.41	118.42	108.58
1	C	301	TYR	N-CA-C	5.38	118.77	110.42
1	Y	78	LEU	N-CA-C	5.38	117.85	109.52
1	Z	172	ARG	N-CA-C	-5.38	105.06	111.03
1	D	104	VAL	N-CA-C	5.36	116.30	108.58
1	Y	6	ALA	N-CA-C	5.31	117.50	111.02
1	B	68	SER	N-CA-C	-5.31	106.39	112.92
1	Z	161	LEU	N-CA-C	-5.30	106.98	113.50
1	A	172	ARG	N-CA-C	-5.29	105.16	111.03
1	B	78	LEU	N-CA-C	5.26	117.68	109.52
1	A	301	TYR	N-CA-C	5.25	118.63	110.17
1	C	146	LYS	N-CA-C	5.25	117.85	110.14
1	Y	231	ASN	N-CA-C	-5.23	103.78	110.53
1	X	301	TYR	N-CA-C	5.21	118.50	110.42
1	Z	79	PHE	N-CA-C	-5.21	101.20	109.96
1	W	301	TYR	N-CA-C	5.20	118.48	110.42
1	A	295	TRP	N-CA-C	5.13	117.78	109.06
1	B	344	HIS	N-CA-C	5.13	117.52	108.24
1	Z	301	TYR	N-CA-C	5.12	118.42	110.17
1	D	301	TYR	N-CA-C	5.12	118.35	110.42
1	Y	182	LEU	N-CA-C	5.11	116.53	110.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	X	190	VAL	N-CA-C	-5.10	99.90	107.51
1	X	121	GLU	N-CA-C	-5.08	104.16	110.41
1	Z	108	LEU	N-CA-C	5.07	119.18	112.89
1	C	148	ARG	CA-C-N	5.07	126.17	119.84
1	C	148	ARG	C-N-CA	5.07	126.17	119.84
1	Z	133	ARG	N-CA-C	-5.07	105.46	111.69
1	C	148	ARG	N-CA-C	5.07	122.36	107.37
1	B	4	PHE	CA-C-N	5.06	125.30	119.83
1	B	4	PHE	C-N-CA	5.06	125.30	119.83
1	X	246	GLU	N-CA-C	-5.03	105.50	111.69
1	W	295	TRP	N-CA-C	5.03	117.61	109.06
1	W	283	LEU	N-CA-C	-5.01	105.82	111.28

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	213	TYR	Sidechain
1	C	213	TYR	Sidechain
1	C	84	TYR	Sidechain
1	W	213	TYR	Sidechain
1	Y	213	TYR	Sidechain

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	2331	0	2359	231	0
1	B	2298	0	2313	270	0
1	C	2527	0	2555	288	0
1	D	2282	0	2301	230	0
1	W	2274	0	2293	215	0
1	X	2523	0	2538	283	0
1	Y	2318	0	2338	260	0
1	Z	2318	0	2345	235	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	10	0	0	0	0
2	W	5	0	0	0	0
2	X	5	0	0	0	0
2	Y	10	0	0	0	0
3	A	4	0	0	0	0
3	B	4	0	0	0	0
3	C	3	0	0	2	0
3	D	2	0	0	0	0
3	W	2	0	0	0	0
3	X	1	0	0	0	0
3	Y	2	0	0	0	0
3	Z	3	0	0	1	0
All	All	18932	0	19042	1985	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 52.

All (1985) 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:W:303:ARG:H	1:W:303:ARG:HD2	1.05	1.19
1:B:303:ARG:H	1:B:303:ARG:HD2	1.02	1.17
1:Z:228:LEU:HG	1:Z:230:PRO:HD3	1.26	1.17
1:C:303:ARG:H	1:C:303:ARG:HD2	1.03	1.17
1:C:149:PRO:HG3	1:C:170:LEU:HD11	1.20	1.17
1:D:303:ARG:H	1:D:303:ARG:HD2	1.05	1.17
1:W:228:LEU:HG	1:W:230:PRO:HD3	1.27	1.15
1:X:228:LEU:HG	1:X:230:PRO:HD3	1.24	1.15
1:D:228:LEU:HG	1:D:230:PRO:HD3	1.29	1.13
1:C:178:GLN:HE22	1:C:222:TYR:HB3	1.08	1.13
1:Y:228:LEU:HG	1:Y:230:PRO:HD3	1.23	1.12
1:X:149:PRO:HG3	1:X:170:LEU:HD11	1.26	1.12
1:A:228:LEU:HG	1:A:230:PRO:HD3	1.25	1.12
1:A:303:ARG:H	1:A:303:ARG:HD2	1.05	1.11
1:C:228:LEU:HG	1:C:230:PRO:HD3	1.26	1.11
1:Y:303:ARG:H	1:Y:303:ARG:HD2	1.02	1.11
1:X:178:GLN:HE22	1:X:222:TYR:HB3	1.15	1.10
1:X:303:ARG:H	1:X:303:ARG:HD2	1.03	1.10
1:Z:303:ARG:H	1:Z:303:ARG:HD2	1.04	1.09
1:B:228:LEU:HG	1:B:230:PRO:HD3	1.24	1.08
1:Y:149:PRO:HG3	1:Y:170:LEU:HD11	1.22	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:216:LEU:HD23	1:C:221:VAL:HG21	1.39	1.04
1:Y:216:LEU:HD23	1:Y:221:VAL:HG21	1.38	1.03
1:X:145:GLY:O	1:X:185:ILE:HG22	1.58	1.03
1:X:216:LEU:HD23	1:X:221:VAL:HG21	1.40	1.03
1:B:127:LEU:H	1:B:127:LEU:HD12	1.24	1.02
1:B:216:LEU:HD23	1:B:221:VAL:HG21	1.41	1.01
1:C:68:SER:OG	1:C:328:MET:HE1	1.60	1.01
1:W:216:LEU:HD23	1:W:221:VAL:HG21	1.44	1.00
1:B:49:GLU:HG2	1:Y:49:GLU:HG2	1.43	1.00
1:A:127:LEU:H	1:A:127:LEU:HD12	1.26	1.00
1:D:216:LEU:HD23	1:D:221:VAL:HG21	1.45	0.98
1:Z:216:LEU:HD23	1:Z:221:VAL:HG21	1.45	0.97
1:Z:232:MET:HE2	1:Z:286:ILE:HD12	1.48	0.96
1:C:149:PRO:CG	1:C:170:LEU:HD11	1.96	0.96
1:X:186:VAL:HG12	1:X:188:PRO:HD3	1.45	0.95
1:C:234:THR:HG22	1:C:248:VAL:HG13	1.48	0.94
1:X:68:SER:OG	1:X:328:MET:HE1	1.68	0.94
1:W:186:VAL:HG12	1:W:188:PRO:HD3	1.48	0.93
1:C:149:PRO:HD3	1:C:170:LEU:HD21	1.51	0.93
1:X:149:PRO:CG	1:X:170:LEU:HD11	1.99	0.92
1:A:216:LEU:HD23	1:A:221:VAL:HG21	1.50	0.91
1:C:186:VAL:HG12	1:C:188:PRO:HD3	1.52	0.91
1:A:18:ILE:O	1:A:22:ILE:HG13	1.70	0.91
1:D:18:ILE:O	1:D:22:ILE:HG13	1.71	0.91
1:D:186:VAL:HG12	1:D:188:PRO:HD3	1.53	0.90
1:Z:18:ILE:O	1:Z:22:ILE:HG13	1.72	0.90
1:Y:303:ARG:HD2	1:Y:303:ARG:N	1.88	0.89
1:D:204:VAL:O	1:D:208:VAL:HG23	1.72	0.89
1:D:89:GLN:HE21	1:D:89:GLN:HA	1.37	0.89
1:W:89:GLN:HE21	1:W:89:GLN:HA	1.36	0.89
1:W:18:ILE:O	1:W:22:ILE:HG13	1.73	0.89
1:C:147:TRP:HD1	1:C:170:LEU:HD23	1.38	0.89
1:B:303:ARG:HD2	1:B:303:ARG:N	1.87	0.88
1:X:303:ARG:H	1:X:303:ARG:CD	1.87	0.88
1:C:146:LYS:HG2	1:C:147:TRP:N	1.87	0.88
1:Y:303:ARG:H	1:Y:303:ARG:CD	1.85	0.87
1:X:204:VAL:O	1:X:208:VAL:HG23	1.75	0.87
1:C:303:ARG:HD2	1:C:303:ARG:N	1.88	0.87
1:W:303:ARG:HD2	1:W:303:ARG:N	1.90	0.86
1:D:303:ARG:HD2	1:D:303:ARG:N	1.90	0.86
1:X:303:ARG:HD2	1:X:303:ARG:N	1.89	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:303:ARG:H	1:A:303:ARG:CD	1.88	0.85
1:B:186:VAL:HG12	1:B:188:PRO:HD3	1.59	0.85
1:B:127:LEU:H	1:B:127:LEU:CD1	1.89	0.85
1:A:204:VAL:O	1:A:208:VAL:HG23	1.77	0.85
1:A:303:ARG:HD2	1:A:303:ARG:N	1.90	0.85
1:Y:204:VAL:O	1:Y:208:VAL:HG23	1.77	0.85
1:Z:204:VAL:O	1:Z:208:VAL:HG23	1.75	0.85
1:W:204:VAL:O	1:W:208:VAL:HG23	1.75	0.85
1:Z:151:LEU:HD21	1:Z:166:ASN:ND2	1.92	0.84
1:X:108:LEU:HD13	1:X:130:LEU:HD11	1.57	0.84
1:Y:18:ILE:O	1:Y:22:ILE:HG13	1.77	0.84
1:X:18:ILE:O	1:X:22:ILE:HG13	1.76	0.84
1:Z:303:ARG:HD2	1:Z:303:ARG:N	1.89	0.83
1:W:173:TYR:HE1	1:W:177:CYS:HG	1.25	0.83
1:C:18:ILE:O	1:C:22:ILE:HG13	1.77	0.83
1:C:204:VAL:O	1:C:208:VAL:HG23	1.78	0.83
1:B:18:ILE:O	1:B:22:ILE:HG13	1.77	0.83
1:X:124:ILE:HD11	1:X:149:PRO:HA	1.61	0.83
1:Z:147:TRP:HB3	1:Z:173:TYR:CE2	2.13	0.83
1:D:226:THR:CG2	1:D:227:LEU:N	2.42	0.83
1:B:208:VAL:O	1:B:212:VAL:HG23	1.79	0.83
1:C:178:GLN:HE22	1:C:222:TYR:CB	1.92	0.82
1:Z:58:PHE:HB2	1:Z:313:TRP:CZ3	2.14	0.82
1:B:146:LYS:HA	1:B:185:ILE:HG22	1.61	0.82
1:B:185:ILE:HG23	1:B:185:ILE:O	1.77	0.82
1:B:204:VAL:O	1:B:208:VAL:HG23	1.79	0.82
1:Y:147:TRP:HB3	1:Y:173:TYR:CD2	2.15	0.81
1:A:226:THR:CG2	1:A:227:LEU:N	2.43	0.81
1:B:106:ILE:HG22	1:B:142:VAL:HG11	1.61	0.81
1:Y:234:THR:HG22	1:Y:248:VAL:HG13	1.60	0.81
1:C:114:PRO:HA	1:C:122:THR:HG22	1.63	0.81
1:Z:232:MET:HE2	1:Z:286:ILE:CD1	2.11	0.81
1:Y:130:LEU:HD12	1:Y:133:ARG:HD3	1.63	0.81
1:Z:226:THR:CG2	1:Z:227:LEU:N	2.42	0.81
1:A:94:ARG:HD2	1:A:140:ASP:O	1.80	0.80
1:Y:51:THR:HG22	1:Y:52:GLU:H	1.46	0.80
1:Y:226:THR:CG2	1:Y:227:LEU:N	2.44	0.80
1:B:146:LYS:HG2	1:B:147:TRP:N	1.96	0.80
1:Y:149:PRO:HG3	1:Y:170:LEU:CD1	2.09	0.80
1:Z:244:THR:HG23	1:Z:247:GLN:HG3	1.63	0.80
1:B:226:THR:CG2	1:B:227:LEU:N	2.45	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:208:VAL:O	1:Y:212:VAL:HG23	1.82	0.79
1:C:151:LEU:HD22	1:C:208:VAL:HG13	1.62	0.79
1:D:143:ASP:O	1:D:182:LEU:HA	1.83	0.79
1:Z:186:VAL:HG12	1:Z:188:PRO:HD3	1.62	0.79
1:C:208:VAL:O	1:C:212:VAL:HG23	1.83	0.79
1:A:185:ILE:HD11	1:A:229:LYS:HD2	1.65	0.79
1:D:178:GLN:HE21	1:D:184:PRO:HG3	1.48	0.79
1:W:226:THR:CG2	1:W:227:LEU:N	2.43	0.79
1:X:119:ASN:HB3	1:X:157:CYS:SG	2.23	0.79
1:X:208:VAL:O	1:X:212:VAL:HG23	1.83	0.79
1:D:226:THR:CG2	1:D:227:LEU:H	1.96	0.78
1:C:149:PRO:HG3	1:C:170:LEU:CD1	2.09	0.78
1:D:234:THR:HG22	1:D:248:VAL:HG13	1.64	0.78
1:W:226:THR:CG2	1:W:227:LEU:H	1.97	0.78
1:A:208:VAL:O	1:A:212:VAL:HG23	1.83	0.78
1:B:51:THR:HG22	1:B:52:GLU:H	1.48	0.78
1:W:178:GLN:HE21	1:W:184:PRO:HG3	1.48	0.78
1:C:118:THR:HG21	1:C:121:GLU:HB2	1.66	0.77
1:C:226:THR:CG2	1:C:227:LEU:N	2.47	0.77
1:C:148:ARG:HB2	1:C:187:GLU:HB3	1.67	0.77
1:X:226:THR:CG2	1:X:227:LEU:N	2.47	0.77
1:Z:185:ILE:HD11	1:Z:229:LYS:HD2	1.65	0.77
1:X:149:PRO:HG3	1:X:170:LEU:CD1	2.11	0.77
1:Y:147:TRP:HB3	1:Y:173:TYR:CE2	2.19	0.77
1:Z:208:VAL:O	1:Z:212:VAL:HG23	1.84	0.77
1:A:226:THR:CG2	1:A:227:LEU:H	1.98	0.77
1:B:146:LYS:HG2	1:B:147:TRP:H	1.50	0.76
1:X:178:GLN:HE22	1:X:222:TYR:CB	1.98	0.76
1:Y:39:MET:HA	1:Y:39:MET:HE3	1.68	0.76
1:Y:212:VAL:O	1:Y:216:LEU:HD12	1.85	0.76
1:B:226:THR:CG2	1:B:227:LEU:H	1.99	0.76
1:Z:94:ARG:HD2	1:Z:140:ASP:O	1.84	0.76
1:A:226:THR:HG22	1:A:227:LEU:N	2.01	0.76
1:B:146:LYS:HA	1:B:185:ILE:CG2	2.14	0.76
1:D:244:THR:HG22	1:D:247:GLN:HG3	1.67	0.76
1:X:198:LEU:HD22	1:X:243:TYR:HD2	1.49	0.76
1:Y:226:THR:HG22	1:Y:227:LEU:N	2.01	0.76
1:C:124:ILE:HD11	1:C:149:PRO:HA	1.67	0.75
1:B:39:MET:HA	1:B:39:MET:HE3	1.67	0.75
1:C:18:ILE:HD13	1:C:143:ASP:HB3	1.68	0.75
1:X:149:PRO:HD3	1:X:170:LEU:HD21	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:234:THR:HG22	1:X:248:VAL:HG13	1.66	0.75
1:A:7:LEU:HD21	1:A:178:GLN:HB3	1.67	0.75
1:D:246:GLU:CD	1:D:246:GLU:H	1.94	0.75
1:W:226:THR:HG22	1:W:227:LEU:N	2.01	0.75
1:B:249:ALA:O	1:B:253:VAL:HG23	1.86	0.75
1:C:145:GLY:O	1:C:185:ILE:HG22	1.86	0.75
1:C:178:GLN:NE2	1:C:222:TYR:HB3	1.94	0.75
1:D:226:THR:HG22	1:D:227:LEU:N	2.00	0.75
1:C:196:HIS:HD2	1:C:201:CYS:HB2	1.52	0.74
1:B:226:THR:HG22	1:B:227:LEU:N	2.02	0.74
1:C:151:LEU:H	1:C:151:LEU:HD12	1.52	0.74
1:X:166:ASN:O	1:X:169:ALA:HB3	1.86	0.74
1:Y:18:ILE:HD13	1:Y:143:ASP:HB3	1.69	0.74
1:C:303:ARG:H	1:C:303:ARG:CD	1.86	0.74
1:Y:226:THR:CG2	1:Y:227:LEU:H	2.00	0.74
1:C:186:VAL:HG12	1:C:188:PRO:CD	2.17	0.74
1:Z:226:THR:HG22	1:Z:227:LEU:N	2.00	0.74
1:Z:198:LEU:HD12	1:Z:234:THR:HA	1.69	0.74
1:A:58:PHE:HB2	1:A:313:TRP:CZ3	2.23	0.73
1:C:58:PHE:CE2	1:C:310:LEU:HD13	2.23	0.73
1:W:249:ALA:O	1:W:253:VAL:HG23	1.88	0.73
1:X:245:PRO:O	1:X:285:ALA:HB1	1.88	0.73
1:Z:226:THR:CG2	1:Z:227:LEU:H	1.98	0.73
1:W:63:PHE:CD1	1:W:97:LEU:HD21	2.24	0.73
1:X:116:ALA:C	1:X:118:THR:H	1.94	0.73
1:X:153:ILE:HD12	1:X:196:HIS:HB3	1.71	0.73
1:B:330:ARG:HH11	1:B:330:ARG:HG3	1.54	0.73
1:A:127:LEU:H	1:A:127:LEU:CD1	2.01	0.73
1:C:56:ARG:HB2	1:C:85:GLN:NE2	2.04	0.73
1:C:87:ASP:OD1	1:C:91:LYS:HB3	1.89	0.72
1:D:208:VAL:O	1:D:212:VAL:HG23	1.89	0.72
1:X:56:ARG:HB2	1:X:85:GLN:NE2	2.04	0.72
1:X:106:ILE:HG22	1:X:142:VAL:HG11	1.71	0.72
1:B:232:MET:CE	1:B:274:MET:HE1	2.19	0.72
1:W:94:ARG:HG2	1:W:94:ARG:HH11	1.54	0.72
1:Y:249:ALA:O	1:Y:253:VAL:HG23	1.89	0.72
1:A:228:LEU:CG	1:A:230:PRO:HD3	2.13	0.72
1:W:208:VAL:O	1:W:212:VAL:HG23	1.88	0.72
1:X:41:ASN:O	1:X:44:GLN:HB3	1.89	0.72
1:Z:243:TYR:HA	1:Z:247:GLN:OE1	1.89	0.72
1:D:94:ARG:HG2	1:D:94:ARG:HH11	1.54	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:249:ALA:O	1:D:253:VAL:HG23	1.90	0.72
1:D:226:THR:HG23	1:D:227:LEU:H	1.54	0.72
1:Y:185:ILE:HG23	1:Y:185:ILE:O	1.88	0.72
1:C:198:LEU:HD12	1:C:234:THR:HA	1.72	0.72
1:B:106:ILE:CG2	1:B:142:VAL:HG11	2.20	0.72
1:Z:18:ILE:HD13	1:Z:143:ASP:HB3	1.72	0.71
1:Z:185:ILE:HD11	1:Z:229:LYS:CD	2.20	0.71
1:A:244:THR:CG2	1:A:247:GLN:HG3	2.21	0.71
1:W:226:THR:HG23	1:W:227:LEU:H	1.54	0.71
1:X:58:PHE:CE2	1:X:310:LEU:HD13	2.25	0.71
1:Y:228:LEU:CG	1:Y:230:PRO:HD3	2.14	0.71
1:C:95:ASN:O	1:C:99:GLU:HG3	1.90	0.71
1:C:166:ASN:O	1:C:169:ALA:HB3	1.90	0.71
1:C:249:ALA:O	1:C:253:VAL:HG23	1.91	0.71
1:C:41:ASN:O	1:C:44:GLN:HB3	1.89	0.71
1:D:344:HIS:O	1:D:345:THR:HB	1.89	0.71
1:X:249:ALA:O	1:X:253:VAL:HG23	1.90	0.71
1:D:316:LYS:HB2	1:D:319:ASN:ND2	2.06	0.71
1:Y:12:LYS:HD2	1:Y:222:TYR:CE1	2.25	0.71
1:A:38:THR:HA	1:A:41:ASN:HD22	1.55	0.71
1:W:58:PHE:HB2	1:W:313:TRP:CZ3	2.25	0.71
1:B:316:LYS:HB2	1:B:319:ASN:ND2	2.06	0.71
1:W:146:LYS:HG2	1:W:147:TRP:N	2.06	0.71
1:X:87:ASP:OD1	1:X:91:LYS:HB3	1.90	0.71
1:A:316:LYS:HB2	1:A:319:ASN:ND2	2.06	0.71
1:C:226:THR:CG2	1:C:227:LEU:H	2.04	0.71
1:D:63:PHE:CD1	1:D:97:LEU:HD21	2.25	0.71
1:X:148:ARG:HD2	1:X:187:GLU:CD	2.15	0.71
1:Z:38:THR:HA	1:Z:41:ASN:HD22	1.55	0.71
1:Z:60:GLU:HA	1:Z:93:PHE:CE1	2.25	0.71
1:C:138:LYS:HB2	1:C:182:LEU:CD1	2.21	0.70
1:X:134:CYS:O	1:X:136:GLN:N	2.24	0.70
1:Z:56:ARG:HB2	1:Z:85:GLN:NE2	2.07	0.70
1:C:226:THR:HG22	1:C:227:LEU:N	2.05	0.70
1:C:119:ASN:HB3	1:C:157:CYS:SG	2.31	0.70
1:C:138:LYS:NZ	1:C:143:ASP:OD1	2.23	0.70
1:X:51:THR:HG22	1:X:53:GLU:H	1.55	0.70
1:Z:226:THR:HG23	1:Z:227:LEU:H	1.55	0.70
1:A:60:GLU:HA	1:A:93:PHE:CE1	2.26	0.70
1:C:161:LEU:O	1:C:165:GLU:HB2	1.90	0.70
1:D:26:GLY:HA3	1:D:339:LYS:HD2	1.71	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:108:LEU:HD11	1:W:134:CYS:SG	2.31	0.70
1:X:22:ILE:HG21	1:X:29:ILE:HD11	1.73	0.70
1:X:95:ASN:O	1:X:99:GLU:HG3	1.92	0.70
1:Y:316:LYS:HB2	1:Y:319:ASN:ND2	2.06	0.70
1:Z:65:VAL:HG23	1:Z:324:GLN:HB3	1.73	0.70
1:A:56:ARG:HB2	1:A:85:GLN:NE2	2.06	0.70
1:B:127:LEU:HD12	1:B:127:LEU:N	2.03	0.70
1:B:303:ARG:H	1:B:303:ARG:CD	1.85	0.70
1:W:89:GLN:HE21	1:W:89:GLN:CA	2.03	0.70
1:C:51:THR:HG22	1:C:53:GLU:H	1.55	0.70
1:W:12:LYS:HD2	1:W:222:TYR:CE1	2.27	0.70
1:X:161:LEU:O	1:X:165:GLU:HB2	1.92	0.70
1:Y:15:LEU:HD22	1:Y:182:LEU:O	1.91	0.70
1:B:212:VAL:O	1:B:216:LEU:HD12	1.91	0.70
1:D:303:ARG:H	1:D:303:ARG:CD	1.88	0.70
1:W:28:GLY:HA3	1:W:299:PHE:CZ	2.27	0.70
1:W:185:ILE:O	1:W:185:ILE:HG22	1.90	0.70
1:X:148:ARG:HD2	1:X:187:GLU:OE2	1.92	0.70
1:X:150:VAL:HG13	1:X:191:ILE:HD13	1.72	0.70
1:Z:316:LYS:HB2	1:Z:319:ASN:ND2	2.06	0.70
1:A:226:THR:HG23	1:A:227:LEU:H	1.56	0.70
1:B:57:GLN:O	1:B:58:PHE:C	2.34	0.70
1:B:234:THR:HG22	1:B:248:VAL:HG13	1.74	0.70
1:X:309:ALA:O	1:X:323:THR:HG23	1.92	0.70
1:A:249:ALA:O	1:A:253:VAL:HG23	1.90	0.70
1:B:228:LEU:CG	1:B:230:PRO:HD3	2.15	0.70
1:D:173:TYR:HE1	1:D:177:CYS:SG	2.15	0.70
1:Z:303:ARG:H	1:Z:303:ARG:CD	1.87	0.69
1:D:14:GLU:O	1:D:18:ILE:HG13	1.92	0.69
1:W:303:ARG:H	1:W:303:ARG:CD	1.88	0.69
1:Z:228:LEU:CG	1:Z:230:PRO:HD3	2.15	0.69
1:W:173:TYR:HE1	1:W:177:CYS:SG	2.15	0.69
1:W:186:VAL:HG12	1:W:188:PRO:CD	2.22	0.69
1:C:196:HIS:CD2	1:C:201:CYS:HB2	2.26	0.69
1:D:12:LYS:HD2	1:D:222:TYR:CE1	2.27	0.69
1:Y:281:LEU:HD21	1:Y:344:HIS:CD2	2.26	0.69
1:Z:58:PHE:CE2	1:Z:310:LEU:HD13	2.28	0.69
1:Z:244:THR:CG2	1:Z:247:GLN:HG3	2.22	0.69
1:C:45:ARG:C	1:C:47:LYS:H	2.00	0.69
1:W:316:LYS:HB2	1:W:319:ASN:ND2	2.06	0.69
1:X:226:THR:HG22	1:X:227:LEU:N	2.06	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:186:VAL:HG12	1:A:188:PRO:HD3	1.74	0.69
1:D:77:ILE:HD11	1:D:185:ILE:HD12	1.75	0.69
1:X:146:LYS:HG2	1:X:147:TRP:N	2.08	0.69
1:A:108:LEU:HB3	1:A:130:LEU:HD11	1.73	0.69
1:Y:63:PHE:HD1	1:Y:97:LEU:HD21	1.58	0.69
1:B:226:THR:HG23	1:B:227:LEU:H	1.58	0.68
1:C:199:GLU:CD	1:C:199:GLU:H	2.01	0.68
1:C:309:ALA:O	1:C:323:THR:HG23	1.92	0.68
1:X:228:LEU:CG	1:X:230:PRO:HD3	2.13	0.68
1:A:30:LEU:HB3	1:A:76:VAL:HG13	1.75	0.68
1:A:185:ILE:HD11	1:A:229:LYS:CD	2.22	0.68
1:C:228:LEU:CG	1:C:230:PRO:HD3	2.15	0.68
1:Y:226:THR:HG23	1:Y:227:LEU:H	1.58	0.68
1:C:134:CYS:O	1:C:136:GLN:N	2.26	0.68
1:D:89:GLN:HE21	1:D:89:GLN:CA	2.04	0.68
1:Y:51:THR:HG22	1:Y:52:GLU:N	2.09	0.68
1:Y:232:MET:CE	1:Y:274:MET:HE1	2.23	0.68
1:Z:249:ALA:O	1:Z:253:VAL:HG23	1.92	0.68
1:Y:146:LYS:HA	1:Y:185:ILE:HG22	1.74	0.68
1:Y:309:ALA:O	1:Y:323:THR:HG23	1.94	0.68
1:C:109:ASP:OD1	1:C:147:TRP:HA	1.94	0.68
1:X:122:THR:OG1	1:X:123:THR:N	2.23	0.68
1:X:164:GLN:O	1:X:168:ASN:ND2	2.23	0.68
1:Y:330:ARG:HH11	1:Y:330:ARG:HG3	1.58	0.68
1:D:147:TRP:HB3	1:D:173:TYR:CE2	2.29	0.68
1:D:335:CYS:O	1:D:339:LYS:HD3	1.93	0.68
1:X:226:THR:CG2	1:X:227:LEU:H	2.06	0.68
1:Z:309:ALA:O	1:Z:323:THR:HG23	1.94	0.68
1:X:146:LYS:HG2	1:X:147:TRP:H	1.58	0.68
1:C:234:THR:CG2	1:C:248:VAL:HG13	2.24	0.68
1:W:14:GLU:O	1:W:18:ILE:HG13	1.94	0.68
1:Y:57:GLN:O	1:Y:58:PHE:C	2.37	0.68
1:Z:143:ASP:O	1:Z:182:LEU:HA	1.94	0.68
1:A:46:ILE:HG12	1:A:314:GLY:HA2	1.75	0.68
1:C:62:LEU:O	1:C:65:VAL:HB	1.94	0.67
1:D:186:VAL:HG12	1:D:188:PRO:CD	2.25	0.67
1:X:198:LEU:HB2	1:X:243:TYR:CE2	2.30	0.67
1:B:309:ALA:O	1:B:323:THR:HG23	1.95	0.67
1:B:12:LYS:HD2	1:B:222:TYR:CE1	2.29	0.67
1:W:232:MET:CE	1:W:274:MET:HE1	2.24	0.67
1:X:45:ARG:C	1:X:47:LYS:H	2.00	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:86:LYS:HD3	1:Y:90:GLY:O	1.94	0.67
1:Z:212:VAL:O	1:Z:216:LEU:HD12	1.94	0.67
1:B:63:PHE:HD1	1:B:97:LEU:HD21	1.60	0.67
1:B:178:GLN:HE21	1:B:184:PRO:HG3	1.60	0.67
1:W:228:LEU:CG	1:W:230:PRO:HD3	2.15	0.67
1:X:316:LYS:HB2	1:X:319:ASN:ND2	2.10	0.67
1:C:226:THR:HG23	1:C:227:LEU:H	1.60	0.67
1:W:94:ARG:HD2	1:W:140:ASP:O	1.94	0.67
1:C:149:PRO:CD	1:C:170:LEU:HD21	2.25	0.67
1:Z:40:GLY:HA3	1:Z:50:ASN:ND2	2.09	0.67
1:X:106:ILE:CG2	1:X:142:VAL:HG11	2.25	0.67
1:B:60:GLU:OE1	1:B:88:SER:N	2.25	0.67
1:B:316:LYS:C	1:B:318:ALA:H	2.02	0.67
1:D:28:GLY:HA3	1:D:299:PHE:CZ	2.30	0.67
1:Y:198:LEU:HD22	1:Y:243:TYR:CE2	2.30	0.67
1:C:330:ARG:HG3	1:C:330:ARG:HH11	1.60	0.66
1:X:118:THR:HG21	1:X:121:GLU:HB2	1.75	0.66
1:B:51:THR:HG22	1:B:52:GLU:N	2.11	0.66
1:B:58:PHE:O	1:B:61:ILE:HB	1.95	0.66
1:D:106:ILE:HG23	1:D:106:ILE:O	1.93	0.66
1:C:147:TRP:CD1	1:C:170:LEU:HD23	2.25	0.66
1:W:143:ASP:O	1:W:182:LEU:HA	1.94	0.66
1:W:27:LYS:HD3	1:W:70:ASN:O	1.96	0.66
1:W:106:ILE:HG23	1:W:106:ILE:O	1.95	0.66
1:W:180:ASN:O	1:W:182:LEU:HD12	1.95	0.66
1:X:276:GLU:HB3	1:X:330:ARG:HH11	1.61	0.66
1:Y:22:ILE:HG21	1:Y:29:ILE:HD11	1.78	0.66
1:A:309:ALA:O	1:A:323:THR:HG23	1.96	0.66
1:D:58:PHE:HB2	1:D:313:TRP:CZ3	2.31	0.66
1:Y:59:ARG:HB3	1:Y:63:PHE:CE2	2.31	0.66
1:Z:234:THR:HG22	1:Z:248:VAL:HG13	1.78	0.66
1:A:40:GLY:HA3	1:A:50:ASN:ND2	2.11	0.66
1:B:22:ILE:HG21	1:B:29:ILE:HD11	1.77	0.66
1:B:86:LYS:HD3	1:B:90:GLY:O	1.96	0.66
1:A:59:ARG:NH1	1:A:82:THR:OG1	2.29	0.65
1:A:60:GLU:HA	1:A:93:PHE:HE1	1.62	0.65
1:A:202:GLN:HG2	1:A:206:GLU:OE2	1.96	0.65
1:A:277:GLU:O	1:A:281:LEU:HG	1.96	0.65
1:C:316:LYS:HB2	1:C:319:ASN:ND2	2.11	0.65
1:D:339:LYS:HB3	1:D:341:GLN:HE21	1.61	0.65
1:W:80:HIS:HD2	1:W:137:TYR:OH	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:228:LEU:HG	1:X:230:PRO:CD	2.16	0.65
1:Z:40:GLY:HA3	1:Z:50:ASN:HD22	1.61	0.65
1:Z:60:GLU:HA	1:Z:93:PHE:HE1	1.61	0.65
1:D:94:ARG:HD2	1:D:140:ASP:O	1.95	0.65
1:D:144:PHE:C	1:D:182:LEU:HD23	2.21	0.65
1:W:212:VAL:O	1:W:216:LEU:HD12	1.97	0.65
1:Y:66:ASP:O	1:Y:68:SER:N	2.29	0.65
1:C:127:LEU:H	1:C:127:LEU:HD12	1.61	0.65
1:D:108:LEU:HD11	1:D:134:CYS:SG	2.37	0.65
1:X:226:THR:HG23	1:X:227:LEU:H	1.61	0.65
1:Y:58:PHE:O	1:Y:61:ILE:HB	1.95	0.65
1:A:38:THR:HA	1:A:41:ASN:ND2	2.11	0.65
1:W:309:ALA:O	1:W:323:THR:HG23	1.96	0.65
1:Y:106:ILE:HG22	1:Y:142:VAL:HG11	1.78	0.65
1:Y:232:MET:HE3	1:Y:274:MET:HE1	1.79	0.65
1:Z:38:THR:HA	1:Z:41:ASN:ND2	2.10	0.65
1:A:22:ILE:HG21	1:A:29:ILE:HD11	1.78	0.65
1:C:12:LYS:HD2	1:C:222:TYR:CE1	2.31	0.65
1:C:121:GLU:O	1:C:122:THR:HG23	1.97	0.65
1:Y:134:CYS:O	1:Y:136:GLN:N	2.30	0.65
1:Z:330:ARG:HH11	1:Z:330:ARG:HG3	1.62	0.65
1:A:309:ALA:HA	1:A:326:ALA:HB3	1.79	0.65
1:C:164:GLN:O	1:C:168:ASN:ND2	2.26	0.65
1:W:134:CYS:O	1:W:136:GLN:N	2.30	0.65
1:X:125:GLN:NE2	1:X:125:GLN:H	1.95	0.65
1:Y:148:ARG:HD2	1:Y:187:GLU:OE2	1.96	0.65
1:B:134:CYS:O	1:B:136:GLN:N	2.30	0.65
1:B:232:MET:O	1:B:234:THR:HG23	1.97	0.65
1:C:22:ILE:HG21	1:C:29:ILE:HD11	1.79	0.65
1:X:267:ILE:HD12	1:X:295:TRP:CE3	2.32	0.65
1:Z:22:ILE:HG21	1:Z:29:ILE:HD11	1.78	0.65
1:B:15:LEU:HD22	1:B:182:LEU:O	1.96	0.65
1:B:66:ASP:O	1:B:68:SER:N	2.30	0.65
1:D:309:ALA:O	1:D:323:THR:HG23	1.96	0.65
1:Y:178:GLN:HE21	1:Y:184:PRO:HG3	1.61	0.65
1:Z:78:LEU:HD12	1:Z:83:LEU:HD12	1.78	0.65
1:Z:277:GLU:O	1:Z:281:LEU:HG	1.96	0.65
1:A:78:LEU:HD12	1:A:83:LEU:HD12	1.77	0.64
1:C:276:GLU:HB3	1:C:330:ARG:HH11	1.61	0.64
1:X:249:ALA:HB1	1:X:286:ILE:HA	1.78	0.64
1:A:316:LYS:C	1:A:318:ALA:H	2.04	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:243:TYR:HA	1:B:247:GLN:OE1	1.97	0.64
1:X:125:GLN:H	1:X:125:GLN:CD	2.05	0.64
1:Y:277:GLU:O	1:Y:281:LEU:HG	1.97	0.64
1:Z:228:LEU:HG	1:Z:230:PRO:CD	2.17	0.64
1:C:28:GLY:HA3	1:C:299:PHE:CZ	2.32	0.64
1:C:146:LYS:HA	1:C:185:ILE:HG23	1.79	0.64
1:W:77:ILE:HD11	1:W:185:ILE:HD12	1.79	0.64
1:Z:276:GLU:HB3	1:Z:330:ARG:HH11	1.61	0.64
1:Z:316:LYS:C	1:Z:318:ALA:H	2.05	0.64
1:A:276:GLU:HB3	1:A:330:ARG:HH11	1.62	0.64
1:B:83:LEU:HG	1:B:83:LEU:O	1.98	0.64
1:B:229:LYS:HE3	1:B:300:SER:HB3	1.79	0.64
1:C:198:LEU:HB2	1:C:243:TYR:CZ	2.32	0.64
1:Y:316:LYS:C	1:Y:318:ALA:H	2.03	0.64
1:A:144:PHE:HB2	1:A:183:VAL:O	1.98	0.64
1:X:330:ARG:HH11	1:X:330:ARG:HG3	1.61	0.64
1:A:69:ILE:HD13	1:A:328:MET:SD	2.38	0.64
1:C:65:VAL:HG23	1:C:324:GLN:HG2	1.80	0.64
1:W:246:GLU:N	1:W:246:GLU:CD	2.56	0.64
1:W:267:ILE:HD12	1:W:295:TRP:CE3	2.33	0.64
1:A:212:VAL:O	1:A:216:LEU:HD12	1.98	0.64
1:B:89:GLN:HA	1:B:89:GLN:HE21	1.63	0.64
1:D:234:THR:CG2	1:D:248:VAL:HG13	2.28	0.64
1:D:277:GLU:O	1:D:281:LEU:HG	1.97	0.64
1:W:144:PHE:HB2	1:W:183:VAL:O	1.96	0.64
1:Z:34:GLU:HB2	1:Z:39:MET:SD	2.38	0.64
1:B:342:TYR:HE2	1:B:344:HIS:HB2	1.61	0.64
1:D:126:GLY:O	1:D:128:ASP:N	2.31	0.64
1:D:144:PHE:HB2	1:D:183:VAL:O	1.97	0.64
1:D:212:VAL:O	1:D:216:LEU:HD12	1.98	0.64
1:Z:35:SER:HB3	1:Z:38:THR:OG1	1.97	0.64
1:Z:59:ARG:NH1	1:Z:82:THR:OG1	2.31	0.64
1:W:276:GLU:HB3	1:W:330:ARG:HH11	1.62	0.63
1:W:277:GLU:O	1:W:281:LEU:HG	1.98	0.63
1:X:56:ARG:HB2	1:X:85:GLN:HE22	1.63	0.63
1:A:134:CYS:O	1:A:136:GLN:N	2.32	0.63
1:D:131:SER:O	1:D:180:ASN:ND2	2.31	0.63
1:D:309:ALA:HA	1:D:326:ALA:HB3	1.80	0.63
1:A:249:ALA:HB1	1:A:286:ILE:HA	1.80	0.63
1:B:183:VAL:HG13	1:B:225:GLY:O	1.99	0.63
1:B:309:ALA:HA	1:B:326:ALA:HB3	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:232:MET:HE2	1:D:286:ILE:HD12	1.79	0.63
1:B:59:ARG:HB3	1:B:63:PHE:CE2	2.33	0.63
1:B:249:ALA:HB1	1:B:286:ILE:HA	1.80	0.63
1:C:309:ALA:HA	1:C:326:ALA:HB3	1.81	0.63
1:D:180:ASN:O	1:D:182:LEU:HD12	1.98	0.63
1:W:330:ARG:HH11	1:W:330:ARG:HG3	1.63	0.63
1:X:316:LYS:C	1:X:318:ALA:H	2.06	0.63
1:B:277:GLU:O	1:B:281:LEU:HG	1.98	0.63
1:B:330:ARG:HG3	1:B:330:ARG:NH1	2.12	0.63
1:D:106:ILE:HB	1:D:142:VAL:HG11	1.78	0.63
1:D:147:TRP:CD1	1:D:148:ARG:N	2.66	0.63
1:A:40:GLY:HA3	1:A:50:ASN:HD22	1.63	0.63
1:A:125:GLN:N	1:A:147:TRP:CZ2	2.67	0.63
1:D:27:LYS:HD3	1:D:70:ASN:O	1.99	0.63
1:D:202:GLN:HG2	1:D:206:GLU:OE2	1.99	0.63
1:X:138:LYS:HB2	1:X:182:LEU:CD1	2.29	0.63
1:A:17:GLU:O	1:A:21:SER:HB3	1.99	0.63
1:B:76:VAL:HG23	1:B:102:ILE:HG21	1.81	0.63
1:W:56:ARG:HB2	1:W:85:GLN:NE2	2.14	0.63
1:X:66:ASP:OD2	1:X:66:ASP:N	2.30	0.63
1:X:132:GLU:HA	1:X:132:GLU:OE2	1.98	0.63
1:Y:66:ASP:C	1:Y:68:SER:H	2.06	0.63
1:Y:309:ALA:HA	1:Y:326:ALA:HB3	1.81	0.63
1:D:134:CYS:O	1:D:136:GLN:N	2.32	0.63
1:W:316:LYS:C	1:W:318:ALA:H	2.06	0.63
1:X:149:PRO:CD	1:X:170:LEU:HD21	2.29	0.63
1:Y:106:ILE:CG2	1:Y:142:VAL:HG11	2.28	0.63
1:B:63:PHE:CD1	1:B:97:LEU:HD21	2.34	0.63
1:W:66:ASP:O	1:W:68:SER:N	2.32	0.63
1:C:106:ILE:HG23	1:C:106:ILE:O	1.99	0.62
1:W:22:ILE:HG21	1:W:29:ILE:HD11	1.81	0.62
1:X:309:ALA:HA	1:X:326:ALA:HB3	1.81	0.62
1:Y:15:LEU:CD2	1:Y:182:LEU:O	2.47	0.62
1:Y:63:PHE:CD1	1:Y:97:LEU:HD21	2.32	0.62
1:Y:67:SER:HA	1:Y:100:LYS:HD3	1.81	0.62
1:Y:76:VAL:HG23	1:Y:102:ILE:HG21	1.81	0.62
1:A:330:ARG:HH11	1:A:330:ARG:HG3	1.63	0.62
1:C:40:GLY:HA3	1:C:50:ASN:HD22	1.64	0.62
1:C:106:ILE:HG22	1:C:142:VAL:HG11	1.80	0.62
1:Y:183:VAL:HG13	1:Y:225:GLY:O	1.98	0.62
1:C:249:ALA:HB1	1:C:286:ILE:HA	1.79	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:66:ASP:O	1:D:68:SER:N	2.32	0.62
1:D:330:ARG:HH11	1:D:330:ARG:HG3	1.63	0.62
1:Z:30:LEU:HB3	1:Z:76:VAL:HG13	1.80	0.62
1:Z:56:ARG:HB2	1:Z:85:GLN:HE22	1.64	0.62
1:C:56:ARG:HB2	1:C:85:GLN:HE22	1.63	0.62
1:X:277:GLU:O	1:X:281:LEU:HG	2.00	0.62
1:Z:309:ALA:HA	1:Z:326:ALA:HB3	1.81	0.62
1:B:66:ASP:C	1:B:68:SER:H	2.07	0.62
1:C:66:ASP:OD2	1:C:66:ASP:N	2.30	0.62
1:Y:234:THR:HG22	1:Y:248:VAL:CG1	2.29	0.62
1:Z:18:ILE:HB	1:Z:183:VAL:HG21	1.81	0.62
1:Z:134:CYS:O	1:Z:136:GLN:N	2.33	0.62
1:C:136:GLN:HE21	1:C:136:GLN:HA	1.63	0.62
1:D:56:ARG:HB2	1:D:85:GLN:NE2	2.14	0.62
1:W:77:ILE:HA	1:W:105:GLY:HA3	1.82	0.62
1:Y:56:ARG:HG2	1:Y:56:ARG:HH11	1.63	0.62
1:Y:60:GLU:OE1	1:Y:88:SER:N	2.25	0.62
1:A:56:ARG:HB2	1:A:85:GLN:HE22	1.63	0.62
1:C:108:LEU:HD13	1:C:130:LEU:HD11	1.80	0.62
1:C:267:ILE:HD12	1:C:295:TRP:CE3	2.34	0.62
1:D:65:VAL:O	1:D:100:LYS:HE2	2.00	0.62
1:D:105:GLY:CA	1:D:144:PHE:CE1	2.83	0.62
1:A:18:ILE:HB	1:A:183:VAL:HG21	1.81	0.62
1:B:67:SER:HA	1:B:100:LYS:HD3	1.82	0.62
1:D:80:HIS:HD2	1:D:137:TYR:OH	1.82	0.62
1:D:136:GLN:HA	1:D:136:GLN:HE21	1.65	0.62
1:W:144:PHE:C	1:W:182:LEU:HD23	2.25	0.62
1:X:12:LYS:HD2	1:X:222:TYR:CE1	2.35	0.62
1:X:40:GLY:HA3	1:X:50:ASN:HD22	1.64	0.62
1:C:58:PHE:HB2	1:C:313:TRP:CZ3	2.35	0.62
1:D:276:GLU:HB3	1:D:330:ARG:HH11	1.63	0.62
1:W:136:GLN:HA	1:W:136:GLN:HE21	1.63	0.62
1:X:18:ILE:HD13	1:X:143:ASP:HB3	1.80	0.62
1:X:196:HIS:CD2	1:X:201:CYS:HB2	2.34	0.62
1:A:51:THR:HB	1:A:54:ASN:ND2	2.15	0.62
1:W:198:LEU:HD22	1:W:243:TYR:CD2	2.35	0.62
1:W:309:ALA:HA	1:W:326:ALA:HB3	1.80	0.62
1:D:46:ILE:HG13	1:D:48:VAL:HG23	1.81	0.61
1:W:65:VAL:O	1:W:100:LYS:HE2	2.00	0.61
1:X:127:LEU:H	1:X:127:LEU:HD12	1.64	0.61
1:X:62:LEU:O	1:X:65:VAL:HB	1.98	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:143:ASP:O	1:Y:182:LEU:HA	2.00	0.61
1:A:151:LEU:O	1:A:190:VAL:HA	2.01	0.61
1:W:32:ALA:HB3	1:W:78:LEU:HD23	1.82	0.61
1:X:136:GLN:HA	1:X:136:GLN:HE21	1.65	0.61
1:X:212:VAL:O	1:X:216:LEU:HD12	2.00	0.61
1:Y:149:PRO:CG	1:Y:170:LEU:HD11	2.13	0.61
1:B:342:TYR:CE2	1:B:344:HIS:HB2	2.35	0.61
1:C:212:VAL:O	1:C:216:LEU:HD12	2.00	0.61
1:C:228:LEU:HG	1:C:230:PRO:CD	2.18	0.61
1:C:277:GLU:O	1:C:281:LEU:HG	2.00	0.61
1:Y:249:ALA:HB1	1:Y:286:ILE:HA	1.81	0.61
1:A:82:THR:HA	1:A:85:GLN:HG3	1.83	0.61
1:B:48:VAL:HG12	1:B:49:GLU:N	2.16	0.61
1:D:316:LYS:C	1:D:318:ALA:H	2.06	0.61
1:Y:59:ARG:HB3	1:Y:63:PHE:HE2	1.65	0.61
1:Y:178:GLN:OE1	1:Y:222:TYR:HB3	2.01	0.61
1:Z:106:ILE:HG12	1:Z:137:TYR:CE1	2.36	0.61
1:D:185:ILE:O	1:D:185:ILE:HG22	1.99	0.61
1:D:339:LYS:HB3	1:D:341:GLN:NE2	2.16	0.61
1:Z:267:ILE:HD12	1:Z:295:TRP:CE3	2.36	0.61
1:A:51:THR:HB	1:A:54:ASN:HD22	1.65	0.61
1:D:173:TYR:CE1	1:D:177:CYS:SG	2.92	0.61
1:D:267:ILE:HD12	1:D:295:TRP:CE3	2.36	0.61
1:Y:89:GLN:HA	1:Y:89:GLN:HE21	1.66	0.61
1:Y:276:GLU:HB3	1:Y:330:ARG:HH11	1.65	0.61
1:A:59:ARG:HD3	1:A:82:THR:CG2	2.30	0.61
1:C:146:LYS:CG	1:C:147:TRP:N	2.63	0.61
1:Y:301:TYR:HE1	1:Y:334:ASN:ND2	1.99	0.61
1:Z:249:ALA:HB1	1:Z:286:ILE:HA	1.83	0.61
1:A:143:ASP:O	1:A:182:LEU:HA	2.00	0.60
1:B:32:ALA:HB1	1:B:63:PHE:HZ	1.66	0.60
1:Y:83:LEU:O	1:Y:83:LEU:HG	2.00	0.60
1:W:221:VAL:HG12	1:W:222:TYR:N	2.16	0.60
1:A:58:PHE:CE2	1:A:310:LEU:HD13	2.36	0.60
1:B:28:GLY:HA3	1:B:299:PHE:CZ	2.36	0.60
1:B:128:ASP:HB2	1:C:128:ASP:OD1	2.00	0.60
1:B:138:LYS:NZ	1:B:143:ASP:OD1	2.33	0.60
1:C:229:LYS:HE3	1:C:300:SER:HB3	1.83	0.60
1:D:232:MET:HE2	1:D:286:ILE:CD1	2.32	0.60
1:Y:171:ALA:O	1:Y:174:ALA:HB3	2.00	0.60
1:X:124:ILE:HB	1:X:147:TRP:HE1	1.65	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:136:GLN:HE21	1:Y:136:GLN:HA	1.65	0.60
1:B:301:TYR:HE1	1:B:334:ASN:ND2	1.99	0.60
1:B:316:LYS:C	1:B:318:ALA:N	2.58	0.60
1:W:126:GLY:N	1:W:147:TRP:HH2	1.98	0.60
1:W:232:MET:HE1	1:W:274:MET:HE1	1.83	0.60
1:Z:28:GLY:HA3	1:Z:299:PHE:CZ	2.36	0.60
1:B:146:LYS:HE3	1:B:187:GLU:OE1	2.01	0.60
1:B:147:TRP:HB3	1:B:173:TYR:CE2	2.37	0.60
1:B:185:ILE:O	1:B:185:ILE:CG2	2.48	0.60
1:C:198:LEU:HD22	1:C:243:TYR:CD2	2.36	0.60
1:W:147:TRP:HB3	1:W:173:TYR:CZ	2.37	0.60
1:Y:51:THR:HB	1:Y:54:ASN:HD22	1.67	0.60
1:Y:316:LYS:C	1:Y:318:ALA:N	2.59	0.60
1:A:59:ARG:HB3	1:A:63:PHE:HE2	1.67	0.60
1:D:244:THR:O	1:D:248:VAL:HG23	2.01	0.60
1:W:46:ILE:HG13	1:W:48:VAL:HG23	1.83	0.60
1:Y:48:VAL:HG12	1:Y:49:GLU:N	2.15	0.60
1:Z:147:TRP:HB3	1:Z:173:TYR:CD2	2.36	0.60
1:A:65:VAL:HG23	1:A:324:GLN:HB3	1.84	0.60
1:B:59:ARG:HB3	1:B:63:PHE:HE2	1.67	0.60
1:B:136:GLN:HA	1:B:136:GLN:HE21	1.65	0.60
1:B:171:ALA:O	1:B:174:ALA:HB3	2.02	0.60
1:D:72:SER:O	1:D:73:ILE:HD13	2.01	0.60
1:Z:59:ARG:HD3	1:Z:82:THR:CG2	2.32	0.60
1:A:59:ARG:HD3	1:A:82:THR:HG23	1.84	0.60
1:D:77:ILE:HA	1:D:105:GLY:HA3	1.83	0.60
1:W:146:LYS:HG2	1:W:147:TRP:H	1.64	0.60
1:X:186:VAL:O	1:X:188:PRO:HD2	2.02	0.60
1:C:202:GLN:O	1:C:206:GLU:HG3	2.01	0.60
1:D:66:ASP:C	1:D:68:SER:H	2.09	0.60
1:W:234:THR:CG2	1:W:248:VAL:HG13	2.32	0.60
1:Y:221:VAL:HG12	1:Y:222:TYR:N	2.16	0.60
1:A:267:ILE:HD12	1:A:295:TRP:CE3	2.37	0.59
1:B:221:VAL:HG12	1:B:222:TYR:N	2.17	0.59
1:D:228:LEU:CG	1:D:230:PRO:HD3	2.18	0.59
1:X:106:ILE:O	1:X:106:ILE:HG23	2.01	0.59
1:Z:59:ARG:HB3	1:Z:63:PHE:HE2	1.67	0.59
1:B:301:TYR:CE1	1:B:334:ASN:ND2	2.70	0.59
1:W:244:THR:O	1:W:248:VAL:HG23	2.02	0.59
1:X:221:VAL:HG12	1:X:222:TYR:N	2.18	0.59
1:Y:330:ARG:HG3	1:Y:330:ARG:NH1	2.15	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:51:THR:CB	1:B:54:ASN:HD22	2.16	0.59
1:D:127:LEU:HG	1:D:147:TRP:CH2	2.37	0.59
1:W:30:LEU:HB3	1:W:76:VAL:HG22	1.84	0.59
1:Y:51:THR:CB	1:Y:54:ASN:HD22	2.16	0.59
1:Z:198:LEU:CD1	1:Z:234:THR:HA	2.33	0.59
1:A:65:VAL:O	1:A:100:LYS:NZ	2.30	0.59
1:C:221:VAL:HG12	1:C:222:TYR:N	2.17	0.59
1:X:145:GLY:O	1:X:185:ILE:CG2	2.43	0.59
1:Z:51:THR:HB	1:Z:54:ASN:ND2	2.16	0.59
1:A:83:LEU:HD11	1:A:142:VAL:HG22	1.84	0.59
1:C:223:LEU:O	1:C:226:THR:HB	2.03	0.59
1:D:221:VAL:HG12	1:D:222:TYR:N	2.16	0.59
1:Y:168:ASN:O	1:Y:172:ARG:HG3	2.02	0.59
1:A:56:ARG:HG3	1:A:85:GLN:HB3	1.85	0.59
1:B:56:ARG:HH11	1:B:56:ARG:HG2	1.67	0.59
1:D:22:ILE:HG21	1:D:29:ILE:HD11	1.85	0.59
1:X:223:LEU:O	1:X:226:THR:HB	2.01	0.59
1:Z:51:THR:HB	1:Z:54:ASN:HD22	1.67	0.59
1:Z:65:VAL:O	1:Z:100:LYS:NZ	2.29	0.59
1:A:12:LYS:HD2	1:A:222:TYR:CE1	2.37	0.59
1:B:86:LYS:HG2	1:B:92:LEU:HD23	1.84	0.59
1:C:65:VAL:HG23	1:C:324:GLN:CG	2.33	0.59
1:X:146:LYS:HA	1:X:185:ILE:HG23	1.85	0.59
1:X:202:GLN:HG3	1:X:206:GLU:OE2	2.02	0.59
1:A:18:ILE:HD13	1:A:143:ASP:HB3	1.85	0.59
1:A:173:TYR:CE1	1:A:177:CYS:SG	2.96	0.59
1:B:51:THR:HB	1:B:54:ASN:HD22	1.67	0.59
1:B:186:VAL:O	1:B:188:PRO:HD2	2.02	0.59
1:C:78:LEU:HD22	1:C:82:THR:HB	1.85	0.59
1:C:316:LYS:C	1:C:318:ALA:H	2.10	0.59
1:Y:63:PHE:CD1	1:Y:97:LEU:HD11	2.37	0.59
1:C:267:ILE:O	1:C:267:ILE:HG22	2.01	0.59
1:D:32:ALA:HB3	1:D:78:LEU:HD23	1.83	0.59
1:A:147:TRP:HB3	1:A:173:TYR:CE2	2.38	0.59
1:A:244:THR:HG22	1:A:247:GLN:HG3	1.83	0.59
1:B:168:ASN:O	1:B:172:ARG:HG3	2.03	0.58
1:C:58:PHE:CD2	1:C:310:LEU:HD13	2.37	0.58
1:C:196:HIS:HB2	1:C:200:HIS:HB3	1.85	0.58
1:Z:136:GLN:HA	1:Z:136:GLN:HE21	1.67	0.58
1:A:136:GLN:HE21	1:A:136:GLN:HA	1.66	0.58
1:B:80:HIS:HD2	1:B:137:TYR:OH	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:205:THR:HG21	1:B:233:VAL:HG22	1.85	0.58
1:C:106:ILE:HG12	1:C:137:TYR:CE1	2.38	0.58
1:C:330:ARG:HG3	1:C:330:ARG:NH1	2.17	0.58
1:Z:69:ILE:HD13	1:Z:328:MET:SD	2.43	0.58
1:A:92:LEU:HD12	1:A:95:ASN:ND2	2.19	0.58
1:X:202:GLN:NE2	1:X:255:ALA:HB2	2.19	0.58
1:X:229:LYS:HE3	1:X:300:SER:HB3	1.85	0.58
1:Z:82:THR:HA	1:Z:85:GLN:HG3	1.83	0.58
1:A:14:GLU:O	1:A:18:ILE:HG13	2.03	0.58
1:W:66:ASP:C	1:W:68:SER:H	2.10	0.58
1:X:78:LEU:HD22	1:X:82:THR:HB	1.85	0.58
1:X:243:TYR:HA	1:X:247:GLN:OE1	2.03	0.58
1:X:267:ILE:O	1:X:267:ILE:HG22	2.03	0.58
1:Y:301:TYR:CE1	1:Y:334:ASN:ND2	2.71	0.58
1:Z:58:PHE:CD2	1:Z:310:LEU:HD13	2.39	0.58
1:Z:221:VAL:HG12	1:Z:222:TYR:N	2.18	0.58
1:A:129:GLY:O	1:A:133:ARG:HB2	2.04	0.58
1:C:50:ASN:OD1	1:C:55:ARG:NH1	2.37	0.58
1:D:187:GLU:OE2	1:D:229:LYS:HD3	2.03	0.58
1:W:58:PHE:O	1:W:61:ILE:HB	2.04	0.58
1:W:198:LEU:HB2	1:W:243:TYR:CE2	2.38	0.58
1:Y:160:SER:O	1:Y:164:GLN:HG3	2.03	0.58
1:Z:56:ARG:HG3	1:Z:85:GLN:HB3	1.86	0.58
1:Z:267:ILE:HG22	1:Z:267:ILE:O	2.03	0.58
1:C:146:LYS:HG2	1:C:147:TRP:H	1.67	0.58
1:W:106:ILE:HB	1:W:142:VAL:HG11	1.84	0.58
1:Y:148:ARG:CZ	1:Y:150:VAL:HG22	2.34	0.58
1:Z:151:LEU:O	1:Z:190:VAL:HA	2.04	0.58
1:Z:330:ARG:HG3	1:Z:330:ARG:NH1	2.19	0.58
1:B:276:GLU:HB3	1:B:330:ARG:HH11	1.68	0.58
1:C:185:ILE:HD11	1:C:229:LYS:HD2	1.84	0.58
1:X:28:GLY:HA3	1:X:299:PHE:CZ	2.39	0.58
1:X:65:VAL:HG23	1:X:324:GLN:HG2	1.84	0.58
1:Z:59:ARG:HD3	1:Z:82:THR:HG23	1.85	0.58
1:A:8:THR:O	1:A:9:GLN:C	2.47	0.58
1:B:234:THR:HG22	1:B:248:VAL:CG1	2.34	0.58
1:C:198:LEU:CD1	1:C:234:THR:HA	2.34	0.58
1:X:336:GLN:O	1:X:340:GLY:N	2.36	0.58
1:Y:32:ALA:HB1	1:Y:63:PHE:HZ	1.68	0.58
1:Z:202:GLN:HG2	1:Z:206:GLU:OE2	2.04	0.58
1:A:166:ASN:O	1:A:169:ALA:HB3	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:144:PHE:HA	1:B:183:VAL:H	1.69	0.58
1:C:68:SER:HG	1:C:328:MET:HE1	1.66	0.58
1:C:100:LYS:HG2	1:C:100:LYS:O	2.04	0.58
1:X:330:ARG:HG3	1:X:330:ARG:NH1	2.17	0.58
1:B:244:THR:C	1:B:246:GLU:N	2.59	0.57
1:D:126:GLY:C	1:D:128:ASP:H	2.12	0.57
1:X:32:ALA:O	1:X:78:LEU:HA	2.04	0.57
1:X:50:ASN:OD1	1:X:55:ARG:NH1	2.37	0.57
1:Y:41:ASN:O	1:Y:44:GLN:HB3	2.04	0.57
1:B:67:SER:O	1:B:67:SER:OG	2.20	0.57
1:C:149:PRO:CD	1:C:170:LEU:HD11	2.34	0.57
1:B:228:LEU:HG	1:B:230:PRO:CD	2.17	0.57
1:A:301:TYR:HE1	1:A:334:ASN:ND2	2.02	0.57
1:B:316:LYS:O	1:B:318:ALA:N	2.37	0.57
1:A:301:TYR:CE1	1:A:334:ASN:ND2	2.72	0.57
1:D:30:LEU:HB3	1:D:76:VAL:HG22	1.85	0.57
1:W:267:ILE:HG22	1:W:267:ILE:O	2.04	0.57
1:X:180:ASN:O	1:X:182:LEU:N	2.38	0.57
1:X:276:GLU:HB3	1:X:330:ARG:NH1	2.19	0.57
1:Y:67:SER:O	1:Y:67:SER:OG	2.21	0.57
1:Y:228:LEU:HG	1:Y:230:PRO:CD	2.16	0.57
1:Z:166:ASN:O	1:Z:169:ALA:HB3	2.05	0.57
1:D:164:GLN:NE2	1:D:165:GLU:HG2	2.19	0.57
1:W:249:ALA:HB1	1:W:286:ILE:HA	1.85	0.57
1:W:330:ARG:HG3	1:W:330:ARG:NH1	2.20	0.57
1:A:28:GLY:HA3	1:A:299:PHE:CZ	2.40	0.57
1:A:34:GLU:HB2	1:A:39:MET:SD	2.45	0.57
1:A:59:ARG:HB3	1:A:63:PHE:CE2	2.40	0.57
1:X:281:LEU:HD21	1:X:344:HIS:HD2	1.70	0.57
1:Z:87:ASP:OD1	1:Z:91:LYS:N	2.37	0.57
1:A:267:ILE:HG22	1:A:267:ILE:O	2.05	0.57
1:X:89:GLN:HA	1:X:89:GLN:HE21	1.70	0.57
1:X:100:LYS:O	1:X:100:LYS:HG2	2.05	0.57
1:Y:106:ILE:HG12	1:Y:137:TYR:CD1	2.40	0.57
1:Z:99:GLU:OE1	1:Z:99:GLU:HA	2.04	0.57
1:W:289:CYS:SG	1:W:291:LEU:HD23	2.44	0.57
1:Y:86:LYS:HG2	1:Y:92:LEU:HD23	1.85	0.57
1:C:124:ILE:HD13	1:C:124:ILE:N	2.20	0.57
1:D:58:PHE:O	1:D:61:ILE:HB	2.04	0.57
1:D:267:ILE:HG22	1:D:267:ILE:O	2.05	0.57
1:W:28:GLY:HA3	1:W:299:PHE:CE1	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:14:GLU:O	1:Z:18:ILE:HG13	2.05	0.57
1:B:18:ILE:HD13	1:B:143:ASP:HB3	1.85	0.56
1:B:87:ASP:C	1:B:89:GLN:H	2.13	0.56
1:W:202:GLN:HG2	1:W:206:GLU:OE2	2.04	0.56
1:W:316:LYS:C	1:W:318:ALA:N	2.63	0.56
1:B:15:LEU:CD2	1:B:182:LEU:O	2.53	0.56
1:B:63:PHE:CD1	1:B:97:LEU:HD11	2.40	0.56
1:C:32:ALA:O	1:C:78:LEU:HA	2.05	0.56
1:C:200:HIS:O	1:C:204:VAL:HG23	2.06	0.56
1:C:276:GLU:HB3	1:C:330:ARG:NH1	2.19	0.56
1:A:221:VAL:HG12	1:A:222:TYR:N	2.19	0.56
1:W:223:LEU:O	1:W:226:THR:HB	2.05	0.56
1:X:138:LYS:NZ	1:X:143:ASP:OD1	2.37	0.56
1:Z:36:VAL:O	1:Z:50:ASN:ND2	2.29	0.56
1:Z:138:LYS:NZ	1:Z:143:ASP:OD1	2.29	0.56
1:Z:276:GLU:HB3	1:Z:330:ARG:NH1	2.20	0.56
1:B:86:LYS:HG2	1:B:92:LEU:CD2	2.35	0.56
1:C:76:VAL:HG23	1:C:102:ILE:HG21	1.87	0.56
1:Y:87:ASP:C	1:Y:89:GLN:H	2.14	0.56
1:Z:59:ARG:HB3	1:Z:63:PHE:CE2	2.41	0.56
1:Z:301:TYR:HE1	1:Z:334:ASN:ND2	2.04	0.56
1:A:228:LEU:HG	1:A:230:PRO:CD	2.16	0.56
1:W:58:PHE:CE2	1:W:310:LEU:HD13	2.40	0.56
1:Y:99:GLU:C	1:Y:101:GLY:H	2.13	0.56
1:Z:147:TRP:CD1	1:Z:147:TRP:C	2.84	0.56
1:A:138:LYS:HA	1:A:142:VAL:O	2.04	0.56
1:B:76:VAL:HG23	1:B:102:ILE:CG2	2.35	0.56
1:C:134:CYS:C	1:C:136:GLN:N	2.64	0.56
1:D:330:ARG:HG3	1:D:330:ARG:NH1	2.20	0.56
1:Y:223:LEU:O	1:Y:226:THR:HB	2.05	0.56
1:Z:144:PHE:HB2	1:Z:183:VAL:O	2.05	0.56
1:A:87:ASP:OD1	1:A:91:LYS:N	2.37	0.56
1:C:30:LEU:HB3	1:C:76:VAL:HG22	1.88	0.56
1:C:148:ARG:HD2	1:C:187:GLU:OE2	2.06	0.56
1:W:164:GLN:NE2	1:W:165:GLU:HG2	2.20	0.56
1:Z:301:TYR:CE1	1:Z:334:ASN:ND2	2.74	0.56
1:W:72:SER:O	1:W:73:ILE:HD13	2.06	0.56
1:W:83:LEU:HD23	1:W:84:TYR:CE2	2.41	0.56
1:X:124:ILE:CD1	1:X:149:PRO:HA	2.33	0.56
1:X:244:THR:O	1:X:247:GLN:N	2.35	0.56
1:B:99:GLU:C	1:B:101:GLY:H	2.13	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:148:ARG:HB2	1:X:187:GLU:HB3	1.87	0.56
1:C:301:TYR:HE1	1:C:334:ASN:ND2	2.04	0.56
1:D:138:LYS:HA	1:D:142:VAL:O	2.06	0.56
1:W:301:TYR:HE1	1:W:334:ASN:ND2	2.04	0.56
1:B:186:VAL:HG12	1:B:188:PRO:CD	2.34	0.55
1:D:213:TYR:OH	1:D:228:LEU:HB2	2.06	0.55
1:A:66:ASP:C	1:A:68:SER:H	2.14	0.55
1:A:276:GLU:HB3	1:A:330:ARG:NH1	2.21	0.55
1:B:41:ASN:O	1:B:44:GLN:HB3	2.05	0.55
1:W:276:GLU:HB3	1:W:330:ARG:NH1	2.21	0.55
1:X:134:CYS:C	1:X:136:GLN:N	2.63	0.55
1:Y:86:LYS:HG2	1:Y:92:LEU:CD2	2.36	0.55
1:Y:187:GLU:O	1:Y:188:PRO:O	2.25	0.55
1:B:108:LEU:HD11	1:B:134:CYS:SG	2.46	0.55
1:B:178:GLN:OE1	1:B:222:TYR:HB3	2.06	0.55
1:D:223:LEU:O	1:D:226:THR:HB	2.06	0.55
1:W:51:THR:HG22	1:W:54:ASN:ND2	2.21	0.55
1:X:179:GLN:NE2	1:X:179:GLN:HA	2.20	0.55
1:Y:15:LEU:HD13	1:Y:178:GLN:HG2	1.88	0.55
1:Y:43:LEU:HD23	1:Y:46:ILE:HD11	1.88	0.55
1:A:69:ILE:C	1:A:71:GLN:H	2.14	0.55
1:A:316:LYS:C	1:A:318:ALA:N	2.61	0.55
1:B:82:THR:C	1:B:84:TYR:H	2.15	0.55
1:D:249:ALA:HB1	1:D:286:ILE:HA	1.87	0.55
1:X:58:PHE:HB2	1:X:313:TRP:CZ3	2.42	0.55
1:X:199:GLU:O	1:X:202:GLN:HB3	2.07	0.55
1:X:301:TYR:HE1	1:X:334:ASN:ND2	2.05	0.55
1:Z:66:ASP:C	1:Z:68:SER:H	2.14	0.55
1:Z:92:LEU:HD12	1:Z:95:ASN:ND2	2.20	0.55
1:A:305:LEU:HD23	1:A:330:ARG:HB3	1.87	0.55
1:A:330:ARG:HG3	1:A:330:ARG:NH1	2.20	0.55
1:B:53:GLU:O	1:B:54:ASN:C	2.48	0.55
1:B:200:HIS:C	1:B:202:GLN:N	2.64	0.55
1:D:301:TYR:HE1	1:D:334:ASN:ND2	2.05	0.55
1:Z:216:LEU:HD23	1:Z:221:VAL:CG2	2.30	0.55
1:W:301:TYR:CE1	1:W:334:ASN:ND2	2.74	0.55
1:Y:87:ASP:OD1	1:Y:91:LYS:HB3	2.07	0.55
1:Z:76:VAL:HG23	1:Z:102:ILE:HG21	1.89	0.55
1:Z:173:TYR:CE1	1:Z:177:CYS:SG	3.00	0.55
1:A:231:ASN:HD22	1:A:231:ASN:H	1.54	0.55
1:B:232:MET:HE3	1:B:274:MET:HE1	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:126:GLY:N	1:W:147:TRP:CH2	2.75	0.55
1:X:14:GLU:O	1:X:18:ILE:HG13	2.07	0.55
1:X:59:ARG:HD3	1:X:82:THR:HG21	1.88	0.55
1:X:146:LYS:HA	1:X:185:ILE:CG2	2.36	0.55
1:X:176:ILE:O	1:X:179:GLN:HB2	2.07	0.55
1:Y:76:VAL:HG23	1:Y:102:ILE:CG2	2.36	0.55
1:Z:99:GLU:O	1:Z:100:LYS:C	2.49	0.55
1:C:89:GLN:HA	1:C:89:GLN:HE21	1.71	0.55
1:C:179:GLN:NE2	1:C:179:GLN:HA	2.21	0.55
1:W:232:MET:SD	1:W:282:ASN:HB3	2.47	0.55
1:X:336:GLN:HA	1:X:339:LYS:HB2	1.89	0.55
1:Y:106:ILE:HG12	1:Y:137:TYR:CE1	2.42	0.55
1:C:138:LYS:HB2	1:C:182:LEU:HD12	1.88	0.55
1:C:180:ASN:O	1:C:182:LEU:N	2.39	0.55
1:C:216:LEU:HD23	1:C:221:VAL:CG2	2.27	0.55
1:D:28:GLY:HA3	1:D:299:PHE:CE1	2.42	0.55
1:W:213:TYR:OH	1:W:228:LEU:HB2	2.07	0.55
1:X:245:PRO:O	1:X:285:ALA:CB	2.54	0.55
1:Y:53:GLU:O	1:Y:54:ASN:C	2.48	0.55
1:Z:127:LEU:O	1:Z:130:LEU:HB2	2.05	0.55
1:Z:316:LYS:C	1:Z:318:ALA:N	2.62	0.55
1:B:43:LEU:HD23	1:B:46:ILE:HD11	1.89	0.54
1:C:80:HIS:HD2	1:C:137:TYR:OH	1.89	0.54
1:D:18:ILE:HD13	1:D:143:ASP:HB3	1.88	0.54
1:D:67:SER:O	1:D:70:ASN:OD1	2.25	0.54
1:D:276:GLU:HB3	1:D:330:ARG:NH1	2.22	0.54
1:X:191:ILE:CG2	1:X:193:ASP:CG	2.80	0.54
1:Z:40:GLY:CA	1:Z:50:ASN:ND2	2.70	0.54
1:Z:69:ILE:C	1:Z:71:GLN:H	2.14	0.54
1:D:18:ILE:HB	1:D:183:VAL:HG21	1.90	0.54
1:D:145:GLY:N	1:D:182:LEU:HD23	2.22	0.54
1:D:344:HIS:O	1:D:345:THR:CB	2.53	0.54
1:C:106:ILE:CG2	1:C:142:VAL:HG11	2.36	0.54
1:C:232:MET:HE3	1:C:274:MET:HE1	1.88	0.54
1:D:83:LEU:HD23	1:D:84:TYR:CE2	2.41	0.54
1:D:301:TYR:CE1	1:D:334:ASN:ND2	2.75	0.54
1:X:179:GLN:HA	1:X:179:GLN:HE21	1.72	0.54
1:B:289:CYS:SG	1:B:291:LEU:HD23	2.47	0.54
1:C:108:LEU:HD11	1:C:134:CYS:SG	2.48	0.54
1:C:176:ILE:O	1:C:179:GLN:HB2	2.07	0.54
1:W:65:VAL:HG22	1:W:66:ASP:N	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:254:THR:HA	1:X:257:HIS:ND1	2.22	0.54
1:Z:138:LYS:HA	1:Z:142:VAL:O	2.07	0.54
1:Z:335:CYS:O	1:Z:339:LYS:HD3	2.06	0.54
1:B:216:LEU:HD23	1:B:221:VAL:CG2	2.27	0.54
1:B:223:LEU:O	1:B:226:THR:HB	2.07	0.54
1:C:301:TYR:CE1	1:C:334:ASN:ND2	2.76	0.54
1:X:56:ARG:NH1	1:X:86:LYS:O	2.40	0.54
1:B:43:LEU:HA	1:B:46:ILE:HD11	1.89	0.54
1:B:143:ASP:O	1:B:182:LEU:HA	2.08	0.54
1:X:244:THR:O	1:X:246:GLU:N	2.41	0.54
1:Y:216:LEU:HD23	1:Y:221:VAL:CG2	2.25	0.54
1:C:56:ARG:HG3	1:C:85:GLN:HB3	1.89	0.54
1:X:65:VAL:HG23	1:X:324:GLN:CG	2.38	0.54
1:X:76:VAL:HG23	1:X:102:ILE:HG21	1.89	0.54
1:Z:17:GLU:O	1:Z:21:SER:HB3	2.07	0.54
1:Z:205:THR:HG22	1:Z:209:LEU:HD12	1.89	0.54
1:Z:223:LEU:O	1:Z:226:THR:HB	2.07	0.54
1:A:163:ILE:HG22	1:A:164:GLN:N	2.22	0.54
1:B:66:ASP:C	1:B:68:SER:N	2.66	0.54
1:B:222:TYR:CZ	1:B:224:GLU:HB2	2.42	0.54
1:C:254:THR:HA	1:C:257:HIS:ND1	2.23	0.54
1:Y:28:GLY:HA3	1:Y:299:PHE:CZ	2.43	0.54
1:Y:229:LYS:HE3	1:Y:300:SER:HB3	1.88	0.54
1:A:40:GLY:CA	1:A:50:ASN:ND2	2.71	0.54
1:A:76:VAL:HG23	1:A:102:ILE:HG21	1.89	0.54
1:B:46:ILE:HB	1:B:314:GLY:HA2	1.89	0.54
1:C:153:ILE:O	1:C:153:ILE:HG22	2.07	0.54
1:C:222:TYR:CZ	1:C:224:GLU:HB2	2.43	0.54
1:Y:144:PHE:HA	1:Y:183:VAL:H	1.72	0.54
1:A:205:THR:HG22	1:A:209:LEU:HD12	1.89	0.54
1:X:59:ARG:HD3	1:X:82:THR:CG2	2.38	0.54
1:Z:145:GLY:N	1:Z:182:LEU:HD23	2.23	0.54
1:B:75:GLY:HA2	1:B:103:VAL:O	2.08	0.53
1:C:232:MET:SD	1:C:282:ASN:HB3	2.48	0.53
1:D:109:ASP:C	1:D:109:ASP:OD1	2.50	0.53
1:D:187:GLU:O	1:D:188:PRO:C	2.50	0.53
1:W:138:LYS:HA	1:W:142:VAL:O	2.09	0.53
1:W:246:GLU:CD	1:W:246:GLU:H	2.15	0.53
1:Y:276:GLU:HB3	1:Y:330:ARG:NH1	2.23	0.53
1:A:106:ILE:HG22	1:A:142:VAL:HG11	1.90	0.53
1:A:229:LYS:HE3	1:A:300:SER:HB3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:43:LEU:O	1:B:46:ILE:HG13	2.08	0.53
1:C:14:GLU:O	1:C:18:ILE:HG13	2.08	0.53
1:C:28:GLY:HA3	1:C:299:PHE:CE1	2.43	0.53
1:W:145:GLY:N	1:W:182:LEU:HD23	2.23	0.53
1:Z:232:MET:SD	1:Z:274:MET:HE1	2.47	0.53
1:C:169:ALA:C	1:C:171:ALA:N	2.65	0.53
1:C:313:TRP:HB2	1:C:323:THR:OG1	2.09	0.53
1:D:46:ILE:HB	1:D:314:GLY:HA2	1.91	0.53
1:D:246:GLU:CD	1:D:246:GLU:N	2.64	0.53
1:D:294:PRO:HG2	1:D:295:TRP:NE1	2.23	0.53
1:W:198:LEU:HD22	1:W:243:TYR:HD2	1.71	0.53
1:X:118:THR:CG2	1:X:121:GLU:HB2	2.37	0.53
1:Y:38:THR:HA	1:Y:41:ASN:ND2	2.23	0.53
1:Y:316:LYS:O	1:Y:318:ALA:N	2.41	0.53
1:Z:305:LEU:HD23	1:Z:330:ARG:HB3	1.90	0.53
1:D:127:LEU:HG	1:D:147:TRP:HH2	1.72	0.53
1:W:17:GLU:O	1:W:21:SER:HB3	2.08	0.53
1:W:178:GLN:HE21	1:W:184:PRO:CG	2.21	0.53
1:X:301:TYR:CE1	1:X:334:ASN:ND2	2.77	0.53
1:Y:271:SER:O	1:Y:272:GLY:C	2.52	0.53
1:A:223:LEU:O	1:A:226:THR:HB	2.08	0.53
1:D:289:CYS:SG	1:D:291:LEU:HD23	2.48	0.53
1:X:58:PHE:CD2	1:X:310:LEU:HD13	2.42	0.53
1:Y:43:LEU:O	1:Y:46:ILE:HG13	2.08	0.53
1:A:134:CYS:C	1:A:136:GLN:N	2.67	0.53
1:A:222:TYR:CZ	1:A:224:GLU:HB2	2.43	0.53
1:C:121:GLU:CD	1:C:162:ALA:HB2	2.34	0.53
1:C:147:TRP:HB3	1:C:173:TYR:CE2	2.43	0.53
1:C:169:ALA:C	1:C:171:ALA:H	2.16	0.53
1:D:306:GLN:O	1:D:307:ALA:C	2.52	0.53
1:W:179:GLN:CA	1:W:179:GLN:HE21	2.21	0.53
1:B:305:LEU:HD23	1:B:330:ARG:HB3	1.89	0.53
1:D:179:GLN:CA	1:D:179:GLN:HE21	2.21	0.53
1:X:56:ARG:HG3	1:X:85:GLN:HB3	1.90	0.53
1:Y:94:ARG:HD2	1:Y:140:ASP:O	2.09	0.53
1:Y:134:CYS:C	1:Y:136:GLN:N	2.65	0.53
1:Z:58:PHE:CE1	1:Z:310:LEU:HA	2.44	0.53
1:A:22:ILE:O	1:A:74:GLY:HA3	2.09	0.53
1:B:218:ASP:C	1:B:220:HIS:H	2.17	0.53
1:C:147:TRP:HD1	1:C:170:LEU:CD2	2.16	0.53
1:W:186:VAL:CG1	1:W:188:PRO:HD3	2.31	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:169:ALA:C	1:X:171:ALA:N	2.67	0.53
1:Z:270:LEU:C	1:Z:270:LEU:HD12	2.34	0.53
1:B:38:THR:HA	1:B:41:ASN:ND2	2.24	0.53
1:D:51:THR:HG22	1:D:54:ASN:ND2	2.23	0.53
1:W:67:SER:O	1:W:70:ASN:OD1	2.26	0.53
1:W:134:CYS:C	1:W:136:GLN:N	2.66	0.53
1:Y:213:TYR:OH	1:Y:228:LEU:HB2	2.09	0.53
1:Z:12:LYS:HD2	1:Z:222:TYR:CE1	2.44	0.53
1:A:244:THR:HG22	1:A:247:GLN:CD	2.34	0.53
1:B:94:ARG:HD2	1:B:140:ASP:O	2.08	0.53
1:B:276:GLU:HB3	1:B:330:ARG:NH1	2.23	0.53
1:C:56:ARG:NH1	1:C:86:LYS:O	2.41	0.53
1:C:336:GLN:O	1:C:340:GLY:N	2.41	0.53
1:D:134:CYS:C	1:D:136:GLN:N	2.67	0.53
1:X:316:LYS:C	1:X:318:ALA:N	2.63	0.53
1:Y:82:THR:C	1:Y:84:TYR:H	2.16	0.53
1:Z:151:LEU:HB2	1:Z:189:GLU:O	2.09	0.53
1:B:82:THR:HA	1:B:85:GLN:HG3	1.91	0.52
1:C:59:ARG:HD3	1:C:82:THR:CG2	2.38	0.52
1:C:59:ARG:HD3	1:C:82:THR:HG21	1.90	0.52
1:X:153:ILE:HG12	1:X:154:ALA:N	2.18	0.52
1:X:205:THR:HG22	1:X:209:LEU:HD12	1.91	0.52
1:Y:222:TYR:CZ	1:Y:224:GLU:HB2	2.43	0.52
1:A:65:VAL:CG1	1:A:69:ILE:HB	2.38	0.52
1:A:78:LEU:HD13	1:A:83:LEU:HA	1.91	0.52
1:A:99:GLU:OE1	1:A:99:GLU:HA	2.06	0.52
1:C:268:CYS:O	1:C:269:PHE:O	2.28	0.52
1:W:7:LEU:HD12	1:W:222:TYR:HB2	1.91	0.52
1:Z:213:TYR:OH	1:Z:228:LEU:HB2	2.08	0.52
1:B:233:VAL:HB	1:B:252:THR:HA	1.92	0.52
1:D:41:ASN:O	1:D:44:GLN:HB3	2.10	0.52
1:Y:43:LEU:HA	1:Y:46:ILE:HD11	1.90	0.52
1:Z:222:TYR:CZ	1:Z:224:GLU:HB2	2.44	0.52
1:A:213:TYR:OH	1:A:228:LEU:HB2	2.09	0.52
1:B:254:THR:HA	1:B:257:HIS:ND1	2.24	0.52
1:C:129:GLY:HA2	1:C:132:GLU:OE2	2.10	0.52
1:W:305:LEU:HD23	1:W:330:ARG:HB3	1.92	0.52
1:W:306:GLN:O	1:W:307:ALA:C	2.52	0.52
1:X:196:HIS:HD2	1:X:201:CYS:HB2	1.74	0.52
1:Y:148:ARG:CZ	1:Y:150:VAL:CG2	2.86	0.52
1:Y:254:THR:HA	1:Y:257:HIS:ND1	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:87:ASP:O	1:A:89:GLN:N	2.43	0.52
1:A:106:ILE:HG12	1:A:137:TYR:CE1	2.45	0.52
1:C:316:LYS:C	1:C:318:ALA:N	2.65	0.52
1:D:56:ARG:HG2	1:D:56:ARG:HH11	1.75	0.52
1:D:316:LYS:C	1:D:318:ALA:N	2.63	0.52
1:W:173:TYR:HA	1:W:176:ILE:HD12	1.91	0.52
1:Y:75:GLY:HA2	1:Y:103:VAL:O	2.09	0.52
1:Y:258:ARG:NE	1:Z:224:GLU:OE2	2.41	0.52
1:Z:65:VAL:CG1	1:Z:69:ILE:HB	2.39	0.52
1:Z:87:ASP:O	1:Z:89:GLN:N	2.42	0.52
1:Z:134:CYS:C	1:Z:136:GLN:N	2.67	0.52
1:C:116:ALA:C	1:C:118:THR:H	2.15	0.52
1:C:213:TYR:OH	1:C:228:LEU:HB2	2.09	0.52
1:X:169:ALA:C	1:X:171:ALA:H	2.18	0.52
1:X:222:TYR:CZ	1:X:224:GLU:HB2	2.45	0.52
1:Y:289:CYS:SG	1:Y:291:LEU:HD23	2.48	0.52
1:D:17:GLU:O	1:D:21:SER:HB3	2.09	0.52
1:D:65:VAL:HG22	1:D:66:ASP:N	2.24	0.52
1:X:243:TYR:CD1	1:X:243:TYR:N	2.78	0.52
1:Y:82:THR:HA	1:Y:85:GLN:HG3	1.91	0.52
1:Y:305:LEU:HD23	1:Y:330:ARG:HB3	1.90	0.52
1:Z:173:TYR:CD1	1:Z:173:TYR:C	2.88	0.52
1:B:129:GLY:H	1:C:125:GLN:CD	2.18	0.52
1:C:185:ILE:O	1:C:185:ILE:HG12	2.09	0.52
1:W:41:ASN:O	1:W:44:GLN:HB3	2.08	0.52
1:A:173:TYR:CD1	1:A:173:TYR:C	2.87	0.52
1:W:205:THR:HG22	1:W:209:LEU:HD12	1.90	0.52
1:W:254:THR:HA	1:W:257:HIS:ND1	2.25	0.52
1:Y:66:ASP:C	1:Y:68:SER:N	2.68	0.52
1:Z:27:LYS:HG3	1:Z:71:GLN:O	2.10	0.52
1:Z:163:ILE:HG22	1:Z:164:GLN:N	2.24	0.52
1:A:128:ASP:HB2	1:D:128:ASP:OD2	2.10	0.52
1:A:270:LEU:C	1:A:270:LEU:HD12	2.34	0.52
1:C:179:GLN:HA	1:C:179:GLN:HE21	1.73	0.52
1:D:305:LEU:HD23	1:D:330:ARG:HB3	1.92	0.52
1:W:56:ARG:HG2	1:W:56:ARG:HH11	1.75	0.52
1:Y:58:PHE:HB2	1:Y:313:TRP:CZ3	2.45	0.52
1:A:218:ASP:C	1:A:220:HIS:H	2.18	0.51
1:B:17:GLU:O	1:B:21:SER:HB3	2.10	0.51
1:B:180:ASN:O	1:B:182:LEU:N	2.43	0.51
1:D:173:TYR:HA	1:D:176:ILE:HD12	1.90	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:30:LEU:HB3	1:X:76:VAL:HG22	1.92	0.51
1:X:123:THR:HG22	1:X:124:ILE:N	2.25	0.51
1:X:187:GLU:O	1:X:189:GLU:N	2.43	0.51
1:Y:83:LEU:HG	1:Y:94:ARG:HE	1.75	0.51
1:Y:180:ASN:O	1:Y:182:LEU:N	2.42	0.51
1:A:99:GLU:O	1:A:100:LYS:C	2.52	0.51
1:A:173:TYR:HE1	1:A:177:CYS:SG	2.33	0.51
1:A:289:CYS:SG	1:A:291:LEU:HD23	2.50	0.51
1:B:87:ASP:O	1:B:89:GLN:N	2.44	0.51
1:B:313:TRP:HB2	1:B:323:THR:OG1	2.10	0.51
1:C:151:LEU:HD22	1:C:208:VAL:CG1	2.39	0.51
1:W:129:GLY:C	1:W:131:SER:N	2.66	0.51
1:X:191:ILE:HG23	1:X:193:ASP:CG	2.36	0.51
1:Y:342:TYR:HE2	1:Y:344:HIS:HB2	1.74	0.51
1:Z:58:PHE:O	1:Z:61:ILE:HB	2.10	0.51
1:Z:78:LEU:HD13	1:Z:83:LEU:HA	1.91	0.51
1:A:58:PHE:O	1:A:61:ILE:HB	2.11	0.51
1:D:218:ASP:C	1:D:220:HIS:H	2.18	0.51
1:X:76:VAL:HG23	1:X:102:ILE:CG2	2.40	0.51
1:Y:218:ASP:C	1:Y:220:HIS:H	2.16	0.51
1:Z:22:ILE:O	1:Z:74:GLY:HA3	2.10	0.51
1:A:128:ASP:OD1	1:D:128:ASP:OD2	2.29	0.51
1:X:134:CYS:O	1:X:135:ALA:C	2.52	0.51
1:X:306:GLN:O	1:X:307:ALA:C	2.54	0.51
1:Z:316:LYS:O	1:Z:318:ALA:N	2.43	0.51
1:A:151:LEU:HD21	1:A:166:ASN:ND2	2.25	0.51
1:D:167:ALA:O	1:D:169:ALA:N	2.43	0.51
1:W:106:ILE:HG12	1:W:137:TYR:CD1	2.45	0.51
1:W:219:HIS:HA	1:Z:161:LEU:CD2	2.40	0.51
1:X:198:LEU:HD22	1:X:243:TYR:CD2	2.38	0.51
1:X:213:TYR:OH	1:X:228:LEU:HB2	2.11	0.51
1:Y:38:THR:HA	1:Y:41:ASN:HD22	1.75	0.51
1:Z:289:CYS:SG	1:Z:291:LEU:HD23	2.51	0.51
1:A:316:LYS:O	1:A:318:ALA:N	2.44	0.51
1:B:32:ALA:O	1:B:78:LEU:HA	2.10	0.51
1:C:306:GLN:O	1:C:307:ALA:C	2.54	0.51
1:W:218:ASP:C	1:W:220:HIS:H	2.18	0.51
1:X:59:ARG:NH1	1:X:82:THR:OG1	2.43	0.51
1:X:106:ILE:HG12	1:X:137:TYR:CE1	2.45	0.51
1:X:121:GLU:CD	1:X:162:ALA:HB2	2.36	0.51
1:Y:202:GLN:HG3	1:Y:233:VAL:HG11	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:277:GLU:OE2	1:Y:344:HIS:CD2	2.64	0.51
1:Z:306:GLN:O	1:Z:307:ALA:C	2.54	0.51
1:B:138:LYS:HB2	1:B:182:LEU:CD1	2.41	0.51
1:W:147:TRP:CD1	1:W:147:TRP:C	2.89	0.51
1:X:17:GLU:O	1:X:21:SER:HB3	2.11	0.51
1:X:151:LEU:N	1:X:151:LEU:HD22	2.26	0.51
1:Y:79:PHE:CD1	1:Y:80:HIS:N	2.79	0.51
1:Y:147:TRP:C	1:Y:147:TRP:CD1	2.88	0.51
1:Z:31:ALA:HB3	1:Z:302:GLY:CA	2.41	0.51
1:A:43:LEU:HD23	1:A:310:LEU:HD11	1.93	0.51
1:B:79:PHE:CD1	1:B:80:HIS:N	2.78	0.51
1:B:130:LEU:O	1:B:131:SER:C	2.54	0.51
1:B:134:CYS:C	1:B:136:GLN:N	2.66	0.51
1:B:205:THR:HG22	1:B:209:LEU:HD12	1.92	0.51
1:Y:50:ASN:OD1	1:Y:55:ARG:NH1	2.44	0.51
1:B:38:THR:HA	1:B:41:ASN:HD22	1.75	0.51
1:C:76:VAL:HG23	1:C:102:ILE:CG2	2.41	0.51
1:C:138:LYS:HA	1:C:142:VAL:O	2.11	0.51
1:W:18:ILE:HB	1:W:183:VAL:HG21	1.91	0.51
1:X:268:CYS:O	1:X:269:PHE:O	2.29	0.51
1:Y:138:LYS:HA	1:Y:142:VAL:O	2.11	0.51
1:Y:301:TYR:HE1	1:Y:334:ASN:HD21	1.58	0.51
1:Z:147:TRP:CD1	1:Z:148:ARG:N	2.79	0.51
1:Z:178:GLN:OE1	1:Z:222:TYR:HB3	2.11	0.51
1:B:28:GLY:HA3	1:B:299:PHE:CE1	2.46	0.51
1:B:306:GLN:O	1:B:307:ALA:C	2.54	0.51
1:C:205:THR:HG22	1:C:209:LEU:HD12	1.93	0.51
1:X:45:ARG:C	1:X:47:LYS:N	2.69	0.51
1:A:138:LYS:NZ	1:A:143:ASP:OD1	2.39	0.50
1:A:178:GLN:OE1	1:A:222:TYR:HB3	2.11	0.50
1:B:14:GLU:O	1:B:18:ILE:HG13	2.11	0.50
1:B:87:ASP:OD1	1:B:91:LYS:HB3	2.10	0.50
1:B:178:GLN:HG3	1:B:184:PRO:HD3	1.93	0.50
1:W:167:ALA:O	1:W:169:ALA:N	2.44	0.50
1:Y:205:THR:HG22	1:Y:209:LEU:HD12	1.92	0.50
1:B:213:TYR:OH	1:B:228:LEU:HB2	2.11	0.50
1:D:178:GLN:HE21	1:D:184:PRO:CG	2.22	0.50
1:Y:306:GLN:O	1:Y:307:ALA:C	2.54	0.50
1:A:185:ILE:O	1:A:185:ILE:HG12	2.10	0.50
1:B:271:SER:O	1:B:272:GLY:C	2.53	0.50
1:D:205:THR:HG22	1:D:209:LEU:HD12	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:254:THR:HA	1:D:257:HIS:ND1	2.26	0.50
1:W:31:ALA:HB3	1:W:302:GLY:CA	2.41	0.50
1:X:130:LEU:O	1:X:133:ARG:N	2.41	0.50
1:Z:200:HIS:O	1:Z:200:HIS:HD2	1.93	0.50
1:W:147:TRP:HB3	1:W:173:TYR:CE2	2.46	0.50
1:X:66:ASP:O	1:X:68:SER:N	2.44	0.50
1:Z:72:SER:HB3	1:Z:331:ALA:O	2.11	0.50
1:A:30:LEU:HD23	1:A:76:VAL:CG1	2.41	0.50
1:B:82:THR:O	1:B:84:TYR:N	2.44	0.50
1:C:45:ARG:C	1:C:47:LYS:N	2.69	0.50
1:D:46:ILE:HG21	1:D:310:LEU:HG	1.92	0.50
1:D:147:TRP:CD1	1:D:147:TRP:C	2.89	0.50
1:X:149:PRO:CD	1:X:170:LEU:HD11	2.41	0.50
1:X:305:LEU:HD23	1:X:330:ARG:HB3	1.93	0.50
1:Z:26:GLY:HA3	1:Z:339:LYS:HD2	1.92	0.50
1:Z:130:LEU:HD12	1:Z:133:ARG:HD3	1.91	0.50
1:A:224:GLU:OE2	1:B:258:ARG:NE	2.43	0.50
1:B:50:ASN:OD1	1:B:55:ARG:NH1	2.44	0.50
1:C:66:ASP:O	1:C:68:SER:N	2.44	0.50
1:D:89:GLN:CA	1:D:89:GLN:NE2	2.74	0.50
1:W:50:ASN:OD1	1:W:55:ARG:NH1	2.44	0.50
1:W:68:SER:OG	1:W:328:MET:HE1	2.11	0.50
1:Y:17:GLU:O	1:Y:21:SER:HB3	2.12	0.50
1:Z:60:GLU:OE1	1:Z:88:SER:N	2.34	0.50
1:B:301:TYR:HE1	1:B:334:ASN:HD21	1.57	0.50
1:W:280:THR:HG21	1:W:342:TYR:CE1	2.47	0.50
1:X:138:LYS:HB2	1:X:182:LEU:HD12	1.92	0.50
1:X:147:TRP:CE3	1:X:173:TYR:HB2	2.47	0.50
1:Y:78:LEU:HD22	1:Y:82:THR:CG2	2.42	0.50
1:Z:232:MET:O	1:Z:234:THR:HG23	2.12	0.50
1:B:138:LYS:HA	1:B:142:VAL:O	2.11	0.50
1:C:17:GLU:O	1:C:21:SER:HB3	2.11	0.50
1:W:216:LEU:HD23	1:W:221:VAL:CG2	2.30	0.50
1:Y:46:ILE:HB	1:Y:314:GLY:HA2	1.94	0.50
1:Y:106:ILE:HG23	1:Y:106:ILE:O	2.11	0.50
1:A:214:LYS:HB2	1:B:214:LYS:HD3	1.93	0.50
1:D:222:TYR:CZ	1:D:224:GLU:HB2	2.47	0.50
1:W:294:PRO:HG2	1:W:295:TRP:NE1	2.27	0.50
1:Y:87:ASP:O	1:Y:89:GLN:N	2.45	0.50
1:Z:254:THR:HA	1:Z:257:HIS:ND1	2.27	0.50
1:C:57:GLN:O	1:C:58:PHE:C	2.54	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:134:CYS:O	1:C:137:TYR:N	2.45	0.49
1:C:218:ASP:C	1:C:220:HIS:H	2.18	0.49
1:C:305:LEU:HD23	1:C:330:ARG:HB3	1.94	0.49
1:W:234:THR:HG23	1:W:248:VAL:HG13	1.94	0.49
1:X:186:VAL:HG12	1:X:188:PRO:CD	2.31	0.49
1:X:189:GLU:HG3	1:X:270:LEU:HD21	1.94	0.49
1:C:100:LYS:O	1:C:100:LYS:CG	2.60	0.49
1:X:134:CYS:O	1:X:137:TYR:N	2.45	0.49
1:Y:178:GLN:HG3	1:Y:184:PRO:HD3	1.94	0.49
1:Z:246:GLU:OE1	1:Z:246:GLU:N	2.45	0.49
1:C:244:THR:O	1:C:246:GLU:N	2.45	0.49
1:D:50:ASN:OD1	1:D:55:ARG:NH1	2.44	0.49
1:B:89:GLN:HA	1:B:89:GLN:NE2	2.25	0.49
1:B:244:THR:C	1:B:246:GLU:H	2.19	0.49
1:C:59:ARG:NH1	1:C:82:THR:OG1	2.45	0.49
1:Z:218:ASP:C	1:Z:220:HIS:H	2.20	0.49
1:C:134:CYS:O	1:C:135:ALA:C	2.54	0.49
1:D:13:LYS:O	1:D:17:GLU:HB2	2.13	0.49
1:D:216:LEU:O	1:D:221:VAL:HG23	2.12	0.49
1:X:106:ILE:HG12	1:X:137:TYR:CD1	2.48	0.49
1:A:306:GLN:O	1:A:307:ALA:C	2.55	0.49
1:B:78:LEU:HD22	1:B:82:THR:CG2	2.42	0.49
1:C:106:ILE:HG12	1:C:137:TYR:CD1	2.48	0.49
1:D:58:PHE:CE2	1:D:310:LEU:HD13	2.47	0.49
1:D:160:SER:O	1:D:161:LEU:C	2.55	0.49
1:W:46:ILE:HG21	1:W:310:LEU:HG	1.94	0.49
1:X:218:ASP:C	1:X:220:HIS:H	2.19	0.49
1:Z:198:LEU:HB2	1:Z:243:TYR:CZ	2.47	0.49
1:A:189:GLU:OE2	1:A:191:ILE:HG22	2.11	0.49
1:A:254:THR:HA	1:A:257:HIS:ND1	2.27	0.49
1:W:228:LEU:HG	1:W:230:PRO:CD	2.19	0.49
1:W:336:GLN:O	1:W:340:GLY:N	2.45	0.49
1:X:57:GLN:O	1:X:58:PHE:C	2.55	0.49
1:Y:14:GLU:O	1:Y:18:ILE:HG13	2.12	0.49
1:C:149:PRO:HD3	1:C:170:LEU:CD2	2.34	0.49
1:X:186:VAL:O	1:X:188:PRO:CD	2.61	0.49
1:Y:244:THR:O	1:Y:245:PRO:C	2.54	0.49
1:A:130:LEU:HD23	1:A:130:LEU:O	2.13	0.49
1:B:134:CYS:O	1:B:135:ALA:C	2.56	0.49
1:C:187:GLU:HG2	1:C:187:GLU:O	2.13	0.49
1:W:180:ASN:O	1:W:182:LEU:N	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:134:CYS:O	1:Y:135:ALA:C	2.55	0.49
1:Y:138:LYS:HB2	1:Y:182:LEU:CD1	2.43	0.49
1:B:83:LEU:HG	1:B:94:ARG:HE	1.77	0.49
1:B:128:ASP:O	1:B:129:GLY:C	2.55	0.49
1:B:147:TRP:CD1	1:B:147:TRP:C	2.90	0.49
1:C:232:MET:CE	1:C:274:MET:HE1	2.43	0.49
1:X:80:HIS:HD2	1:X:137:TYR:OH	1.95	0.49
1:X:294:PRO:HG2	1:X:295:TRP:NE1	2.28	0.49
1:Z:28:GLY:HA3	1:Z:299:PHE:CE1	2.48	0.49
1:Z:294:PRO:HG2	1:Z:295:TRP:NE1	2.28	0.49
1:B:283:LEU:HD22	1:B:299:PHE:HB3	1.95	0.48
1:D:180:ASN:O	1:D:182:LEU:N	2.46	0.48
1:W:316:LYS:O	1:W:318:ALA:N	2.46	0.48
1:Y:32:ALA:O	1:Y:78:LEU:HA	2.13	0.48
1:Y:93:PHE:HA	1:Y:96:ILE:HB	1.93	0.48
1:A:13:LYS:O	1:A:17:GLU:HB2	2.13	0.48
1:A:246:GLU:OE1	1:A:246:GLU:N	2.46	0.48
1:D:87:ASP:OD1	1:D:91:LYS:N	2.46	0.48
1:D:176:ILE:O	1:D:177:CYS:C	2.55	0.48
1:X:176:ILE:HG22	1:X:177:CYS:N	2.28	0.48
1:X:269:PHE:CZ	1:X:286:ILE:HD13	2.47	0.48
1:X:271:SER:O	1:X:272:GLY:C	2.57	0.48
1:A:161:LEU:CD2	1:D:219:HIS:HA	2.43	0.48
1:B:8:THR:O	1:B:9:GLN:C	2.57	0.48
1:B:294:PRO:HG2	1:B:295:TRP:CD1	2.48	0.48
1:C:121:GLU:OE1	1:C:162:ALA:HB2	2.13	0.48
1:C:173:TYR:O	1:C:176:ILE:HB	2.14	0.48
1:C:289:CYS:SG	1:C:291:LEU:HD23	2.53	0.48
1:D:216:LEU:HD23	1:D:221:VAL:CG2	2.31	0.48
1:Z:106:ILE:HG23	1:Z:106:ILE:O	2.13	0.48
1:B:106:ILE:HG12	1:B:137:TYR:CE1	2.48	0.48
1:C:283:LEU:HD22	1:C:299:PHE:HB3	1.95	0.48
1:W:301:TYR:HE1	1:W:334:ASN:HD21	1.61	0.48
1:X:100:LYS:O	1:X:100:LYS:CG	2.61	0.48
1:A:134:CYS:O	1:A:135:ALA:C	2.56	0.48
1:B:58:PHE:HB2	1:B:313:TRP:CZ3	2.49	0.48
1:D:175:SER:O	1:D:179:GLN:HB2	2.13	0.48
1:W:176:ILE:O	1:W:177:CYS:C	2.56	0.48
1:A:27:LYS:HG3	1:A:71:GLN:O	2.13	0.48
1:B:12:LYS:O	1:B:13:LYS:C	2.57	0.48
1:D:46:ILE:HG22	1:D:311:ALA:HA	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:316:LYS:O	1:D:318:ALA:N	2.46	0.48
1:W:66:ASP:C	1:W:68:SER:N	2.71	0.48
1:W:222:TYR:CZ	1:W:224:GLU:HB2	2.48	0.48
1:X:316:LYS:O	1:X:318:ALA:N	2.46	0.48
1:B:200:HIS:C	1:B:202:GLN:H	2.20	0.48
1:B:244:THR:HG22	1:B:245:PRO:HD2	1.94	0.48
1:D:313:TRP:HB2	1:D:323:THR:OG1	2.14	0.48
1:W:87:ASP:OD1	1:W:91:LYS:N	2.46	0.48
1:X:294:PRO:HG2	1:X:295:TRP:CD1	2.48	0.48
1:Y:48:VAL:HG12	1:Y:49:GLU:H	1.79	0.48
1:Y:63:PHE:HE1	1:Y:76:VAL:HG11	1.79	0.48
1:Y:214:LYS:HB2	1:Z:214:LYS:HD3	1.96	0.48
1:Y:271:SER:HA	1:Y:274:MET:HE2	1.94	0.48
1:Y:283:LEU:HD22	1:Y:299:PHE:HB3	1.95	0.48
1:A:216:LEU:O	1:A:221:VAL:HG23	2.13	0.48
1:B:271:SER:HA	1:B:274:MET:HE2	1.95	0.48
1:C:144:PHE:HA	1:C:183:VAL:H	1.79	0.48
1:W:175:SER:O	1:W:179:GLN:HB2	2.14	0.48
1:X:116:ALA:C	1:X:118:THR:N	2.64	0.48
1:X:126:GLY:H	1:Y:128:ASP:CG	2.22	0.48
1:X:180:ASN:O	1:X:181:GLY:C	2.57	0.48
1:A:56:ARG:HG2	1:A:56:ARG:HH11	1.79	0.48
1:C:186:VAL:O	1:C:188:PRO:HD2	2.14	0.48
1:C:316:LYS:O	1:C:318:ALA:N	2.47	0.48
1:X:153:ILE:HG21	1:X:196:HIS:ND1	2.28	0.48
1:Y:313:TRP:HB2	1:Y:323:THR:OG1	2.14	0.48
1:C:173:TYR:CE1	1:C:177:CYS:SG	3.07	0.48
1:C:294:PRO:HG2	1:C:295:TRP:CD1	2.49	0.48
1:D:60:GLU:HA	1:D:93:PHE:CE1	2.48	0.48
1:W:13:LYS:O	1:W:17:GLU:HB2	2.14	0.48
1:X:12:LYS:O	1:X:13:LYS:C	2.57	0.48
1:X:216:LEU:HD23	1:X:221:VAL:CG2	2.27	0.48
1:Z:92:LEU:C	1:Z:94:ARG:N	2.71	0.48
1:A:244:THR:HG23	1:A:247:GLN:HG3	1.93	0.47
1:C:269:PHE:CZ	1:C:286:ILE:HD13	2.49	0.47
1:Y:82:THR:C	1:Y:84:TYR:N	2.72	0.47
1:A:65:VAL:HG13	1:A:66:ASP:N	2.29	0.47
1:C:244:THR:O	1:C:247:GLN:N	2.43	0.47
1:D:56:ARG:HG3	1:D:85:GLN:HB3	1.97	0.47
1:D:59:ARG:HD3	1:D:82:THR:CG2	2.44	0.47
1:D:66:ASP:C	1:D:68:SER:N	2.72	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:126:GLY:N	1:D:147:TRP:CH2	2.82	0.47
1:D:301:TYR:HE1	1:D:334:ASN:HD21	1.62	0.47
1:W:60:GLU:HA	1:W:93:PHE:CE1	2.49	0.47
1:X:187:GLU:O	1:X:187:GLU:HG2	2.14	0.47
1:Y:11:GLN:O	1:Y:15:LEU:HG	2.14	0.47
1:Y:106:ILE:HB	1:Y:142:VAL:HG11	1.95	0.47
1:Z:7:LEU:CD2	1:Z:178:GLN:HB3	2.44	0.47
1:Z:280:THR:HG21	1:Z:342:TYR:CE1	2.49	0.47
1:Z:313:TRP:HB2	1:Z:323:THR:OG1	2.14	0.47
1:A:67:SER:HA	1:A:100:LYS:HD3	1.97	0.47
1:A:294:PRO:HG2	1:A:295:TRP:NE1	2.29	0.47
1:C:77:ILE:HG12	1:C:144:PHE:CZ	2.50	0.47
1:C:126:GLY:C	1:C:128:ASP:H	2.22	0.47
1:C:199:GLU:OE2	1:C:199:GLU:N	2.39	0.47
1:D:245:PRO:HB2	1:D:246:GLU:OE2	2.13	0.47
1:X:51:THR:HG22	1:X:52:GLU:N	2.30	0.47
1:X:189:GLU:HG2	1:X:191:ILE:HD12	1.95	0.47
1:Y:89:GLN:HA	1:Y:89:GLN:NE2	2.27	0.47
1:Y:106:ILE:CB	1:Y:142:VAL:HG11	2.44	0.47
1:Z:232:MET:HG2	1:Z:269:PHE:CD2	2.49	0.47
1:A:32:ALA:HB3	1:A:78:LEU:HD23	1.96	0.47
1:A:106:ILE:HG23	1:A:106:ILE:O	2.14	0.47
1:B:78:LEU:N	1:B:105:GLY:O	2.47	0.47
1:C:276:GLU:O	3:C:367:HOH:O	2.20	0.47
1:D:294:PRO:HG2	1:D:295:TRP:CD1	2.49	0.47
1:W:134:CYS:O	1:W:135:ALA:C	2.57	0.47
1:W:163:ILE:HG22	1:W:164:GLN:N	2.30	0.47
1:X:49:GLU:O	1:X:54:ASN:ND2	2.47	0.47
1:X:124:ILE:HB	1:X:147:TRP:NE1	2.28	0.47
1:A:67:SER:O	1:A:70:ASN:OD1	2.32	0.47
1:A:313:TRP:HB2	1:A:323:THR:OG1	2.15	0.47
1:B:57:GLN:O	1:B:60:GLU:N	2.48	0.47
1:C:12:LYS:O	1:C:13:LYS:C	2.57	0.47
1:C:147:TRP:HB2	1:C:173:TYR:CE1	2.49	0.47
1:D:186:VAL:CG1	1:D:188:PRO:HD3	2.34	0.47
1:W:56:ARG:HG3	1:W:85:GLN:HB3	1.97	0.47
1:X:79:PHE:O	1:X:80:HIS:C	2.57	0.47
1:X:178:GLN:NE2	1:X:222:TYR:HB3	2.00	0.47
1:X:313:TRP:HB2	1:X:323:THR:OG1	2.14	0.47
1:Y:232:MET:O	1:Y:234:THR:HG23	2.14	0.47
1:A:92:LEU:C	1:A:94:ARG:N	2.71	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:LEU:C	1:A:99:GLU:N	2.71	0.47
1:X:69:ILE:CG2	1:X:102:ILE:HD11	2.45	0.47
1:Y:243:TYR:HA	1:Y:247:GLN:OE1	2.15	0.47
1:Z:13:LYS:O	1:Z:17:GLU:HB2	2.15	0.47
1:Z:33:ASP:HB2	1:Z:107:LYS:HD2	1.96	0.47
1:A:40:GLY:O	1:A:44:GLN:HB2	2.15	0.47
1:A:76:VAL:HG23	1:A:102:ILE:CG2	2.45	0.47
1:A:105:GLY:HA3	1:A:144:PHE:CE1	2.50	0.47
1:A:283:LEU:HD22	1:A:299:PHE:HB3	1.97	0.47
1:A:301:TYR:HE1	1:A:334:ASN:HD21	1.60	0.47
1:B:65:VAL:HG23	1:B:324:GLN:HB3	1.96	0.47
1:D:106:ILE:HG12	1:D:137:TYR:CD1	2.49	0.47
1:D:134:CYS:O	1:D:135:ALA:C	2.57	0.47
1:W:134:CYS:O	1:W:137:TYR:N	2.48	0.47
1:X:138:LYS:HA	1:X:142:VAL:O	2.14	0.47
1:X:198:LEU:HB2	1:X:243:TYR:HE2	1.79	0.47
1:Y:185:ILE:O	1:Y:185:ILE:CG2	2.60	0.47
1:Z:173:TYR:HE1	1:Z:177:CYS:SG	2.38	0.47
1:W:216:LEU:O	1:W:221:VAL:HG23	2.15	0.47
1:X:147:TRP:CZ3	1:X:173:TYR:HB2	2.50	0.47
1:Y:12:LYS:O	1:Y:13:LYS:C	2.58	0.47
1:Y:51:THR:HB	1:Y:54:ASN:ND2	2.29	0.47
1:Y:161:LEU:O	1:Y:162:ALA:C	2.58	0.47
1:Z:106:ILE:HG12	1:Z:137:TYR:CZ	2.49	0.47
1:Z:134:CYS:O	1:Z:135:ALA:C	2.57	0.47
1:Z:162:ALA:O	1:Z:163:ILE:C	2.58	0.47
1:B:92:LEU:O	1:B:93:PHE:C	2.58	0.47
1:B:146:LYS:HA	1:B:185:ILE:HG21	1.96	0.47
1:C:15:LEU:HD11	1:C:178:GLN:HB3	1.97	0.47
1:D:53:GLU:OE2	1:D:56:ARG:NH2	2.48	0.47
1:X:283:LEU:HD22	1:X:299:PHE:HB3	1.96	0.47
1:Y:107:LYS:HE2	1:Y:109:ASP:HB2	1.97	0.47
1:Y:146:LYS:HA	1:Y:185:ILE:CG2	2.43	0.47
1:Y:250:MET:O	1:Y:251:ALA:C	2.57	0.47
1:Z:180:ASN:O	1:Z:181:GLY:C	2.58	0.47
1:A:32:ALA:O	1:A:78:LEU:HA	2.15	0.47
1:A:253:VAL:O	1:A:254:THR:C	2.58	0.47
1:B:51:THR:HB	1:B:54:ASN:ND2	2.29	0.47
1:C:294:PRO:HG2	1:C:295:TRP:NE1	2.30	0.47
1:W:12:LYS:O	1:W:13:LYS:C	2.58	0.47
1:W:172:ARG:O	1:W:176:ILE:HG13	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:219:HIS:HA	1:Z:161:LEU:HD22	1.97	0.47
1:W:245:PRO:HA	1:W:248:VAL:HB	1.97	0.47
1:X:69:ILE:HG23	1:X:102:ILE:HD11	1.97	0.47
1:Z:97:LEU:C	1:Z:99:GLU:N	2.72	0.47
1:A:244:THR:HG22	1:A:247:GLN:CG	2.44	0.46
1:B:253:VAL:O	1:B:254:THR:C	2.58	0.46
1:C:94:ARG:O	1:C:98:LYS:HD2	2.15	0.46
1:C:176:ILE:HG22	1:C:177:CYS:N	2.29	0.46
1:D:283:LEU:HD22	1:D:299:PHE:HB3	1.97	0.46
1:W:161:LEU:HD12	1:W:164:GLN:HE22	1.80	0.46
1:Y:57:GLN:O	1:Y:60:GLU:N	2.48	0.46
1:Y:92:LEU:O	1:Y:93:PHE:C	2.57	0.46
1:Y:127:LEU:HD13	1:Y:172:ARG:HD2	1.97	0.46
1:Z:56:ARG:HG2	1:Z:56:ARG:HH11	1.80	0.46
1:B:11:GLN:O	1:B:15:LEU:HG	2.15	0.46
1:B:93:PHE:HA	1:B:96:ILE:HB	1.97	0.46
1:B:160:SER:O	1:B:164:GLN:HG3	2.14	0.46
1:B:339:LYS:O	1:B:341:GLN:HG3	2.15	0.46
1:C:180:ASN:O	1:C:181:GLY:C	2.58	0.46
1:D:161:LEU:HD12	1:D:164:GLN:HE22	1.80	0.46
1:W:58:PHE:CZ	1:W:310:LEU:HD13	2.50	0.46
1:X:85:GLN:O	1:X:92:LEU:HD23	2.15	0.46
1:X:190:VAL:HB	1:X:231:ASN:ND2	2.29	0.46
1:X:250:MET:SD	1:X:291:LEU:HD21	2.56	0.46
1:Z:146:LYS:HE3	1:Z:187:GLU:OE1	2.16	0.46
1:Z:301:TYR:HE1	1:Z:334:ASN:HD21	1.61	0.46
1:B:65:VAL:O	1:B:66:ASP:C	2.58	0.46
1:D:59:ARG:O	1:D:60:GLU:C	2.58	0.46
1:D:183:VAL:HA	1:D:184:PRO:HD2	1.78	0.46
1:Z:65:VAL:HG13	1:Z:66:ASP:N	2.30	0.46
1:B:82:THR:C	1:B:84:TYR:N	2.71	0.46
1:B:173:TYR:OH	1:B:185:ILE:HG22	2.14	0.46
1:B:269:PHE:CZ	1:B:286:ILE:HD13	2.50	0.46
1:C:46:ILE:O	1:C:48:VAL:HG23	2.15	0.46
1:C:51:THR:HG22	1:C:52:GLU:N	2.29	0.46
1:Z:76:VAL:HG23	1:Z:102:ILE:CG2	2.46	0.46
1:A:164:GLN:O	1:A:168:ASN:HB2	2.16	0.46
1:B:63:PHE:HE1	1:B:76:VAL:HG11	1.78	0.46
1:B:101:GLY:O	1:B:102:ILE:HG13	2.16	0.46
1:B:147:TRP:HB3	1:B:173:TYR:CZ	2.51	0.46
1:B:292:PRO:C	1:B:293:LYS:HG3	2.40	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:150:VAL:C	1:X:151:LEU:HD22	2.41	0.46
1:Z:12:LYS:O	1:Z:13:LYS:C	2.56	0.46
1:A:216:LEU:HD23	1:A:221:VAL:HG11	1.97	0.46
1:C:49:GLU:O	1:C:54:ASN:ND2	2.48	0.46
1:C:159:SER:H	1:C:162:ALA:HB3	1.80	0.46
1:C:187:GLU:O	1:C:189:GLU:N	2.47	0.46
1:C:271:SER:O	1:C:272:GLY:C	2.58	0.46
1:D:172:ARG:O	1:D:176:ILE:HG13	2.15	0.46
1:W:173:TYR:CD1	1:W:173:TYR:O	2.68	0.46
1:Y:8:THR:O	1:Y:9:GLN:C	2.59	0.46
1:C:127:LEU:HD12	1:C:127:LEU:N	2.27	0.46
1:D:244:THR:C	1:D:248:VAL:HG23	2.40	0.46
1:D:293:LYS:O	1:D:295:TRP:N	2.49	0.46
1:W:57:GLN:O	1:W:58:PHE:C	2.59	0.46
1:W:280:THR:HG21	1:W:342:TYR:CD1	2.50	0.46
1:W:313:TRP:HB2	1:W:323:THR:OG1	2.16	0.46
1:X:173:TYR:O	1:X:176:ILE:HB	2.16	0.46
1:Z:67:SER:O	1:Z:70:ASN:OD1	2.33	0.46
1:A:46:ILE:HG12	1:A:314:GLY:CA	2.44	0.46
1:C:69:ILE:CG2	1:C:102:ILE:HD11	2.46	0.46
1:C:216:LEU:O	1:C:221:VAL:HG23	2.15	0.46
1:D:106:ILE:O	1:D:106:ILE:CG2	2.63	0.46
1:D:173:TYR:O	1:D:173:TYR:CD1	2.68	0.46
1:X:60:GLU:CD	1:X:87:ASP:HB2	2.41	0.46
1:X:173:TYR:CE1	1:X:177:CYS:SG	3.09	0.46
1:Y:13:LYS:O	1:Y:17:GLU:HB2	2.16	0.46
1:Y:82:THR:O	1:Y:84:TYR:N	2.49	0.46
1:Y:253:VAL:O	1:Y:254:THR:C	2.59	0.46
1:Y:294:PRO:HG2	1:Y:295:TRP:CD1	2.49	0.46
1:A:59:ARG:HD3	1:A:82:THR:HG21	1.98	0.46
1:B:15:LEU:HD13	1:B:178:GLN:HG2	1.96	0.46
1:C:36:VAL:HG22	1:C:79:PHE:HE2	1.81	0.46
1:C:116:ALA:C	1:C:118:THR:N	2.71	0.46
1:C:158:PRO:HB2	1:C:163:ILE:HD11	1.97	0.46
1:D:7:LEU:CD1	1:D:222:TYR:HB2	2.46	0.46
1:D:57:GLN:O	1:D:58:PHE:C	2.59	0.46
1:D:94:ARG:HG2	1:D:94:ARG:NH1	2.27	0.46
1:D:293:LYS:C	1:D:295:TRP:H	2.24	0.46
1:W:59:ARG:O	1:W:60:GLU:C	2.58	0.46
1:W:293:LYS:O	1:W:295:TRP:N	2.49	0.46
1:X:77:ILE:HG12	1:X:144:PHE:CE2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:121:GLU:OE2	1:X:162:ALA:CB	2.64	0.46
1:Y:200:HIS:C	1:Y:202:GLN:N	2.74	0.46
1:Z:31:ALA:HB3	1:Z:302:GLY:HA3	1.98	0.46
1:Z:40:GLY:O	1:Z:44:GLN:HB2	2.16	0.46
1:Z:185:ILE:CD1	1:Z:229:LYS:HD2	2.41	0.46
1:A:292:PRO:C	1:A:293:LYS:HG3	2.41	0.46
1:B:250:MET:O	1:B:251:ALA:C	2.59	0.46
1:D:61:ILE:O	1:D:62:LEU:C	2.59	0.46
1:D:134:CYS:O	1:D:137:TYR:N	2.49	0.46
1:X:216:LEU:O	1:X:221:VAL:HG23	2.16	0.46
1:X:289:CYS:SG	1:X:291:LEU:HD23	2.56	0.46
1:Y:344:HIS:ND1	1:Y:345:THR:N	2.63	0.46
1:A:60:GLU:OE1	1:A:88:SER:N	2.34	0.45
1:A:162:ALA:O	1:A:163:ILE:C	2.59	0.45
1:B:36:VAL:HG22	1:B:79:PHE:HE2	1.81	0.45
1:C:89:GLN:C	1:C:91:LYS:H	2.22	0.45
1:C:130:LEU:O	1:C:133:ARG:N	2.49	0.45
1:D:179:GLN:HE21	1:D:179:GLN:C	2.24	0.45
1:W:59:ARG:HD3	1:W:82:THR:CG2	2.46	0.45
1:W:61:ILE:O	1:W:62:LEU:C	2.58	0.45
1:X:89:GLN:C	1:X:91:LYS:H	2.23	0.45
1:Y:38:THR:O	1:Y:39:MET:C	2.59	0.45
1:Y:58:PHE:CZ	1:Y:310:LEU:HD13	2.51	0.45
1:Z:83:LEU:HD11	1:Z:142:VAL:HG22	1.97	0.45
1:A:127:LEU:N	1:A:147:TRP:HH2	2.14	0.45
1:C:250:MET:SD	1:C:291:LEU:HD21	2.56	0.45
1:C:301:TYR:HE1	1:C:334:ASN:HD21	1.63	0.45
1:W:43:LEU:HD23	1:W:310:LEU:HD11	1.99	0.45
1:X:39:MET:HE3	1:X:39:MET:HA	1.98	0.45
1:Y:269:PHE:CZ	1:Y:286:ILE:HD13	2.51	0.45
1:Z:161:LEU:O	1:Z:165:GLU:HB2	2.17	0.45
1:Z:164:GLN:O	1:Z:168:ASN:HB2	2.16	0.45
1:Z:341:GLN:O	1:Z:342:TYR:C	2.58	0.45
1:A:125:GLN:O	1:D:128:ASP:OD1	2.35	0.45
1:A:134:CYS:O	1:A:137:TYR:N	2.50	0.45
1:B:161:LEU:O	1:B:162:ALA:C	2.59	0.45
1:B:178:GLN:HE21	1:B:184:PRO:CG	2.27	0.45
1:B:330:ARG:NE	1:B:330:ARG:HA	2.31	0.45
1:C:13:LYS:O	1:C:17:GLU:HB2	2.16	0.45
1:C:69:ILE:HG23	1:C:102:ILE:HD11	1.98	0.45
1:D:127:LEU:HD13	1:D:172:ARG:HD2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:11:GLN:O	1:W:15:LEU:HG	2.16	0.45
1:W:46:ILE:HG22	1:W:311:ALA:HA	1.96	0.45
1:W:146:LYS:HE3	1:W:187:GLU:OE2	2.15	0.45
1:X:13:LYS:O	1:X:17:GLU:HB2	2.16	0.45
1:X:174:ALA:HB1	1:X:184:PRO:HG3	1.99	0.45
1:Y:91:LYS:HG2	1:Y:96:ILE:HG13	1.99	0.45
1:Y:198:LEU:C	1:Y:200:HIS:N	2.74	0.45
1:A:105:GLY:CA	1:A:144:PHE:CE1	2.99	0.45
1:A:232:MET:SD	1:A:274:MET:HE1	2.56	0.45
1:B:56:ARG:HG2	1:B:56:ARG:NH1	2.30	0.45
1:B:92:LEU:O	1:B:95:ASN:N	2.48	0.45
1:D:12:LYS:O	1:D:13:LYS:C	2.59	0.45
1:X:185:ILE:HD11	1:X:229:LYS:HD2	1.98	0.45
1:X:330:ARG:NE	1:X:330:ARG:HA	2.31	0.45
1:Z:216:LEU:O	1:Z:221:VAL:HG23	2.16	0.45
1:A:172:ARG:HH12	1:D:172:ARG:NH2	2.14	0.45
1:D:43:LEU:HD23	1:D:310:LEU:HD11	1.99	0.45
1:D:244:THR:HG22	1:D:247:GLN:CG	2.44	0.45
1:D:244:THR:OG1	1:D:245:PRO:HD2	2.17	0.45
1:W:294:PRO:HG2	1:W:295:TRP:CD1	2.51	0.45
1:X:127:LEU:HG	1:X:147:TRP:CH2	2.51	0.45
1:X:250:MET:SD	1:X:291:LEU:CD2	3.05	0.45
1:A:39:MET:O	1:A:43:LEU:HG	2.17	0.45
1:A:172:ARG:HH12	1:D:172:ARG:HH22	1.65	0.45
1:A:180:ASN:O	1:A:181:GLY:C	2.60	0.45
1:A:189:GLU:OE1	1:A:270:LEU:HD22	2.17	0.45
1:B:324:GLN:O	1:B:328:MET:HG2	2.17	0.45
1:W:160:SER:O	1:W:161:LEU:C	2.60	0.45
1:W:293:LYS:C	1:W:295:TRP:H	2.23	0.45
1:X:165:GLU:OE2	1:Y:172:ARG:NH2	2.50	0.45
1:Y:65:VAL:O	1:Y:66:ASP:C	2.59	0.45
1:Y:138:LYS:NZ	1:Y:143:ASP:OD1	2.50	0.45
1:Y:294:PRO:HG2	1:Y:295:TRP:NE1	2.32	0.45
1:Z:104:VAL:HG23	3:Z:364:HOH:O	2.15	0.45
1:Z:202:GLN:O	1:Z:206:GLU:HG3	2.17	0.45
1:A:185:ILE:CD1	1:A:229:LYS:HD2	2.42	0.45
1:A:231:ASN:H	1:A:231:ASN:ND2	2.15	0.45
1:B:216:LEU:HD23	1:B:221:VAL:HG11	1.99	0.45
1:B:232:MET:HE1	1:B:274:MET:HE1	1.98	0.45
1:W:324:GLN:O	1:W:328:MET:HG2	2.17	0.45
1:Y:51:THR:CG2	1:Y:52:GLU:N	2.79	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:149:PRO:HD2	1:Y:187:GLU:O	2.17	0.45
1:Z:67:SER:HA	1:Z:100:LYS:HD3	1.98	0.45
1:A:232:MET:O	1:A:234:THR:HG23	2.16	0.45
1:B:58:PHE:CZ	1:B:310:LEU:HD13	2.52	0.45
1:C:79:PHE:O	1:C:80:HIS:C	2.60	0.45
1:C:85:GLN:O	1:C:92:LEU:HD23	2.16	0.45
1:C:157:CYS:HA	1:C:158:PRO:C	2.42	0.45
1:C:330:ARG:NE	1:C:330:ARG:HA	2.32	0.45
1:D:108:LEU:HA	1:D:108:LEU:HD23	1.72	0.45
1:W:18:ILE:HD13	1:W:143:ASP:HB3	1.98	0.45
1:X:46:ILE:O	1:X:48:VAL:HG23	2.16	0.45
1:Z:253:VAL:O	1:Z:254:THR:C	2.60	0.45
1:A:214:LYS:HD3	1:B:214:LYS:HB2	1.98	0.45
1:C:60:GLU:OE1	1:C:87:ASP:HB2	2.17	0.45
1:D:68:SER:OG	1:D:328:MET:HE1	2.17	0.45
1:D:292:PRO:C	1:D:293:LYS:HG3	2.42	0.45
1:W:187:GLU:OE2	1:W:229:LYS:HD3	2.17	0.45
1:X:232:MET:HG3	1:X:269:PHE:CD2	2.52	0.45
1:X:259:THR:O	1:X:261:PRO:HD3	2.16	0.45
1:Y:159:SER:O	1:Y:160:SER:C	2.59	0.45
1:Z:216:LEU:HD23	1:Z:221:VAL:HG11	1.98	0.45
1:Z:292:PRO:C	1:Z:293:LYS:HG3	2.42	0.45
1:B:48:VAL:HG12	1:B:49:GLU:H	1.81	0.45
1:B:101:GLY:C	1:B:102:ILE:HG13	2.42	0.45
1:B:233:VAL:CG2	1:B:252:THR:HA	2.47	0.45
1:D:146:LYS:NZ	1:D:229:LYS:HZ3	2.15	0.45
1:W:279:ALA:HB1	1:W:301:TYR:CE1	2.52	0.45
1:W:283:LEU:HD22	1:W:299:PHE:HB3	1.98	0.45
1:X:60:GLU:OE1	1:X:87:ASP:HB2	2.17	0.45
1:X:115:LEU:HB2	1:X:122:THR:HA	1.98	0.45
1:X:148:ARG:HA	1:X:149:PRO:HD2	1.92	0.45
1:Y:28:GLY:HA3	1:Y:299:PHE:CE1	2.52	0.45
1:B:294:PRO:HG2	1:B:295:TRP:NE1	2.32	0.44
1:C:108:LEU:HD23	1:C:108:LEU:HA	1.74	0.44
1:W:53:GLU:OE2	1:W:56:ARG:NH2	2.49	0.44
1:X:197:ASP:O	1:X:198:LEU:C	2.60	0.44
1:Y:330:ARG:NE	1:Y:330:ARG:HA	2.31	0.44
1:B:91:LYS:HG2	1:B:96:ILE:HG13	2.00	0.44
1:C:250:MET:O	1:C:251:ALA:C	2.61	0.44
1:D:56:ARG:HG2	1:D:56:ARG:NH1	2.32	0.44
1:W:292:PRO:C	1:W:293:LYS:HG3	2.42	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:101:GLY:C	1:Y:102:ILE:HG13	2.41	0.44
1:Y:178:GLN:HE21	1:Y:184:PRO:CG	2.27	0.44
1:Y:202:GLN:CG	1:Y:233:VAL:HG11	2.47	0.44
1:Z:330:ARG:HA	1:Z:330:ARG:NE	2.32	0.44
1:C:56:ARG:HD2	1:C:86:LYS:O	2.18	0.44
1:C:60:GLU:CD	1:C:87:ASP:HB2	2.42	0.44
1:W:94:ARG:HG2	1:W:94:ARG:NH1	2.27	0.44
1:W:179:GLN:HE21	1:W:179:GLN:C	2.25	0.44
1:X:50:ASN:OD1	1:X:50:ASN:C	2.60	0.44
1:X:250:MET:O	1:X:251:ALA:C	2.60	0.44
1:Y:292:PRO:C	1:Y:293:LYS:HG3	2.43	0.44
1:A:53:GLU:OE2	1:A:57:GLN:HG3	2.18	0.44
1:B:134:CYS:O	1:B:137:TYR:N	2.50	0.44
1:D:330:ARG:HA	1:D:330:ARG:NE	2.32	0.44
1:W:232:MET:HG2	1:W:286:ILE:HD11	2.00	0.44
1:Y:101:GLY:O	1:Y:102:ILE:HG13	2.16	0.44
1:Y:108:LEU:HD11	1:Y:134:CYS:SG	2.57	0.44
1:A:143:ASP:C	1:A:182:LEU:HG	2.42	0.44
1:B:51:THR:CG2	1:B:52:GLU:N	2.81	0.44
1:B:60:GLU:OE1	1:B:87:ASP:HB2	2.17	0.44
1:C:50:ASN:OD1	1:C:50:ASN:C	2.60	0.44
1:D:279:ALA:HB1	1:D:301:TYR:CE1	2.53	0.44
1:X:247:GLN:O	1:X:248:VAL:C	2.61	0.44
1:Y:78:LEU:N	1:Y:105:GLY:O	2.49	0.44
1:Z:39:MET:O	1:Z:43:LEU:HG	2.18	0.44
1:A:233:VAL:O	1:A:233:VAL:HG12	2.17	0.44
1:B:245:PRO:O	1:B:285:ALA:HB1	2.18	0.44
1:C:39:MET:HA	1:C:39:MET:HE3	2.00	0.44
1:C:89:GLN:C	1:C:91:LYS:N	2.75	0.44
1:Z:30:LEU:HD23	1:Z:76:VAL:CG1	2.47	0.44
1:Z:58:PHE:CZ	1:Z:310:LEU:HD13	2.51	0.44
1:B:65:VAL:HG13	1:B:69:ILE:HB	1.99	0.44
1:B:244:THR:HB	1:B:246:GLU:HB2	1.99	0.44
1:B:277:GLU:OE2	1:B:344:HIS:ND1	2.51	0.44
1:C:65:VAL:CG2	1:C:324:GLN:HB3	2.47	0.44
1:C:174:ALA:HB1	1:C:184:PRO:HG3	1.99	0.44
1:C:259:THR:O	1:C:261:PRO:HD3	2.17	0.44
1:D:31:ALA:HB3	1:D:302:GLY:CA	2.48	0.44
1:W:180:ASN:C	1:W:182:LEU:H	2.25	0.44
1:X:99:GLU:C	1:X:101:GLY:H	2.26	0.44
1:X:121:GLU:OE2	1:X:162:ALA:HB2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:227:LEU:HD23	1:X:227:LEU:HA	1.85	0.44
1:Y:80:HIS:HD2	1:Y:137:TYR:OH	2.00	0.44
1:Z:53:GLU:OE2	1:Z:57:GLN:HG3	2.18	0.44
1:A:250:MET:O	1:A:251:ALA:C	2.61	0.44
1:A:257:HIS:HA	1:A:295:TRP:HZ2	1.83	0.44
1:B:51:THR:OG1	1:B:54:ASN:ND2	2.51	0.44
1:B:58:PHE:CE2	1:B:310:LEU:HD13	2.53	0.44
1:B:202:GLN:HG3	1:B:233:VAL:HG11	1.98	0.44
1:C:197:ASP:O	1:C:198:LEU:C	2.61	0.44
1:C:248:VAL:HG11	1:C:282:ASN:ND2	2.33	0.44
1:D:185:ILE:CG2	1:D:229:LYS:HB2	2.48	0.44
1:W:330:ARG:HA	1:W:330:ARG:NE	2.32	0.44
1:X:28:GLY:HA3	1:X:299:PHE:CE1	2.53	0.44
1:Y:108:LEU:HB3	1:Y:130:LEU:HD11	2.00	0.44
1:Y:324:GLN:O	1:Y:328:MET:HG2	2.17	0.44
1:A:58:PHE:CD2	1:A:310:LEU:HD13	2.52	0.44
1:B:232:MET:HG3	1:B:269:PHE:CD2	2.53	0.44
1:C:294:PRO:N	3:C:366:HOH:O	2.51	0.44
1:D:11:GLN:O	1:D:15:LEU:HG	2.18	0.44
1:W:128:ASP:OD2	1:Z:128:ASP:HB2	2.17	0.44
1:X:27:LYS:HG2	1:X:72:SER:C	2.43	0.44
1:X:89:GLN:C	1:X:91:LYS:N	2.76	0.44
1:X:146:LYS:CG	1:X:147:TRP:N	2.80	0.44
1:X:191:ILE:C	1:X:193:ASP:H	2.26	0.44
1:Y:56:ARG:HG2	1:Y:56:ARG:NH1	2.27	0.44
1:Y:79:PHE:O	1:Y:80:HIS:C	2.60	0.44
1:Y:89:GLN:C	1:Y:91:LYS:H	2.26	0.44
1:Y:126:GLY:N	1:Y:147:TRP:HH2	2.16	0.44
1:Y:216:LEU:O	1:Y:221:VAL:HG23	2.18	0.44
1:Z:58:PHE:CZ	1:Z:310:LEU:HB2	2.53	0.44
1:A:12:LYS:O	1:A:13:LYS:C	2.60	0.43
1:B:106:ILE:CB	1:B:142:VAL:HG11	2.48	0.43
1:C:69:ILE:HD12	1:C:69:ILE:HA	1.85	0.43
1:D:183:VAL:HG13	1:D:225:GLY:O	2.17	0.43
1:W:106:ILE:HG12	1:W:137:TYR:CE1	2.52	0.43
1:W:332:MET:O	1:W:336:GLN:HG3	2.18	0.43
1:Y:12:LYS:CD	1:Y:222:TYR:CE1	2.97	0.43
1:Y:51:THR:OG1	1:Y:54:ASN:ND2	2.51	0.43
1:Y:198:LEU:O	1:Y:200:HIS:N	2.51	0.43
1:Z:59:ARG:HD3	1:Z:82:THR:HG21	2.00	0.43
1:Z:197:ASP:OD1	1:Z:199:GLU:HG2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:330:ARG:NE	1:A:330:ARG:HA	2.32	0.43
1:B:231:ASN:HA	1:B:270:LEU:HG	1.99	0.43
1:C:179:GLN:HE21	1:C:179:GLN:CA	2.29	0.43
1:C:198:LEU:HB2	1:C:243:TYR:CE2	2.53	0.43
1:C:324:GLN:O	1:C:328:MET:HG2	2.18	0.43
1:D:163:ILE:HG22	1:D:164:GLN:N	2.32	0.43
1:D:250:MET:O	1:D:251:ALA:C	2.62	0.43
1:X:244:THR:C	1:X:246:GLU:H	2.27	0.43
1:Y:87:ASP:C	1:Y:89:GLN:N	2.76	0.43
1:A:30:LEU:HD23	1:A:76:VAL:HG13	2.00	0.43
1:B:232:MET:O	1:B:234:THR:N	2.51	0.43
1:D:180:ASN:C	1:D:182:LEU:H	2.26	0.43
1:X:117:GLY:HA2	1:Y:6:ALA:N	2.32	0.43
1:X:124:ILE:HG21	1:X:147:TRP:NE1	2.33	0.43
1:X:324:GLN:O	1:X:328:MET:HG2	2.17	0.43
1:Y:65:VAL:HG13	1:Y:69:ILE:HB	1.99	0.43
1:Z:227:LEU:HD23	1:Z:227:LEU:HA	1.83	0.43
1:A:324:GLN:O	1:A:328:MET:HG2	2.19	0.43
1:B:38:THR:O	1:B:39:MET:C	2.59	0.43
1:B:89:GLN:C	1:B:91:LYS:H	2.25	0.43
1:Z:294:PRO:HG2	1:Z:295:TRP:CD1	2.53	0.43
1:C:232:MET:HG2	1:C:269:PHE:CD2	2.54	0.43
1:C:247:GLN:O	1:C:248:VAL:C	2.62	0.43
1:D:324:GLN:O	1:D:328:MET:HG2	2.18	0.43
1:X:56:ARG:HD2	1:X:86:LYS:O	2.18	0.43
1:X:94:ARG:O	1:X:98:LYS:HD2	2.17	0.43
1:X:232:MET:SD	1:X:282:ASN:HB3	2.59	0.43
1:X:292:PRO:C	1:X:293:LYS:HG3	2.43	0.43
1:Y:166:ASN:O	1:Y:169:ALA:HB3	2.19	0.43
1:Z:279:ALA:HB1	1:Z:301:TYR:CE1	2.54	0.43
1:A:76:VAL:CG2	1:A:102:ILE:HG21	2.48	0.43
1:A:161:LEU:O	1:A:165:GLU:HB2	2.19	0.43
1:B:172:ARG:NH2	1:C:165:GLU:OE2	2.51	0.43
1:C:231:ASN:HA	1:C:270:LEU:HG	1.99	0.43
1:D:228:LEU:HG	1:D:230:PRO:CD	2.21	0.43
1:W:201:CYS:SG	1:W:233:VAL:HG13	2.59	0.43
1:Z:43:LEU:HD23	1:Z:310:LEU:HD11	2.00	0.43
1:B:99:GLU:C	1:B:101:GLY:N	2.76	0.43
1:X:68:SER:HG	1:X:328:MET:HE1	1.78	0.43
1:Y:200:HIS:O	1:Y:201:CYS:C	2.61	0.43
1:Z:76:VAL:CG2	1:Z:102:ILE:HG21	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:51:THR:CB	1:A:54:ASN:HD22	2.31	0.43
1:A:147:TRP:CD1	1:A:148:ARG:N	2.86	0.43
1:B:43:LEU:HB3	1:B:48:VAL:HB	2.00	0.43
1:B:79:PHE:O	1:B:80:HIS:C	2.61	0.43
1:C:167:ALA:C	1:C:169:ALA:N	2.76	0.43
1:D:216:LEU:HD23	1:D:221:VAL:HG11	2.01	0.43
1:Z:250:MET:O	1:Z:251:ALA:C	2.62	0.43
1:B:202:GLN:O	1:B:203:TYR:C	2.61	0.43
1:C:87:ASP:CG	1:C:91:LYS:HB3	2.44	0.43
1:W:250:MET:O	1:W:251:ALA:C	2.61	0.43
1:W:339:LYS:HB3	1:W:341:GLN:NE2	2.34	0.43
1:Y:60:GLU:HA	1:Y:93:PHE:CE1	2.54	0.43
1:Y:134:CYS:O	1:Y:137:TYR:N	2.51	0.43
1:Y:202:GLN:O	1:Y:206:GLU:HG3	2.19	0.43
1:Z:283:LEU:HD22	1:Z:299:PHE:HB3	2.00	0.43
1:A:11:GLN:O	1:A:15:LEU:HG	2.18	0.43
1:A:130:LEU:HA	1:A:133:ARG:HB3	2.01	0.43
1:B:168:ASN:HD22	1:B:168:ASN:N	2.15	0.43
1:B:216:LEU:CD2	1:B:221:VAL:HG11	2.49	0.43
1:C:284:ASN:O	1:C:285:ALA:C	2.61	0.43
1:D:83:LEU:HG	1:D:83:LEU:O	2.19	0.43
1:D:146:LYS:NZ	1:D:229:LYS:NZ	2.67	0.43
1:D:257:HIS:HA	1:D:295:TRP:HZ2	1.84	0.43
1:W:56:ARG:HG2	1:W:56:ARG:NH1	2.33	0.43
1:W:63:PHE:CZ	1:W:78:LEU:HD21	2.54	0.43
1:W:109:ASP:OD1	1:W:109:ASP:C	2.61	0.43
1:W:170:LEU:HD13	1:W:212:VAL:HG13	2.00	0.43
1:X:36:VAL:HG22	1:X:79:PHE:HE2	1.84	0.43
1:X:167:ALA:C	1:X:169:ALA:N	2.77	0.43
1:Z:145:GLY:O	1:Z:185:ILE:HG23	2.19	0.43
1:Z:293:LYS:O	1:Z:295:TRP:N	2.52	0.43
1:A:33:ASP:HA	1:A:79:PHE:HB2	2.01	0.42
1:A:199:GLU:OE1	1:A:199:GLU:N	2.52	0.42
1:A:250:MET:SD	1:A:291:LEU:HD21	2.59	0.42
1:C:99:GLU:C	1:C:101:GLY:H	2.26	0.42
1:W:80:HIS:CD2	1:W:137:TYR:OH	2.66	0.42
1:X:87:ASP:CG	1:X:91:LYS:HB3	2.44	0.42
1:X:144:PHE:HA	1:X:183:VAL:H	1.84	0.42
1:X:253:VAL:O	1:X:254:THR:C	2.62	0.42
1:Y:214:LYS:HD3	1:Z:214:LYS:HB2	2.00	0.42
1:Z:205:THR:O	1:Z:209:LEU:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:36:VAL:O	1:A:50:ASN:ND2	2.40	0.42
1:B:4:PHE:CD1	1:B:4:PHE:N	2.88	0.42
1:B:60:GLU:HA	1:B:93:PHE:CE1	2.53	0.42
1:C:172:ARG:O	1:C:173:TYR:C	2.62	0.42
1:C:180:ASN:C	1:C:182:LEU:N	2.76	0.42
1:C:244:THR:CG2	1:C:247:GLN:HG3	2.49	0.42
1:D:336:GLN:O	1:D:340:GLY:N	2.52	0.42
1:W:250:MET:SD	1:W:291:LEU:HD21	2.59	0.42
1:X:134:CYS:C	1:X:136:GLN:H	2.27	0.42
1:X:301:TYR:HE1	1:X:334:ASN:HD21	1.65	0.42
1:Y:60:GLU:OE1	1:Y:87:ASP:HB2	2.18	0.42
1:Y:89:GLN:HE21	1:Y:89:GLN:CA	2.29	0.42
1:Z:46:ILE:HD13	1:Z:311:ALA:HA	2.00	0.42
1:Z:324:GLN:O	1:Z:328:MET:HG2	2.19	0.42
1:A:279:ALA:HB1	1:A:301:TYR:CE1	2.54	0.42
1:B:283:LEU:HD12	1:B:283:LEU:O	2.20	0.42
1:C:283:LEU:HD12	1:C:283:LEU:O	2.19	0.42
1:D:105:GLY:HA2	1:D:144:PHE:CE1	2.55	0.42
1:W:83:LEU:HG	1:W:83:LEU:O	2.19	0.42
1:W:244:THR:OG1	1:W:247:GLN:HG3	2.19	0.42
1:W:244:THR:N	1:W:247:GLN:OE1	2.52	0.42
1:W:253:VAL:O	1:W:254:THR:C	2.61	0.42
1:X:205:THR:O	1:X:209:LEU:HB2	2.19	0.42
1:Y:36:VAL:HG22	1:Y:79:PHE:HE2	1.83	0.42
1:Y:187:GLU:C	1:Y:188:PRO:O	2.62	0.42
1:Y:232:MET:O	1:Y:234:THR:N	2.53	0.42
1:Z:11:GLN:O	1:Z:15:LEU:HG	2.18	0.42
1:Z:134:CYS:O	1:Z:137:TYR:N	2.52	0.42
1:A:293:LYS:C	1:A:295:TRP:H	2.27	0.42
1:B:12:LYS:CD	1:B:222:TYR:CE1	3.00	0.42
1:B:254:THR:HA	1:B:257:HIS:CE1	2.55	0.42
1:C:69:ILE:C	1:C:71:GLN:H	2.28	0.42
1:C:160:SER:O	1:C:164:GLN:HG2	2.19	0.42
1:D:170:LEU:HD13	1:D:212:VAL:HG13	2.01	0.42
1:X:180:ASN:C	1:X:182:LEU:N	2.75	0.42
1:B:247:GLN:O	1:B:248:VAL:C	2.62	0.42
1:C:205:THR:O	1:C:209:LEU:HB2	2.18	0.42
1:C:293:LYS:C	1:C:295:TRP:H	2.26	0.42
1:D:94:ARG:NH1	1:D:94:ARG:CG	2.83	0.42
1:D:264:VAL:O	1:D:295:TRP:HB3	2.19	0.42
1:W:205:THR:O	1:W:209:LEU:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:121:GLU:C	1:X:122:THR:HG22	2.44	0.42
1:Y:254:THR:HA	1:Y:257:HIS:CE1	2.55	0.42
1:A:72:SER:HB3	1:A:331:ALA:O	2.20	0.42
1:B:32:ALA:CB	1:B:63:PHE:HZ	2.32	0.42
1:C:86:LYS:HD3	1:C:90:GLY:O	2.19	0.42
1:C:152:ARG:HG3	1:C:152:ARG:HH11	1.84	0.42
1:C:292:PRO:C	1:C:293:LYS:HG3	2.44	0.42
1:D:205:THR:O	1:D:209:LEU:HB2	2.18	0.42
1:W:63:PHE:HZ	1:W:78:LEU:HD21	1.83	0.42
1:W:65:VAL:CG2	1:W:66:ASP:N	2.82	0.42
1:X:92:LEU:O	1:X:93:PHE:C	2.63	0.42
1:Y:218:ASP:C	1:Y:220:HIS:N	2.77	0.42
1:A:53:GLU:O	1:A:54:ASN:C	2.63	0.42
1:A:293:LYS:O	1:A:295:TRP:N	2.52	0.42
1:B:13:LYS:O	1:B:17:GLU:HB2	2.19	0.42
1:B:39:MET:HG2	1:B:55:ARG:CD	2.50	0.42
1:B:40:GLY:O	1:B:44:GLN:N	2.52	0.42
1:B:106:ILE:HG12	1:B:137:TYR:CD1	2.55	0.42
1:B:274:MET:HE3	1:B:279:ALA:HA	2.02	0.42
1:C:121:GLU:O	1:C:122:THR:CG2	2.67	0.42
1:C:126:GLY:C	1:C:128:ASP:N	2.78	0.42
1:C:134:CYS:C	1:C:136:GLN:H	2.27	0.42
1:C:145:GLY:O	1:C:185:ILE:CG2	2.62	0.42
1:C:250:MET:SD	1:C:291:LEU:CD2	3.07	0.42
1:C:253:VAL:O	1:C:254:THR:C	2.63	0.42
1:C:275:SER:O	1:C:278:ASP:N	2.53	0.42
1:D:106:ILE:HG12	1:D:137:TYR:CE1	2.54	0.42
1:D:247:GLN:O	1:D:248:VAL:C	2.63	0.42
1:W:105:GLY:CA	1:W:144:PHE:CE1	3.03	0.42
1:W:166:ASN:N	1:W:166:ASN:HD22	2.17	0.42
1:X:283:LEU:O	1:X:283:LEU:HD12	2.19	0.42
1:Z:51:THR:CB	1:Z:54:ASN:HD22	2.32	0.42
1:A:87:ASP:C	1:A:89:GLN:H	2.28	0.42
1:A:92:LEU:C	1:A:94:ARG:H	2.27	0.42
1:B:131:SER:O	1:B:132:GLU:C	2.62	0.42
1:W:106:ILE:CG2	1:W:142:VAL:HG11	2.50	0.42
1:W:257:HIS:HA	1:W:295:TRP:HZ2	1.84	0.42
1:Y:65:VAL:HG23	1:Y:324:GLN:HB3	2.01	0.42
1:Y:247:GLN:C	1:Y:249:ALA:N	2.77	0.42
1:Y:281:LEU:HD21	1:Y:344:HIS:HD2	1.82	0.42
1:Y:339:LYS:C	1:Y:341:GLN:N	2.75	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:46:ILE:HG12	1:Z:314:GLY:HA2	2.01	0.42
1:A:147:TRP:CD1	1:A:147:TRP:C	2.98	0.42
1:A:199:GLU:OE1	1:A:243:TYR:OH	2.35	0.42
1:B:277:GLU:CD	1:B:344:HIS:CE1	2.97	0.42
1:C:214:LYS:HD3	1:D:214:LYS:HB2	2.02	0.42
1:C:247:GLN:C	1:C:249:ALA:N	2.77	0.42
1:D:65:VAL:CG2	1:D:66:ASP:N	2.83	0.42
1:D:244:THR:N	1:D:247:GLN:OE1	2.52	0.42
1:W:264:VAL:O	1:W:295:TRP:HB3	2.20	0.42
1:X:191:ILE:HA	1:X:192:PRO:HD2	1.79	0.42
1:Y:58:PHE:CE2	1:Y:310:LEU:HD13	2.55	0.42
1:Y:198:LEU:O	1:Y:199:GLU:C	2.62	0.42
1:Z:106:ILE:HG22	1:Z:142:VAL:HG11	2.02	0.42
1:B:51:THR:CB	1:B:54:ASN:ND2	2.82	0.42
1:B:244:THR:O	1:B:247:GLN:N	2.52	0.42
1:C:25:ASN:C	1:C:27:LYS:N	2.78	0.42
1:C:118:THR:HG23	1:C:121:GLU:HG3	2.01	0.42
1:D:33:ASP:HB2	1:D:107:LYS:HD2	2.01	0.42
1:W:173:TYR:CD1	1:W:173:TYR:C	2.97	0.42
1:X:254:THR:HA	1:X:257:HIS:CE1	2.54	0.42
1:Y:39:MET:HG2	1:Y:55:ARG:CD	2.49	0.42
1:Y:284:ASN:N	1:Y:337:ALA:HB1	2.35	0.42
1:Y:293:LYS:C	1:Y:295:TRP:H	2.28	0.42
1:Z:320:LYS:O	1:Z:324:GLN:HG3	2.20	0.42
1:A:169:ALA:O	1:A:170:LEU:C	2.63	0.41
1:B:126:GLY:N	1:B:147:TRP:HH2	2.17	0.41
1:D:166:ASN:N	1:D:166:ASN:HD22	2.18	0.41
1:W:221:VAL:CG1	1:W:222:TYR:N	2.82	0.41
1:X:257:HIS:HA	1:X:295:TRP:HZ2	1.85	0.41
1:Y:92:LEU:O	1:Y:95:ASN:N	2.51	0.41
1:Y:168:ASN:N	1:Y:168:ASN:HD22	2.17	0.41
1:Z:39:MET:HA	1:Z:39:MET:HE3	2.02	0.41
1:Z:189:GLU:OE1	1:Z:270:LEU:HD22	2.20	0.41
1:A:33:ASP:HB2	1:A:107:LYS:HD2	2.02	0.41
1:C:146:LYS:CG	1:C:147:TRP:H	2.29	0.41
1:D:253:VAL:O	1:D:254:THR:C	2.61	0.41
1:X:172:ARG:O	1:X:173:TYR:C	2.63	0.41
1:X:275:SER:O	1:X:278:ASP:N	2.53	0.41
1:X:284:ASN:O	1:X:285:ALA:C	2.62	0.41
1:Y:40:GLY:O	1:Y:44:GLN:N	2.53	0.41
1:Z:109:ASP:OD2	1:Z:109:ASP:C	2.62	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:244:THR:HG22	1:Z:247:GLN:CD	2.45	0.41
1:A:172:ARG:NH1	1:D:172:ARG:HH22	2.18	0.41
1:A:189:GLU:HG3	1:A:231:ASN:HB3	2.02	0.41
1:B:100:LYS:HE3	1:B:100:LYS:HB2	1.93	0.41
1:C:279:ALA:HB1	1:C:301:TYR:CE1	2.56	0.41
1:D:58:PHE:CZ	1:D:310:LEU:HD13	2.56	0.41
1:Y:146:LYS:HE2	1:Y:187:GLU:OE1	2.21	0.41
1:Z:7:LEU:HD21	1:Z:178:GLN:HB3	2.03	0.41
1:Z:257:HIS:HA	1:Z:295:TRP:HZ2	1.84	0.41
1:A:69:ILE:C	1:A:71:GLN:N	2.78	0.41
1:B:178:GLN:HE22	1:B:221:VAL:CG1	2.34	0.41
1:B:216:LEU:O	1:B:221:VAL:HG23	2.20	0.41
1:C:186:VAL:CG1	1:C:188:PRO:HD3	2.36	0.41
1:C:202:GLN:NE2	1:C:251:ALA:HA	2.36	0.41
1:D:173:TYR:CD1	1:D:173:TYR:C	2.96	0.41
1:W:82:THR:C	1:W:84:TYR:H	2.28	0.41
1:X:124:ILE:CG1	1:X:149:PRO:HA	2.50	0.41
1:X:178:GLN:HE21	1:X:178:GLN:HB3	1.64	0.41
1:X:244:THR:C	1:X:246:GLU:N	2.78	0.41
1:Y:51:THR:CG2	1:Y:52:GLU:H	2.24	0.41
1:Y:52:GLU:OE2	1:Y:85:GLN:NE2	2.54	0.41
1:Y:187:GLU:O	1:Y:187:GLU:HG2	2.18	0.41
1:Z:87:ASP:C	1:Z:89:GLN:H	2.28	0.41
1:Z:185:ILE:HD11	1:Z:229:LYS:HB2	2.03	0.41
1:A:28:GLY:HA3	1:A:299:PHE:CE1	2.56	0.41
1:B:130:LEU:O	1:B:133:ARG:HB3	2.21	0.41
1:C:254:THR:HA	1:C:257:HIS:CE1	2.55	0.41
1:W:89:GLN:CA	1:W:89:GLN:NE2	2.74	0.41
1:W:94:ARG:NH1	1:W:94:ARG:CG	2.82	0.41
1:W:106:ILE:O	1:W:106:ILE:CG2	2.65	0.41
1:B:48:VAL:CG1	1:B:49:GLU:N	2.83	0.41
1:B:279:ALA:HB1	1:B:301:TYR:CE1	2.55	0.41
1:D:234:THR:HG22	1:D:248:VAL:CG1	2.43	0.41
1:W:25:ASN:C	1:W:27:LYS:N	2.78	0.41
1:X:279:ALA:HB1	1:X:301:TYR:CE1	2.56	0.41
1:X:293:LYS:C	1:X:295:TRP:H	2.28	0.41
1:A:66:ASP:O	1:A:68:SER:N	2.53	0.41
1:A:80:HIS:HD2	1:A:137:TYR:OH	2.02	0.41
1:A:205:THR:O	1:A:209:LEU:HB2	2.21	0.41
1:A:216:LEU:HD23	1:A:221:VAL:CG2	2.34	0.41
1:B:134:CYS:C	1:B:136:GLN:H	2.29	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:180:ASN:C	1:B:182:LEU:H	2.27	0.41
1:C:31:ALA:HB3	1:C:302:GLY:CA	2.51	0.41
1:C:244:THR:HG22	1:C:247:GLN:HG3	2.01	0.41
1:D:127:LEU:HG	1:D:127:LEU:H	1.39	0.41
1:W:59:ARG:HD3	1:W:82:THR:HG23	2.02	0.41
1:W:243:TYR:N	1:W:243:TYR:CD1	2.88	0.41
1:X:123:THR:CG2	1:X:124:ILE:N	2.83	0.41
1:Y:93:PHE:O	1:Y:94:ARG:C	2.64	0.41
1:Z:53:GLU:O	1:Z:54:ASN:C	2.64	0.41
1:Z:143:ASP:C	1:Z:182:LEU:HG	2.45	0.41
1:B:138:LYS:HB2	1:B:182:LEU:HD11	2.03	0.41
1:B:159:SER:O	1:B:160:SER:C	2.63	0.41
1:C:56:ARG:CB	1:C:85:GLN:NE2	2.81	0.41
1:C:133:ARG:O	1:C:136:GLN:HB3	2.21	0.41
1:C:152:ARG:H	1:C:152:ARG:HG2	1.49	0.41
1:D:221:VAL:CG1	1:D:222:TYR:N	2.83	0.41
1:X:179:GLN:HE21	1:X:179:GLN:CA	2.27	0.41
1:X:332:MET:O	1:X:336:GLN:HG3	2.20	0.41
1:Y:200:HIS:O	1:Y:202:GLN:N	2.53	0.41
1:Y:283:LEU:O	1:Y:283:LEU:HD12	2.21	0.41
1:Z:66:ASP:C	1:Z:68:SER:N	2.78	0.41
1:Z:92:LEU:C	1:Z:94:ARG:H	2.27	0.41
1:Z:264:VAL:O	1:Z:295:TRP:HB3	2.20	0.41
1:A:39:MET:HA	1:A:39:MET:HE3	2.02	0.41
1:B:42:ARG:C	1:B:44:GLN:N	2.78	0.41
1:B:52:GLU:OE2	1:B:85:GLN:NE2	2.54	0.41
1:B:221:VAL:CG1	1:B:222:TYR:N	2.82	0.41
1:B:293:LYS:C	1:B:295:TRP:H	2.28	0.41
1:C:12:LYS:CD	1:C:222:TYR:CE1	3.02	0.41
1:C:33:ASP:HB2	1:C:107:LYS:HD2	2.03	0.41
1:C:92:LEU:O	1:C:93:PHE:C	2.62	0.41
1:C:149:PRO:HG2	1:C:188:PRO:HA	2.03	0.41
1:C:231:ASN:H	1:C:231:ASN:HD22	1.68	0.41
1:C:274:MET:CE	1:C:279:ALA:HA	2.51	0.41
1:C:320:LYS:O	1:C:324:GLN:HG3	2.21	0.41
1:D:147:TRP:HD1	1:D:148:ARG:N	2.17	0.41
1:D:216:LEU:CD2	1:D:221:VAL:HG11	2.51	0.41
1:D:283:LEU:HD11	1:D:297:LEU:O	2.21	0.41
1:X:52:GLU:HA	1:X:55:ARG:NH2	2.36	0.41
1:X:77:ILE:HA	1:X:105:GLY:HA3	2.03	0.41
1:X:86:LYS:HD3	1:X:90:GLY:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:87:ASP:OD1	1:X:87:ASP:N	2.54	0.41
1:Y:43:LEU:HB3	1:Y:48:VAL:HB	2.02	0.41
1:Y:182:LEU:N	1:Y:182:LEU:HD12	2.35	0.41
1:Y:259:THR:O	1:Y:261:PRO:HD3	2.20	0.41
1:Y:267:ILE:O	1:Y:267:ILE:HG22	2.21	0.41
1:Z:149:PRO:HG2	1:Z:149:PRO:O	2.21	0.41
1:Z:176:ILE:O	1:Z:179:GLN:N	2.52	0.41
1:Z:228:LEU:HD12	1:Z:229:LYS:N	2.36	0.41
1:Z:293:LYS:C	1:Z:295:TRP:H	2.28	0.41
1:A:25:ASN:C	1:A:27:LYS:N	2.78	0.41
1:A:151:LEU:C	1:A:152:ARG:HG3	2.46	0.41
1:D:82:THR:C	1:D:84:TYR:H	2.28	0.41
1:D:187:GLU:O	1:D:187:GLU:HG2	2.20	0.41
1:W:283:LEU:HD11	1:W:297:LEU:O	2.21	0.41
1:X:231:ASN:HA	1:X:270:LEU:HG	2.03	0.41
1:Y:32:ALA:CB	1:Y:63:PHE:HZ	2.33	0.41
1:Z:69:ILE:C	1:Z:71:GLN:N	2.79	0.41
1:A:56:ARG:HG2	1:A:56:ARG:NH1	2.35	0.40
1:A:264:VAL:O	1:A:295:TRP:HB3	2.21	0.40
1:B:25:ASN:C	1:B:27:LYS:N	2.79	0.40
1:B:218:ASP:C	1:B:220:HIS:N	2.78	0.40
1:C:11:GLN:O	1:C:15:LEU:HG	2.21	0.40
1:D:59:ARG:HD3	1:D:82:THR:HG23	2.02	0.40
1:D:105:GLY:N	1:D:144:PHE:HE1	2.19	0.40
1:X:247:GLN:O	1:X:250:MET:N	2.54	0.40
1:X:250:MET:HA	1:X:289:CYS:SG	2.61	0.40
1:Y:48:VAL:CG1	1:Y:49:GLU:N	2.82	0.40
1:A:31:ALA:HB3	1:A:302:GLY:CA	2.52	0.40
1:B:69:ILE:C	1:B:71:GLN:H	2.29	0.40
1:B:248:VAL:HG11	1:B:282:ASN:ND2	2.36	0.40
1:C:123:THR:C	1:C:124:ILE:HD13	2.45	0.40
1:C:221:VAL:HG12	1:C:222:TYR:H	1.86	0.40
1:D:63:PHE:HZ	1:D:78:LEU:HD21	1.86	0.40
1:D:340:GLY:C	1:D:341:GLN:HG3	2.46	0.40
1:X:11:GLN:O	1:X:15:LEU:HG	2.22	0.40
1:X:69:ILE:C	1:X:71:GLN:H	2.29	0.40
1:X:83:LEU:HD21	1:X:94:ARG:CD	2.52	0.40
1:Y:284:ASN:O	1:Y:285:ALA:C	2.64	0.40
1:Z:56:ARG:HG2	1:Z:56:ARG:NH1	2.37	0.40
1:A:35:SER:HB3	1:A:38:THR:OG1	2.20	0.40
1:A:66:ASP:C	1:A:68:SER:N	2.78	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:145:GLY:O	1:A:185:ILE:CG2	2.69	0.40
1:A:224:GLU:CD	1:B:258:ARG:HE	2.28	0.40
1:C:37:GLY:O	1:C:38:THR:C	2.64	0.40
1:C:51:THR:HB	1:C:54:ASN:ND2	2.36	0.40
1:C:216:LEU:HD23	1:C:221:VAL:HG11	2.04	0.40
1:W:271:SER:O	1:W:272:GLY:C	2.64	0.40
1:X:51:THR:HB	1:X:54:ASN:ND2	2.36	0.40
1:X:78:LEU:HD22	1:X:82:THR:CG2	2.51	0.40
1:X:127:LEU:HD12	1:X:127:LEU:N	2.34	0.40
1:X:133:ARG:O	1:X:137:TYR:CD2	2.74	0.40
1:Y:69:ILE:C	1:Y:71:GLN:H	2.29	0.40
1:Y:279:ALA:HB1	1:Y:301:TYR:CE1	2.56	0.40
1:A:161:LEU:HD22	1:D:219:HIS:HA	2.03	0.40
1:B:46:ILE:HG21	1:B:310:LEU:O	2.22	0.40
1:B:166:ASN:O	1:B:169:ALA:HB3	2.22	0.40
1:C:291:LEU:HA	1:C:291:LEU:HD13	1.88	0.40
1:W:46:ILE:HB	1:W:314:GLY:HA2	2.04	0.40
1:X:221:VAL:HG12	1:X:222:TYR:H	1.86	0.40
1:A:228:LEU:C	1:A:230:PRO:HD3	2.47	0.40
1:B:244:THR:O	1:B:245:PRO:C	2.62	0.40
1:B:284:ASN:N	1:B:337:ALA:HB1	2.36	0.40
1:B:291:LEU:HD13	1:B:291:LEU:HA	1.90	0.40
1:C:61:ILE:O	1:C:64:SER:N	2.55	0.40
1:D:67:SER:HA	1:D:100:LYS:HD3	2.03	0.40
1:W:129:GLY:C	1:W:131:SER:H	2.29	0.40
1:W:134:CYS:C	1:W:136:GLN:H	2.29	0.40
1:W:214:LYS:HB2	1:X:214:LYS:HD3	2.03	0.40
1:Y:33:ASP:HA	1:Y:79:PHE:HB2	2.03	0.40
1:Y:216:LEU:CD2	1:Y:221:VAL:HG11	2.51	0.40
1:Y:219:HIS:CD2	1:Y:219:HIS:N	2.89	0.40
1:Z:9:GLN:O	1:Z:10:GLU:C	2.64	0.40
1:Z:25:ASN:C	1:Z:27:LYS:N	2.79	0.40
1:Z:180:ASN:O	1:Z:182:LEU:N	2.55	0.40
1:Z:200:HIS:CD2	1:Z:200:HIS:C	3.00	0.40
1:Z:219:HIS:CD2	1:Z:219:HIS:N	2.89	0.40
1:Z:228:LEU:C	1:Z:230:PRO:HD3	2.46	0.40
1:Z:283:LEU:HD12	1:Z:283:LEU:O	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	293/365 (80%)	223 (76%)	55 (19%)	15 (5%)	1	10
1	B	289/365 (79%)	209 (72%)	59 (20%)	21 (7%)	1	4
1	C	321/365 (88%)	244 (76%)	57 (18%)	20 (6%)	1	6
1	D	287/365 (79%)	218 (76%)	51 (18%)	18 (6%)	1	6
1	W	286/365 (78%)	222 (78%)	47 (16%)	17 (6%)	1	7
1	X	323/365 (88%)	246 (76%)	56 (17%)	21 (6%)	1	5
1	Y	292/365 (80%)	214 (73%)	60 (20%)	18 (6%)	1	6
1	Z	291/365 (80%)	219 (75%)	55 (19%)	17 (6%)	1	8
All	All	2382/2920 (82%)	1795 (75%)	440 (18%)	147 (6%)	1	6

All (147) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	67	SER
1	A	149	PRO
1	A	233	VAL
1	B	67	SER
1	B	88	SER
1	B	186	VAL
1	B	269	PHE
1	C	67	SER
1	C	135	ALA
1	C	269	PHE
1	D	67	SER
1	D	127	LEU
1	D	167	ALA
1	D	342	TYR
1	W	67	SER
1	W	135	ALA
1	W	167	ALA

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Mol	Chain	Res	Type
1	X	67	SER
1	X	135	ALA
1	X	269	PHE
1	Y	67	SER
1	Y	135	ALA
1	Z	67	SER
1	A	88	SER
1	A	135	ALA
1	A	181	GLY
1	B	135	ALA
1	B	174	ALA
1	B	181	GLY
1	B	233	VAL
1	B	272	GLY
1	C	181	GLY
1	D	107	LYS
1	D	135	ALA
1	D	168	ASN
1	D	181	GLY
1	D	272	GLY
1	W	107	LYS
1	W	168	ASN
1	W	181	GLY
1	W	272	GLY
1	X	181	GLY
1	X	186	VAL
1	Y	88	SER
1	Y	174	ALA
1	Y	181	GLY
1	Y	188	PRO
1	Y	233	VAL
1	Y	269	PHE
1	Y	272	GLY
1	Z	88	SER
1	Z	127	LEU
1	Z	135	ALA
1	Z	149	PRO
1	Z	181	GLY
1	A	24	ALA
1	A	70	ASN
1	A	250	MET
1	A	272	GLY

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Mol	Chain	Res	Type
1	A	307	ALA
1	B	24	ALA
1	B	83	LEU
1	B	129	GLY
1	B	131	SER
1	B	147	TRP
1	B	250	MET
1	B	307	ALA
1	B	317	ALA
1	C	24	ALA
1	C	245	PRO
1	C	268	CYS
1	C	276	GLU
1	C	307	ALA
1	D	24	ALA
1	D	83	LEU
1	D	108	LEU
1	D	250	MET
1	D	307	ALA
1	W	24	ALA
1	W	160	SER
1	W	250	MET
1	W	307	ALA
1	X	24	ALA
1	X	131	SER
1	X	245	PRO
1	X	276	GLU
1	X	307	ALA
1	Y	24	ALA
1	Y	149	PRO
1	Y	199	GLU
1	Y	250	MET
1	Y	307	ALA
1	Z	24	ALA
1	Z	70	ASN
1	Z	163	ILE
1	Z	250	MET
1	Z	272	GLY
1	Z	307	ALA
1	Z	317	ALA
1	A	163	ILE
1	A	170	LEU

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Mol	Chain	Res	Type
1	A	294	PRO
1	A	317	ALA
1	B	66	ASP
1	C	100	LYS
1	C	250	MET
1	C	272	GLY
1	D	294	PRO
1	W	83	LEU
1	W	108	LEU
1	W	294	PRO
1	W	317	ALA
1	X	187	GLU
1	X	250	MET
1	X	272	GLY
1	X	317	ALA
1	Y	66	ASP
1	Y	83	LEU
1	Y	317	ALA
1	Z	294	PRO
1	C	70	ASN
1	C	147	TRP
1	C	198	LEU
1	C	317	ALA
1	D	317	ALA
1	W	147	TRP
1	X	100	LYS
1	X	268	CYS
1	Z	83	LEU
1	Z	170	LEU
1	Z	341	GLN
1	B	9	GLN
1	B	187	GLU
1	C	46	ILE
1	X	46	ILE
1	X	70	ASN
1	C	61	ILE
1	X	61	ILE
1	X	294	PRO
1	B	294	PRO
1	C	294	PRO
1	D	245	PRO
1	D	267	ILE

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Mol	Chain	Res	Type
1	W	267	ILE
1	X	192	PRO
1	Y	294	PRO
1	C	150	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	247/292 (85%)	226 (92%)	21 (8%)	10	36
1	B	242/292 (83%)	223 (92%)	19 (8%)	11	39
1	C	269/292 (92%)	245 (91%)	24 (9%)	9	34
1	D	241/292 (82%)	218 (90%)	23 (10%)	8	31
1	W	240/292 (82%)	221 (92%)	19 (8%)	11	39
1	X	268/292 (92%)	237 (88%)	31 (12%)	5	23
1	Y	245/292 (84%)	229 (94%)	16 (6%)	15	47
1	Z	245/292 (84%)	225 (92%)	20 (8%)	10	37
All	All	1997/2336 (86%)	1824 (91%)	173 (9%)	9	35

All (173) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	LEU
1	A	65	VAL
1	A	76	VAL
1	A	83	LEU
1	A	127	LEU
1	A	136	GLN
1	A	152	ARG
1	A	168	ASN
1	A	173	TYR
1	A	182	LEU
1	A	185	ILE

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Mol	Chain	Res	Type
1	A	209	LEU
1	A	216	LEU
1	A	226	THR
1	A	231	ASN
1	A	246	GLU
1	A	254	THR
1	A	291	LEU
1	A	295	TRP
1	A	303	ARG
1	A	330	ARG
1	B	7	LEU
1	B	49	GLU
1	B	66	ASP
1	B	94	ARG
1	B	104	VAL
1	B	127	LEU
1	B	128	ASP
1	B	136	GLN
1	B	170	LEU
1	B	189	GLU
1	B	202	GLN
1	B	216	LEU
1	B	226	THR
1	B	244	THR
1	B	254	THR
1	B	291	LEU
1	B	295	TRP
1	B	303	ARG
1	B	330	ARG
1	C	46	ILE
1	C	65	VAL
1	C	66	ASP
1	C	83	LEU
1	C	96	ILE
1	C	104	VAL
1	C	115	LEU
1	C	118	THR
1	C	136	GLN
1	C	151	LEU
1	C	152	ARG
1	C	173	TYR
1	C	176	ILE

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Mol	Chain	Res	Type
1	C	178	GLN
1	C	182	LEU
1	C	185	ILE
1	C	191	ILE
1	C	216	LEU
1	C	226	THR
1	C	254	THR
1	C	291	LEU
1	C	295	TRP
1	C	303	ARG
1	C	330	ARG
1	D	51	THR
1	D	83	LEU
1	D	89	GLN
1	D	96	ILE
1	D	99	GLU
1	D	109	ASP
1	D	127	LEU
1	D	136	GLN
1	D	164	GLN
1	D	173	TYR
1	D	179	GLN
1	D	209	LEU
1	D	216	LEU
1	D	226	THR
1	D	244	THR
1	D	254	THR
1	D	291	LEU
1	D	295	TRP
1	D	303	ARG
1	D	330	ARG
1	D	339	LYS
1	D	344	HIS
1	D	345	THR
1	W	51	THR
1	W	83	LEU
1	W	89	GLN
1	W	96	ILE
1	W	99	GLU
1	W	109	ASP
1	W	127	LEU
1	W	136	GLN

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Mol	Chain	Res	Type
1	W	164	GLN
1	W	173	TYR
1	W	179	GLN
1	W	209	LEU
1	W	216	LEU
1	W	226	THR
1	W	254	THR
1	W	291	LEU
1	W	295	TRP
1	W	303	ARG
1	W	330	ARG
1	X	7	LEU
1	X	46	ILE
1	X	65	VAL
1	X	66	ASP
1	X	83	LEU
1	X	96	ILE
1	X	104	VAL
1	X	115	LEU
1	X	118	THR
1	X	122	THR
1	X	125	GLN
1	X	136	GLN
1	X	152	ARG
1	X	153	ILE
1	X	173	TYR
1	X	176	ILE
1	X	178	GLN
1	X	182	LEU
1	X	185	ILE
1	X	199	GLU
1	X	216	LEU
1	X	226	THR
1	X	232	MET
1	X	233	VAL
1	X	243	TYR
1	X	245	PRO
1	X	254	THR
1	X	291	LEU
1	X	295	TRP
1	X	303	ARG
1	X	330	ARG

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Mol	Chain	Res	Type
1	Y	7	LEU
1	Y	49	GLU
1	Y	66	ASP
1	Y	94	ARG
1	Y	104	VAL
1	Y	136	GLN
1	Y	170	LEU
1	Y	202	GLN
1	Y	216	LEU
1	Y	226	THR
1	Y	254	THR
1	Y	291	LEU
1	Y	295	TRP
1	Y	303	ARG
1	Y	330	ARG
1	Y	343	VAL
1	Z	7	LEU
1	Z	65	VAL
1	Z	76	VAL
1	Z	83	LEU
1	Z	136	GLN
1	Z	149	PRO
1	Z	168	ASN
1	Z	173	TYR
1	Z	182	LEU
1	Z	185	ILE
1	Z	198	LEU
1	Z	209	LEU
1	Z	216	LEU
1	Z	226	THR
1	Z	246	GLU
1	Z	254	THR
1	Z	291	LEU
1	Z	295	TRP
1	Z	303	ARG
1	Z	330	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (123) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	ASN
1	A	44	GLN

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Mol	Chain	Res	Type
1	A	54	ASN
1	A	80	HIS
1	A	85	GLN
1	A	89	GLN
1	A	95	ASN
1	A	136	GLN
1	A	166	ASN
1	A	179	GLN
1	A	231	ASN
1	A	284	ASN
1	A	319	ASN
1	A	334	ASN
1	B	41	ASN
1	B	54	ASN
1	B	57	GLN
1	B	80	HIS
1	B	85	GLN
1	B	89	GLN
1	B	136	GLN
1	B	164	GLN
1	B	168	ASN
1	B	219	HIS
1	B	324	GLN
1	B	334	ASN
1	B	341	GLN
1	C	41	ASN
1	C	44	GLN
1	C	54	ASN
1	C	70	ASN
1	C	80	HIS
1	C	85	GLN
1	C	89	GLN
1	C	95	ASN
1	C	136	GLN
1	C	178	GLN
1	C	179	GLN
1	C	202	GLN
1	C	219	HIS
1	C	231	ASN
1	C	284	ASN
1	C	319	ASN
1	C	324	GLN

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Mol	Chain	Res	Type
1	C	334	ASN
1	D	41	ASN
1	D	80	HIS
1	D	89	GLN
1	D	136	GLN
1	D	164	GLN
1	D	166	ASN
1	D	168	ASN
1	D	179	GLN
1	D	219	HIS
1	D	284	ASN
1	D	306	GLN
1	D	319	ASN
1	D	334	ASN
1	D	341	GLN
1	W	41	ASN
1	W	54	ASN
1	W	80	HIS
1	W	89	GLN
1	W	136	GLN
1	W	164	GLN
1	W	166	ASN
1	W	168	ASN
1	W	179	GLN
1	W	219	HIS
1	W	306	GLN
1	W	319	ASN
1	W	334	ASN
1	X	41	ASN
1	X	44	GLN
1	X	54	ASN
1	X	70	ASN
1	X	80	HIS
1	X	85	GLN
1	X	89	GLN
1	X	95	ASN
1	X	110	GLN
1	X	119	ASN
1	X	125	GLN
1	X	136	GLN
1	X	178	GLN
1	X	179	GLN

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Mol	Chain	Res	Type
1	X	219	HIS
1	X	231	ASN
1	X	319	ASN
1	X	324	GLN
1	X	334	ASN
1	X	344	HIS
1	Y	41	ASN
1	Y	54	ASN
1	Y	57	GLN
1	Y	80	HIS
1	Y	85	GLN
1	Y	89	GLN
1	Y	136	GLN
1	Y	164	GLN
1	Y	168	ASN
1	Y	178	GLN
1	Y	219	HIS
1	Y	231	ASN
1	Y	324	GLN
1	Y	334	ASN
1	Y	344	HIS
1	Z	41	ASN
1	Z	44	GLN
1	Z	54	ASN
1	Z	80	HIS
1	Z	85	GLN
1	Z	89	GLN
1	Z	95	ASN
1	Z	136	GLN
1	Z	166	ASN
1	Z	179	GLN
1	Z	200	HIS
1	Z	202	GLN
1	Z	284	ASN
1	Z	319	ASN
1	Z	324	GLN
1	Z	334	ASN

5.3.3 RNA ⓘ

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](#)

8 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	SO4	A	364	-	4,4,4	0.41	0	6,6,6	0.12	0
2	SO4	B	364	-	4,4,4	0.42	0	6,6,6	0.12	0
2	SO4	W	364	-	4,4,4	0.37	0	6,6,6	0.11	0
2	SO4	X	364	-	4,4,4	0.38	0	6,6,6	0.16	0
2	SO4	C	365	-	4,4,4	0.39	0	6,6,6	0.13	0
2	SO4	C	364	-	4,4,4	0.40	0	6,6,6	0.19	0
2	SO4	Y	365	-	4,4,4	0.44	0	6,6,6	0.11	0
2	SO4	Y	364	-	4,4,4	0.41	0	6,6,6	0.10	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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

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	303/365 (83%)	-1.22	0 100 100	15, 74, 94, 94	0
1	B	299/365 (81%)	-1.34	0 100 100	1, 54, 89, 94	0
1	C	329/365 (90%)	-1.29	0 100 100	9, 65, 94, 94	0
1	D	297/365 (81%)	-1.28	0 100 100	5, 69, 94, 94	0
1	W	296/365 (81%)	-1.23	0 100 100	7, 68, 94, 94	0
1	X	329/365 (90%)	-1.27	0 100 100	7, 68, 94, 94	0
1	Y	302/365 (82%)	-1.27	0 100 100	1, 55, 89, 94	0
1	Z	301/365 (82%)	-1.22	0 100 100	16, 74, 94, 94	0
All	All	2456/2920 (84%)	-1.27	0 100 100	1, 66, 94, 94	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](#)

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($\text{\AA}^2$)	Q<0.9
2	SO4	W	364	5/5	0.96	0.04	93,93,93,93	0
2	SO4	C	365	5/5	0.97	0.06	93,93,93,93	0
2	SO4	B	364	5/5	0.97	0.05	93,93,93,93	0
2	SO4	A	364	5/5	0.98	0.03	93,93,93,93	0
2	SO4	C	364	5/5	0.98	0.07	93,93,93,93	0
2	SO4	Y	364	5/5	0.98	0.03	93,93,93,93	0
2	SO4	Y	365	5/5	0.98	0.05	93,93,93,93	0
2	SO4	X	364	5/5	0.99	0.04	93,93,93,93	0

6.5 Other polymers [i](#)

There are no such residues in this entry.