



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:01 PM UTC

PDB ID : 1M3E / pdb_00001m3e
Title : Succinyl-CoA:3-ketoacid COA transferase from pig heart (selenomethionine)
Authors : Bateman, K.S.; Brownie, E.R.; Wolodko, W.T.; Fraser, M.E.
Deposited on : 2002-06-27
Resolution : 2.50 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

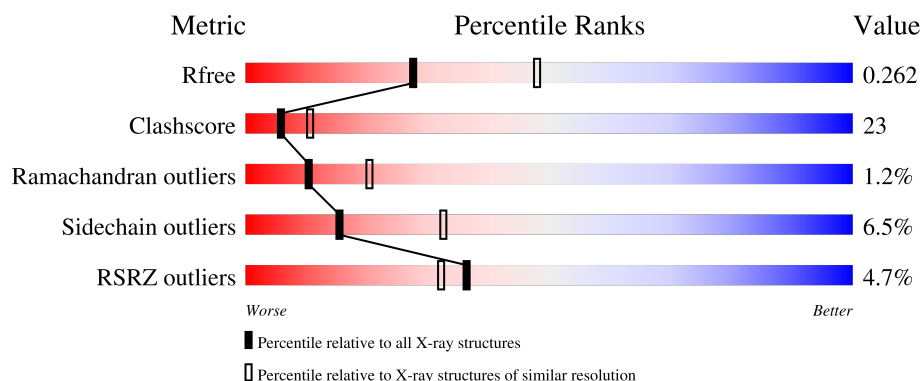
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	481	6% 57% 37% 5%
1	B	481	4% 60% 34% 5%
1	C	481	3% 61% 31% 6%
1	D	481	5% 57% 35% 5%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 15308 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 SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	472	Total	C	N	O	S	Se	0	1	0
			3607	2284	616	689	5	13			
1	B	473	Total	C	N	O	S	Se	0	2	0
			3616	2288	620	690	5	13			
1	C	473	Total	C	N	O	S	Se	0	3	0
			3619	2289	620	692	5	13			
1	D	472	Total	C	N	O	S	Se	0	1	0
			3607	2284	616	689	5	13			

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	72	MSE	MET	modified residue	UNP Q29551
A	195	MSE	MET	modified residue	UNP Q29551
A	278	MSE	MET	modified residue	UNP Q29551
A	298	MSE	MET	modified residue	UNP Q29551
A	349	MSE	MET	modified residue	UNP Q29551
A	359	MSE	MET	modified residue	UNP Q29551
A	363	MSE	MET	modified residue	UNP Q29551
A	375	MSE	MET	modified residue	UNP Q29551
A	384	MSE	MET	modified residue	UNP Q29551
A	388	MSE	MET	modified residue	UNP Q29551
A	402	MSE	MET	modified residue	UNP Q29551
A	414	MSE	MET	modified residue	UNP Q29551
A	476	MSE	MET	modified residue	UNP Q29551
B	72	MSE	MET	modified residue	UNP Q29551
B	195	MSE	MET	modified residue	UNP Q29551
B	278	MSE	MET	modified residue	UNP Q29551
B	298	MSE	MET	modified residue	UNP Q29551
B	349	MSE	MET	modified residue	UNP Q29551
B	359	MSE	MET	modified residue	UNP Q29551
B	363	MSE	MET	modified residue	UNP Q29551

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	375	MSE	MET	modified residue	UNP Q29551
B	384	MSE	MET	modified residue	UNP Q29551
B	388	MSE	MET	modified residue	UNP Q29551
B	402	MSE	MET	modified residue	UNP Q29551
B	414	MSE	MET	modified residue	UNP Q29551
B	476	MSE	MET	modified residue	UNP Q29551
C	72	MSE	MET	modified residue	UNP Q29551
C	195	MSE	MET	modified residue	UNP Q29551
C	278	MSE	MET	modified residue	UNP Q29551
C	298	MSE	MET	modified residue	UNP Q29551
C	349	MSE	MET	modified residue	UNP Q29551
C	359	MSE	MET	modified residue	UNP Q29551
C	363	MSE	MET	modified residue	UNP Q29551
C	375	MSE	MET	modified residue	UNP Q29551
C	384	MSE	MET	modified residue	UNP Q29551
C	388	MSE	MET	modified residue	UNP Q29551
C	402	MSE	MET	modified residue	UNP Q29551
C	414	MSE	MET	modified residue	UNP Q29551
C	476	MSE	MET	modified residue	UNP Q29551
D	72	MSE	MET	modified residue	UNP Q29551
D	195	MSE	MET	modified residue	UNP Q29551
D	278	MSE	MET	modified residue	UNP Q29551
D	298	MSE	MET	modified residue	UNP Q29551
D	349	MSE	MET	modified residue	UNP Q29551
D	359	MSE	MET	modified residue	UNP Q29551
D	363	MSE	MET	modified residue	UNP Q29551
D	375	MSE	MET	modified residue	UNP Q29551
D	384	MSE	MET	modified residue	UNP Q29551
D	388	MSE	MET	modified residue	UNP Q29551
D	402	MSE	MET	modified residue	UNP Q29551
D	414	MSE	MET	modified residue	UNP Q29551
D	476	MSE	MET	modified residue	UNP Q29551

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	167	Total O 167 167	0	0
2	B	269	Total O 269 269	0	0
2	C	256	Total O 256 256	0	0

Continued on next page...

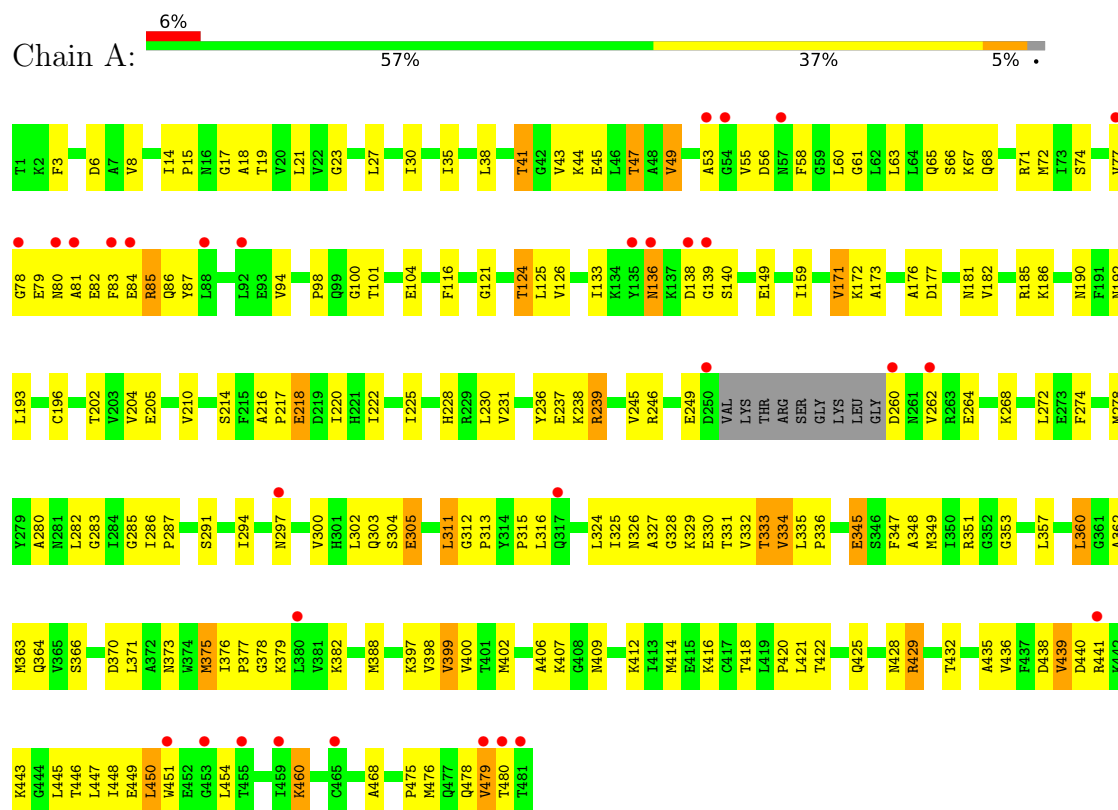
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	167	Total 167	O 167	0	0

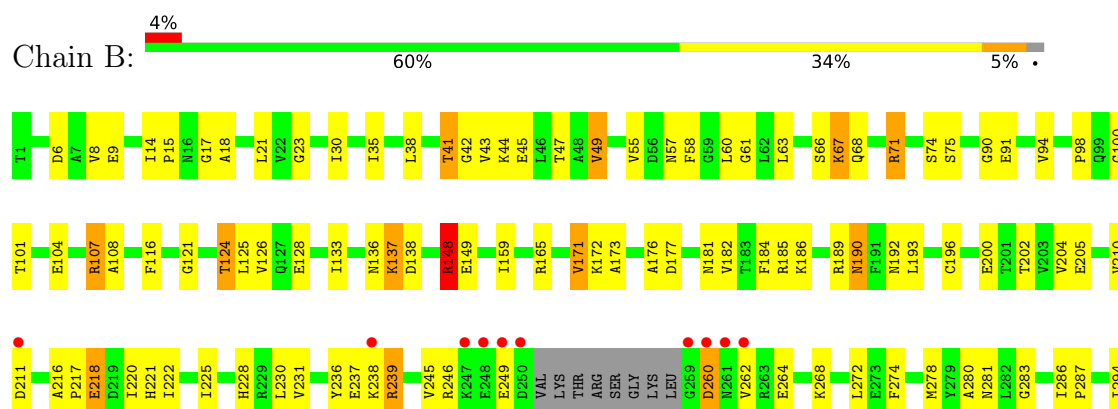
3 Residue-property plots

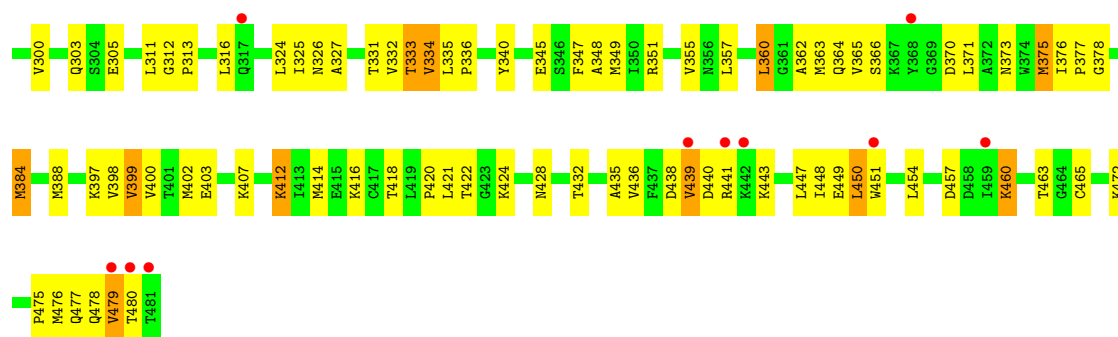
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

• Molecule 1: SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE

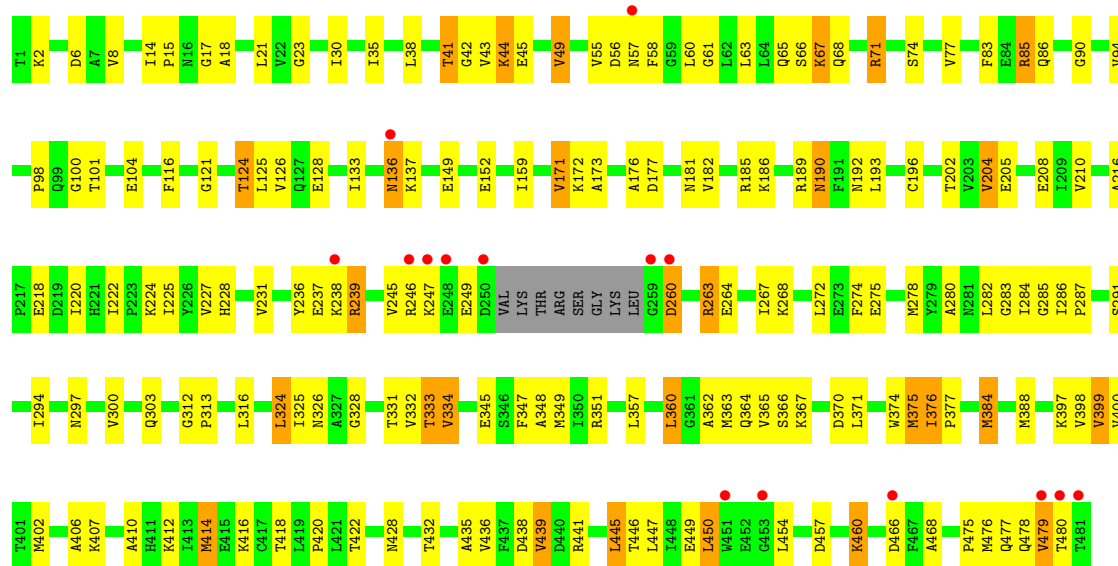


• Molecule 1: SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE

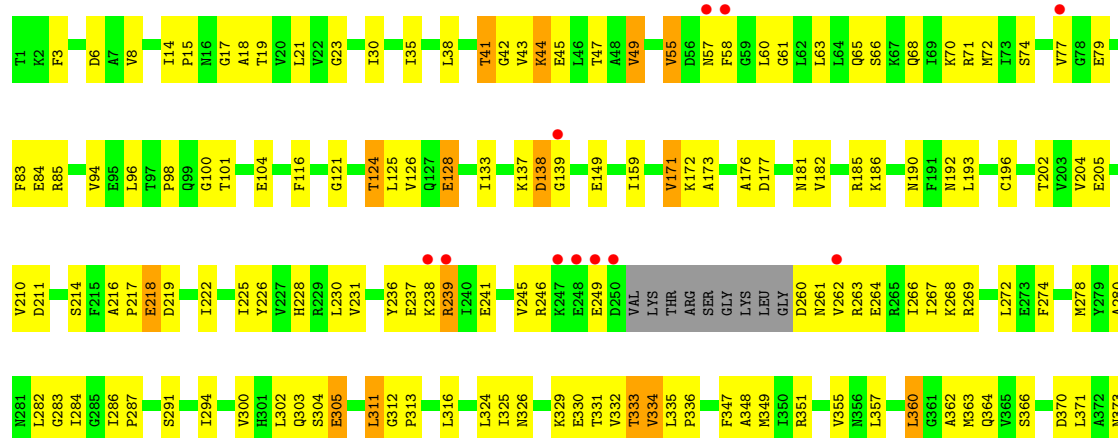


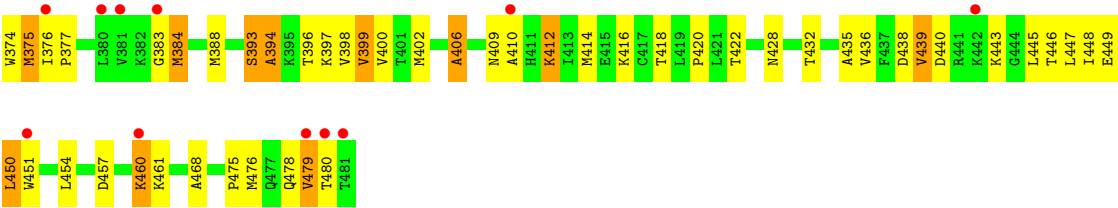


• Molecule 1: SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE



• Molecule 1: SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	60.17Å 264.32Å 62.69Å 90.00° 111.88° 90.00°	Depositor
Resolution (Å)	30.00 – 2.50 30.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	96.7 (30.00-2.50) 96.6 (30.00-2.50)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	8.17 (at 2.51Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.221 , 0.265 0.219 , 0.262	Depositor DCC
R_{free} test set	3199 reflections (5.31%)	wwPDB-VP
Wilson B-factor (Å ²)	21.2	Xtriage
Anisotropy	1.094	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 45.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.033 for l,-k,h	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	15308	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.20% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.42	0/3657	1.01	21/4913 (0.4%)
1	B	0.44	0/3672	1.00	15/4932 (0.3%)
1	C	0.41	0/3680	0.96	13/4943 (0.3%)
1	D	0.41	0/3656	0.95	11/4912 (0.2%)
All	All	0.42	0/14665	0.98	60/19700 (0.3%)

There are no bond length outliers.

All (60) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	71	ARG	NE-CZ-NH2	-11.40	108.94	119.20
1	B	148	ARG	NE-CZ-NH2	-10.94	109.36	119.20
1	A	71	ARG	CD-NE-CZ	10.43	139.00	124.40
1	A	480	THR	N-CA-C	-10.42	100.57	113.28
1	D	480	THR	N-CA-C	-10.38	100.61	113.28
1	C	480	THR	N-CA-C	-10.36	100.64	113.28
1	B	480	THR	N-CA-C	-10.29	100.73	113.28
1	B	148	ARG	CD-NE-CZ	10.25	138.75	124.40
1	C	348	ALA	N-CA-C	-9.75	100.73	111.36
1	A	71	ARG	NE-CZ-NH1	9.57	131.07	121.50
1	B	348	ALA	N-CA-C	-9.57	100.93	111.36
1	A	348	ALA	N-CA-C	-9.46	101.05	111.36
1	B	148	ARG	NE-CZ-NH1	9.34	130.84	121.50
1	D	348	ALA	N-CA-C	-9.02	101.53	111.36
1	A	139	GLY	N-CA-C	-8.65	103.69	114.16
1	A	429	ARG	NE-CZ-NH2	-8.19	111.83	119.20
1	C	44	LYS	N-CA-C	7.44	119.74	109.18
1	B	438	ASP	N-CA-C	-7.25	97.86	109.76
1	C	438	ASP	N-CA-C	-7.25	97.86	109.76
1	A	438	ASP	N-CA-C	-7.25	97.87	109.76
1	D	438	ASP	N-CA-C	-7.14	97.59	109.24
1	A	429	ARG	NE-CZ-NH1	6.96	128.46	121.50
1	A	285	GLY	N-CA-C	6.77	119.47	111.35

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	422	THR	N-CA-C	-6.67	105.30	113.50
1	C	316	LEU	N-CA-C	-6.64	101.96	110.53
1	A	316	LEU	N-CA-C	-6.62	101.99	110.53
1	D	216	ALA	N-CA-C	-6.58	101.36	109.65
1	B	316	LEU	N-CA-C	-6.58	102.05	110.53
1	D	316	LEU	N-CA-C	-6.50	102.14	110.53
1	C	422	THR	N-CA-C	-6.46	105.56	113.50
1	A	422	THR	N-CA-C	-6.39	105.64	113.50
1	B	422	THR	N-CA-C	-6.39	105.64	113.50
1	A	216	ALA	N-CA-C	-6.26	101.77	109.65
1	A	429	ARG	CD-NE-CZ	6.23	133.12	124.40
1	B	216	ALA	N-CA-C	-6.22	101.82	109.65
1	C	182	VAL	N-CA-C	6.17	117.36	108.48
1	B	182	VAL	N-CA-C	6.06	117.21	108.48
1	D	182	VAL	N-CA-C	5.98	117.10	108.48
1	C	376	ILE	N-CA-C	-5.96	102.25	108.15
1	A	182	VAL	N-CA-C	5.86	116.92	108.48
1	B	44	LYS	N-CA-C	5.80	118.04	109.69
1	A	376	ILE	N-CA-C	-5.71	102.50	108.15
1	C	216	ALA	N-CA-C	-5.66	101.04	109.42
1	A	412	LYS	N-CA-C	-5.65	106.93	113.88
1	B	376	ILE	N-CA-C	-5.58	102.63	108.15
1	D	376	ILE	N-CA-C	-5.54	102.66	108.15
1	D	412	LYS	N-CA-C	-5.50	107.11	113.88
1	B	412	LYS	N-CA-C	-5.50	107.12	113.88
1	A	44	LYS	N-CA-C	5.48	116.96	109.18
1	A	71	ARG	CG-CD-NE	-5.45	100.02	112.00
1	A	375	MSE	N-CA-C	5.38	118.16	108.48
1	C	412	LYS	N-CA-C	-5.37	107.28	113.88
1	B	421	LEU	N-CA-C	5.27	117.93	110.50
1	D	375	MSE	N-CA-C	5.25	117.92	108.48
1	A	421	LEU	N-CA-C	5.23	117.87	110.50
1	C	285	GLY	N-CA-C	5.22	117.87	111.45
1	C	375	MSE	N-CA-C	5.15	117.74	108.48
1	C	414	MSE	N-CA-C	5.10	115.26	108.38
1	B	375	MSE	N-CA-C	5.09	117.64	108.48
1	D	44	LYS	N-CA-C	5.04	117.52	109.81

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3607	0	3665	174	0
1	B	3616	0	3673	175	0
1	C	3619	0	3669	170	0
1	D	3607	0	3663	171	0
2	A	167	0	0	8	0
2	B	269	0	0	22	0
2	C	256	0	0	18	0
2	D	167	0	0	12	0
All	All	15308	0	14670	672	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 23.

All (672) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:436:VAL:HG23	1:B:476:MSE:HE2	1.38	1.06
1:D:436:VAL:HG23	1:D:476:MSE:HE2	1.38	1.05
1:A:436:VAL:HG23	1:A:476:MSE:HE2	1.39	1.04
1:C:436:VAL:HG23	1:C:476:MSE:HE2	1.40	1.04
1:A:332:VAL:HG12	1:A:333:THR:H	1.24	0.99
1:D:366:SER:HB3	1:D:370:ASP:HB2	1.45	0.98
1:D:406:ALA:HB3	1:D:410:ALA:HB3	1.47	0.95
1:D:332:VAL:HG12	1:D:333:THR:H	1.28	0.95
1:B:272:LEU:HD21	1:B:479:VAL:HG11	1.49	0.95
1:B:366:SER:HB3	1:B:370:ASP:HB2	1.49	0.95
1:C:238:LYS:HA	2:C:617:HOH:O	1.66	0.95
1:C:85:ARG:HH12	1:C:86:GLN:HG3	1.33	0.94
1:C:445:LEU:HD23	1:C:445:LEU:H	1.32	0.94
1:C:278:MSE:HE3	1:C:280:ALA:HB2	1.50	0.93
1:A:272:LEU:HD21	1:A:479:VAL:HG11	1.51	0.93
1:D:446:THR:HG21	2:D:648:HOH:O	1.68	0.93
1:B:278:MSE:HE3	1:B:280:ALA:HB2	1.49	0.93
1:D:272:LEU:HD21	1:D:479:VAL:HG11	1.51	0.93
1:C:375:MSE:HE2	1:C:420:PRO:HG3	1.50	0.93

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:278:MSE:HE3	1:D:280:ALA:HB2	1.50	0.92
1:A:278:MSE:HE3	1:A:280:ALA:HB2	1.49	0.92
1:B:375:MSE:HE2	1:B:420:PRO:HG3	1.49	0.92
1:A:366:SER:HB3	1:A:370:ASP:HB2	1.48	0.91
1:D:375:MSE:HE2	1:D:420:PRO:HG3	1.51	0.91
1:B:137:LYS:H	1:B:137:LYS:HD2	1.35	0.91
1:C:272:LEU:HD21	1:C:479:VAL:HG11	1.51	0.91
1:C:366:SER:HB3	1:C:370:ASP:HB2	1.50	0.91
1:D:446:THR:HG22	1:D:468:ALA:HB3	1.54	0.89
1:A:78:GLY:HA2	1:A:382:LYS:HE2	1.53	0.88
1:A:375:MSE:HE2	1:A:420:PRO:HG3	1.54	0.88
1:B:41:THR:HG22	1:B:43:VAL:H	1.38	0.88
1:B:313:PRO:O	1:B:333:THR:HB	1.75	0.87
1:D:41:THR:HG22	1:D:43:VAL:H	1.40	0.86
1:D:313:PRO:O	1:D:333:THR:HB	1.76	0.86
1:C:41:THR:HG22	1:C:43:VAL:H	1.39	0.86
1:A:278:MSE:HE1	1:A:357:LEU:HD23	1.57	0.86
1:B:171:VAL:HG22	1:B:204:VAL:HG22	1.59	0.85
1:A:41:THR:HG22	1:A:43:VAL:H	1.40	0.84
1:C:303:GLN:HG3	1:C:349:MSE:HE2	1.56	0.84
1:B:107[A]:ARG:HH12	1:B:108:ALA:HB2	1.42	0.84
1:D:303:GLN:HG3	1:D:349:MSE:HE2	1.59	0.84
1:C:406:ALA:HB3	1:C:410:ALA:HB3	1.56	0.84
1:B:101:THR:HG21	2:B:577:HOH:O	1.78	0.84
1:B:332:VAL:HG12	1:B:333:THR:N	1.91	0.84
1:A:313:PRO:O	1:A:333:THR:HB	1.77	0.83
1:A:81:ALA:O	1:A:85:ARG:HB2	1.77	0.83
1:C:313:PRO:O	1:C:333:THR:HB	1.77	0.83
1:C:278:MSE:HE1	1:C:357:LEU:HD23	1.59	0.83
1:A:171:VAL:HG22	1:A:204:VAL:HG22	1.61	0.83
1:A:303:GLN:HG3	1:A:349:MSE:HE2	1.60	0.82
1:C:363:MSE:HE1	1:C:376:ILE:HD11	1.60	0.82
1:B:278:MSE:HE1	1:B:357:LEU:HD23	1.61	0.81
1:A:202:THR:H	1:A:228:HIS:HD2	1.26	0.81
1:A:332:VAL:HG12	1:A:333:THR:N	1.96	0.81
1:D:65:GLN:HG2	2:D:619:HOH:O	1.80	0.81
1:D:278:MSE:HE1	1:D:357:LEU:HD23	1.60	0.81
1:C:171:VAL:HG22	1:C:204:VAL:HB	1.61	0.81
1:B:202:THR:H	1:B:228:HIS:HD2	1.27	0.81
1:C:225:ILE:HD13	1:D:349:MSE:HE3	1.63	0.80
1:D:263:ARG:HD3	2:D:632:HOH:O	1.80	0.80

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:202:THR:H	1:C:228:HIS:HD2	1.24	0.80
1:B:202:THR:H	1:B:228:HIS:CD2	2.00	0.80
1:C:225:ILE:CD1	1:D:349:MSE:HE3	2.12	0.79
1:D:202:THR:H	1:D:228:HIS:HD2	1.27	0.79
1:D:177:ASP:HA	1:D:210:VAL:O	1.83	0.79
1:B:303:GLN:HG3	1:B:349:MSE:HE2	1.65	0.79
1:C:202:THR:H	1:C:228:HIS:CD2	1.99	0.79
1:A:202:THR:H	1:A:228:HIS:CD2	2.00	0.79
1:C:324:LEU:HD22	1:C:332:VAL:HG23	1.65	0.79
1:D:202:THR:H	1:D:228:HIS:CD2	2.01	0.78
1:C:446:THR:HG22	1:C:468:ALA:HB3	1.66	0.78
1:D:30:ILE:HG22	2:D:559:HOH:O	1.84	0.78
1:A:441:ARG:HG2	1:A:441:ARG:HH11	1.49	0.77
1:C:349:MSE:HE3	1:D:225:ILE:CD1	2.14	0.77
1:A:225:ILE:HD13	1:B:349:MSE:HE3	1.66	0.77
1:A:445:LEU:H	1:A:445:LEU:HD23	1.49	0.77
1:A:19:THR:HA	1:A:47:THR:HG23	1.66	0.77
1:A:218[B]:GLU:CD	1:B:189:ARG:HH21	1.91	0.76
1:A:225:ILE:CD1	1:B:349:MSE:HE3	2.14	0.76
1:A:303:GLN:HG3	1:A:349:MSE:CE	2.15	0.76
1:C:349:MSE:HE3	1:D:225:ILE:HD13	1.66	0.76
1:D:366:SER:CB	1:D:370:ASP:HB2	2.16	0.76
1:B:332:VAL:HG12	1:B:333:THR:H	1.47	0.75
1:C:136:ASN:H	1:C:136:ASN:HD22	1.34	0.75
1:A:349:MSE:HE3	1:B:225:ILE:HD13	1.66	0.75
1:B:332:VAL:CG1	1:B:333:THR:H	1.98	0.75
1:A:82:GLU:O	1:A:86:GLN:HG3	1.86	0.75
1:A:366:SER:CB	1:A:370:ASP:HB2	2.17	0.75
1:D:445:LEU:H	1:D:445:LEU:HD23	1.51	0.74
1:C:124:THR:O	1:C:128:GLU:HG2	1.86	0.74
1:D:171:VAL:HG22	1:D:204:VAL:HG22	1.70	0.74
1:D:96:LEU:HB3	1:D:384:MSE:HE3	1.69	0.73
1:B:366:SER:CB	1:B:370:ASP:HB2	2.18	0.73
1:B:90:GLY:HA2	2:B:576:HOH:O	1.89	0.73
1:A:363:MSE:HE2	1:A:373:ASN:HA	1.70	0.72
1:D:303:GLN:HG3	1:D:349:MSE:CE	2.18	0.72
1:A:104:GLU:HG2	2:A:599:HOH:O	1.89	0.72
1:C:366:SER:CB	1:C:370:ASP:HB2	2.19	0.71
1:A:349:MSE:HE3	1:B:225:ILE:CD1	2.19	0.71
1:B:332:VAL:CG1	1:B:333:THR:N	2.54	0.71
1:C:41:THR:HG21	2:C:614:HOH:O	1.91	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:274:PHE:HD1	1:A:278:MSE:HE2	1.56	0.71
1:B:41:THR:HG21	2:B:692:HOH:O	1.88	0.71
1:D:124:THR:O	1:D:128:GLU:HG2	1.91	0.70
1:B:30:ILE:HD11	1:B:58:PHE:CE2	2.27	0.70
1:A:85:ARG:HH11	1:A:85:ARG:HB3	1.57	0.70
1:D:332:VAL:HG12	1:D:333:THR:N	2.05	0.70
1:C:445:LEU:HD23	1:C:445:LEU:N	2.05	0.70
1:C:30:ILE:HD11	1:C:58:PHE:CE2	2.27	0.69
1:D:104:GLU:HG2	2:D:611:HOH:O	1.90	0.69
1:A:87:TYR:O	2:A:613:HOH:O	2.08	0.69
1:B:274:PHE:HD1	1:B:278:MSE:HE2	1.56	0.69
1:C:85:ARG:NH1	1:C:86:GLN:HG3	2.06	0.69
1:A:441:ARG:HD3	2:A:519:HOH:O	1.91	0.69
1:A:30:ILE:HD11	1:A:58:PHE:CE2	2.28	0.69
1:D:30:ILE:HD11	1:D:58:PHE:CE2	2.28	0.69
1:A:278:MSE:HE1	1:A:357:LEU:CD2	2.23	0.69
1:A:27:LEU:HD21	1:A:55:VAL:HG23	1.74	0.68
1:C:274:PHE:HD1	1:C:278:MSE:HE2	1.58	0.68
1:C:124:THR:CG2	1:C:126:VAL:H	2.06	0.68
1:A:53:ALA:CB	1:A:83:PHE:HD2	2.07	0.68
1:A:177:ASP:HA	1:A:210:VAL:O	1.95	0.68
1:A:124:THR:CG2	1:A:126:VAL:H	2.06	0.67
1:B:124:THR:CG2	1:B:126:VAL:H	2.06	0.67
1:C:284:ILE:HD11	1:C:328:GLY:HA3	1.75	0.67
1:A:171:VAL:CG2	1:A:204:VAL:HG22	2.24	0.67
1:D:274:PHE:HD1	1:D:278:MSE:HE2	1.59	0.67
1:D:278:MSE:HE1	1:D:357:LEU:CD2	2.24	0.67
1:C:303:GLN:HG3	1:C:349:MSE:CE	2.25	0.67
1:C:278:MSE:HE1	1:C:357:LEU:CD2	2.23	0.67
1:B:41:THR:CG2	1:B:43:VAL:H	2.07	0.66
1:B:326:ASN:HB3	1:B:332:VAL:HG21	1.76	0.66
1:C:41:THR:CG2	1:C:43:VAL:H	2.08	0.66
1:B:278:MSE:HE1	1:B:357:LEU:CD2	2.26	0.66
1:A:41:THR:CG2	1:A:43:VAL:H	2.09	0.66
1:B:104:GLU:HG2	2:B:593:HOH:O	1.94	0.66
1:D:326:ASN:HB3	1:D:332:VAL:HG21	1.78	0.66
1:D:357:LEU:HD12	1:D:397:LYS:O	1.96	0.66
1:A:83:PHE:C	1:A:83:PHE:HD1	2.04	0.65
1:B:171:VAL:CG2	1:B:204:VAL:HG22	2.25	0.65
1:C:90:GLY:HA2	2:C:681:HOH:O	1.95	0.65
1:D:35:ILE:HG23	1:D:63:LEU:HD13	1.79	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:332:VAL:CG1	1:A:333:THR:H	2.03	0.65
1:B:67:LYS:HD3	1:B:67:LYS:N	2.12	0.65
1:B:17:GLY:HA2	1:B:45:GLU:O	1.96	0.65
1:A:83:PHE:C	1:A:83:PHE:CD1	2.75	0.65
1:C:171:VAL:CG2	1:C:204:VAL:HB	2.27	0.65
1:C:202:THR:N	1:C:228:HIS:HD2	1.96	0.64
1:B:35:ILE:HG23	1:B:63:LEU:HD13	1.80	0.64
1:D:41:THR:CG2	1:D:43:VAL:H	2.10	0.64
1:B:283:GLY:O	1:B:287:PRO:HG2	1.98	0.64
1:D:19:THR:HA	1:D:47:THR:HG23	1.80	0.64
1:C:238:LYS:HE2	2:C:485:HOH:O	1.98	0.64
1:B:272:LEU:HD21	1:B:479:VAL:CG1	2.26	0.63
1:D:366:SER:HB3	1:D:370:ASP:CB	2.26	0.63
1:D:124:THR:CG2	1:D:126:VAL:H	2.12	0.63
1:A:85:ARG:HB3	1:A:85:ARG:NH1	2.12	0.63
1:B:185:ARG:HG2	1:B:186:LYS:HG2	1.81	0.63
1:B:124:THR:HG22	1:B:126:VAL:H	1.64	0.63
1:D:185:ARG:NH1	2:D:586:HOH:O	2.29	0.63
1:C:85:ARG:HH12	1:C:86:GLN:CG	2.09	0.62
1:D:66:SER:OG	1:D:68:GLN:HG3	1.99	0.62
1:D:302:LEU:O	1:D:311:LEU:HD23	1.99	0.62
1:A:202:THR:N	1:A:228:HIS:HD2	1.97	0.62
1:B:440:ASP:OD2	1:B:443:LYS:HG2	1.99	0.62
1:A:272:LEU:HD21	1:A:479:VAL:CG1	2.28	0.62
1:C:185:ARG:HG2	1:C:186:LYS:HG2	1.82	0.62
1:C:35:ILE:HG23	1:C:63:LEU:HD13	1.80	0.62
1:B:311:LEU:HD22	1:B:332:VAL:HG11	1.80	0.62
1:A:124:THR:HG22	1:A:126:VAL:H	1.63	0.62
1:B:460:LYS:HB2	1:B:460:LYS:NZ	2.15	0.62
1:C:460:LYS:NZ	1:C:460:LYS:HB2	2.15	0.62
1:A:27:LEU:HD11	1:A:55:VAL:HG21	1.82	0.62
1:A:364:GLN:HE22	1:A:418:THR:HB	1.65	0.62
1:B:238:LYS:HE2	2:B:492:HOH:O	1.98	0.62
1:C:124:THR:HG22	1:C:126:VAL:H	1.64	0.61
1:C:435:ALA:C	1:C:476:MSE:HE1	2.24	0.61
1:C:364:GLN:HE22	1:C:418:THR:HB	1.66	0.61
1:D:185:ARG:HG2	1:D:186:LYS:HG2	1.82	0.61
1:A:357:LEU:HD11	1:A:399:VAL:CG1	2.31	0.61
1:D:357:LEU:HD11	1:D:399:VAL:CG1	2.30	0.61
1:A:17:GLY:HA2	1:A:45:GLU:O	1.99	0.61
1:A:441:ARG:HG2	1:A:441:ARG:NH1	2.15	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:202:THR:N	1:B:228:HIS:HD2	1.98	0.61
1:A:217:PRO:HG2	1:A:218[A]:GLU:OE1	2.01	0.61
1:A:260:ASP:OD2	1:A:262:VAL:HG22	1.99	0.61
1:A:326:ASN:HB3	1:A:332:VAL:HG21	1.82	0.61
1:A:345:GLU:HG2	2:A:600:HOH:O	2.00	0.61
1:A:460:LYS:HB2	1:A:460:LYS:NZ	2.16	0.61
1:A:435:ALA:C	1:A:476:MSE:HE1	2.26	0.61
1:D:435:ALA:C	1:D:476:MSE:HE1	2.26	0.61
1:D:98:PRO:HG2	1:D:101:THR:HB	1.82	0.61
1:D:375:MSE:HE3	1:D:377:PRO:HG3	1.82	0.61
1:B:137:LYS:H	1:B:137:LYS:CD	2.09	0.61
1:C:357:LEU:HD11	1:C:399:VAL:CG1	2.31	0.61
1:D:202:THR:N	1:D:228:HIS:HD2	1.97	0.61
1:D:364:GLN:HE22	1:D:418:THR:HB	1.65	0.61
1:A:98:PRO:HG2	1:A:101:THR:HB	1.83	0.60
1:D:460:LYS:HB2	1:D:460:LYS:NZ	2.15	0.60
1:A:35:ILE:HG23	1:A:63:LEU:HD13	1.82	0.60
1:D:272:LEU:HD21	1:D:479:VAL:CG1	2.28	0.60
1:D:393:SER:OG	1:D:396:THR:HB	2.02	0.60
1:D:446:THR:HG23	2:D:582:HOH:O	2.00	0.60
1:B:200:GLU:HG2	2:B:739:HOH:O	2.00	0.60
1:B:435:ALA:C	1:B:476:MSE:HE1	2.26	0.60
1:D:17:GLY:HA2	1:D:45:GLU:O	2.00	0.60
1:D:332:VAL:CG1	1:D:333:THR:H	2.09	0.60
1:A:185:ARG:HG2	1:A:186:LYS:HG2	1.82	0.60
1:B:357:LEU:HD11	1:B:399:VAL:CG1	2.31	0.59
1:D:335:LEU:HB3	1:D:336:PRO:HD2	1.83	0.59
1:A:366:SER:HB3	1:A:370:ASP:CB	2.28	0.59
1:B:137:LYS:HD2	1:B:137:LYS:N	2.13	0.59
1:B:238:LYS:HB3	2:B:744:HOH:O	2.02	0.59
1:D:55:VAL:HG22	2:D:609:HOH:O	2.01	0.59
1:A:78:GLY:CA	1:A:382:LYS:HE2	2.29	0.59
1:B:107[A]:ARG:NH1	1:B:108:ALA:N	2.50	0.59
1:C:272:LEU:HD21	1:C:479:VAL:CG1	2.28	0.59
1:D:311:LEU:HD23	1:D:311:LEU:H	1.67	0.59
1:C:17:GLY:HA2	1:C:45:GLU:O	2.03	0.59
1:C:66:SER:OG	1:C:68:GLN:HG3	2.01	0.59
1:C:152:GLU:HG3	2:C:720:HOH:O	2.03	0.59
1:B:66:SER:OG	1:B:68:GLN:HG3	2.02	0.59
1:B:357:LEU:HD12	1:B:397:LYS:O	2.02	0.59
1:D:393:SER:O	1:D:394:ALA:HB2	2.03	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:375:MSE:HE3	1:B:377:PRO:HG3	1.84	0.59
1:B:364:GLN:HE22	1:B:418:THR:HB	1.68	0.58
1:B:378:GLY:HA2	2:B:665:HOH:O	2.01	0.58
1:C:375:MSE:HE3	1:C:377:PRO:HG3	1.85	0.58
1:D:446:THR:CG2	1:D:468:ALA:HB3	2.29	0.58
1:B:366:SER:HB3	1:B:370:ASP:CB	2.28	0.58
1:A:66:SER:OG	1:A:68:GLN:HG3	2.03	0.58
1:A:283:GLY:O	1:A:287:PRO:HG2	2.03	0.58
1:D:283:GLY:O	1:D:287:PRO:HG2	2.02	0.58
1:A:274:PHE:CD1	1:A:278:MSE:HE2	2.39	0.58
1:B:332:VAL:HG12	1:B:333:THR:O	2.03	0.58
1:B:75:SER:O	1:B:384:MSE:HE2	2.04	0.58
1:C:366:SER:HB3	1:C:370:ASP:CB	2.29	0.58
1:A:210:VAL:HG22	1:A:214:SER:OG	2.04	0.58
1:B:124:THR:HG23	1:B:125:LEU:N	2.19	0.58
1:C:312:GLY:HA3	1:C:333:THR:HG22	1.85	0.58
1:B:274:PHE:CD1	1:B:278:MSE:HE2	2.38	0.58
1:D:217:PRO:HG2	1:D:218:GLU:OE1	2.04	0.57
1:A:72:MSE:HE2	1:A:83:PHE:CE2	2.39	0.57
1:D:436:VAL:HB	1:D:449:GLU:HB2	1.87	0.57
1:B:303:GLN:CG	1:B:349:MSE:HE2	2.33	0.57
1:D:193:LEU:HG	1:D:222:ILE:HD11	1.86	0.57
1:B:424:LYS:HE2	2:B:537:HOH:O	2.03	0.57
1:C:124:THR:HG23	1:C:125:LEU:N	2.19	0.57
1:D:124:THR:HG21	1:D:388:MSE:SE	2.54	0.57
1:B:472:LYS:HG3	2:B:716:HOH:O	2.05	0.57
1:C:104:GLU:HB3	1:C:116:PHE:CZ	2.39	0.57
1:D:3:PHE:CE2	1:D:230:LEU:HD23	2.39	0.57
1:C:136:ASN:H	1:C:136:ASN:ND2	2.02	0.57
1:C:283:GLY:O	1:C:287:PRO:HG2	2.05	0.57
1:C:324:LEU:HD22	1:C:332:VAL:CG2	2.32	0.57
1:C:177:ASP:HA	1:C:210:VAL:O	2.05	0.56
1:A:193:LEU:HG	1:A:222:ILE:HD11	1.86	0.56
1:C:367:LYS:HG3	1:C:445:LEU:CD2	2.36	0.56
1:C:436:VAL:HB	1:C:449:GLU:HB2	1.88	0.56
1:B:104:GLU:HB3	1:B:116:PHE:CZ	2.39	0.56
1:B:312:GLY:HA3	1:B:333:THR:HG22	1.86	0.56
1:A:53:ALA:HB2	1:A:83:PHE:CD2	2.41	0.56
1:C:15:PRO:HG2	1:C:18:ALA:HB2	1.87	0.56
1:C:176:ALA:HA	1:C:181:ASN:O	2.06	0.56
1:A:124:THR:HG23	1:A:125:LEU:N	2.19	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218[B]:GLU:OE2	1:B:189:ARG:NH2	2.36	0.55
1:A:104:GLU:HB3	1:A:116:PHE:CZ	2.42	0.55
1:A:436:VAL:HB	1:A:449:GLU:HB2	1.89	0.55
1:A:445:LEU:HD23	1:A:445:LEU:N	2.21	0.55
1:D:460:LYS:HB2	1:D:460:LYS:HZ2	1.72	0.55
1:C:98:PRO:HG2	1:C:101:THR:HB	1.87	0.55
1:D:104:GLU:HB3	1:D:116:PHE:CZ	2.41	0.55
1:B:15:PRO:HG2	1:B:18:ALA:HB2	1.87	0.55
1:B:193:LEU:HG	1:B:222:ILE:HD11	1.88	0.55
1:D:124:THR:HG22	1:D:126:VAL:H	1.70	0.55
1:D:176:ALA:HA	1:D:181:ASN:O	2.07	0.55
1:A:15:PRO:HG2	1:A:18:ALA:HB2	1.89	0.55
1:B:165:ARG:NH1	2:B:739:HOH:O	2.39	0.55
1:C:136:ASN:ND2	1:C:136:ASN:N	2.55	0.55
1:C:274:PHE:CD1	1:C:278:MSE:HE2	2.40	0.55
1:B:436:VAL:HB	1:B:449:GLU:HB2	1.89	0.54
1:A:80:ASN:O	1:A:84:GLU:HG2	2.07	0.54
1:B:101:THR:HG22	2:B:637:HOH:O	2.05	0.54
1:D:274:PHE:CD1	1:D:278:MSE:HE2	2.41	0.54
1:A:363:MSE:HE2	1:A:373:ASN:CA	2.36	0.54
1:A:55:VAL:HG12	1:A:56:ASP:H	1.73	0.54
1:C:193:LEU:HG	1:C:222:ILE:HD11	1.88	0.54
1:C:239:ARG:NE	2:C:723:HOH:O	2.32	0.54
1:C:445:LEU:HD23	2:C:644:HOH:O	2.07	0.54
1:A:378:GLY:O	1:A:379:LYS:HD2	2.07	0.54
1:A:225:ILE:HD12	1:B:349:MSE:HE3	1.88	0.54
1:A:446:THR:HG22	1:A:468:ALA:HB3	1.89	0.54
1:A:311:LEU:H	1:A:311:LEU:HD23	1.73	0.54
1:D:124:THR:HG23	1:D:125:LEU:N	2.22	0.54
1:A:55:VAL:HG12	1:A:56:ASP:N	2.22	0.54
1:C:260:ASP:O	1:C:264:GLU:HB2	2.08	0.54
1:D:15:PRO:HG2	1:D:18:ALA:HB2	1.90	0.53
1:C:94:VAL:O	1:C:133:ILE:HA	2.08	0.53
1:A:305:GLU:HG3	1:A:327:ALA:HB2	1.89	0.53
1:A:335:LEU:HB3	1:A:336:PRO:HD2	1.90	0.53
1:A:357:LEU:HD11	1:A:399:VAL:HG13	1.91	0.53
1:C:384:MSE:H	1:C:384:MSE:SE	2.41	0.53
1:D:241:GLU:OE1	1:D:329:LYS:HE3	2.08	0.53
1:C:326:ASN:HB3	1:C:332:VAL:HG11	1.91	0.53
1:C:363:MSE:CE	1:C:376:ILE:HD11	2.36	0.53
1:D:94:VAL:O	1:D:133:ILE:HA	2.09	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:171:VAL:CG2	1:D:204:VAL:HG22	2.36	0.53
1:B:107[A]:ARG:HH12	1:B:108:ALA:CB	2.18	0.53
1:B:124:THR:O	1:B:128:GLU:HG2	2.09	0.53
1:A:138:ASP:HB2	1:A:140:SER:OG	2.09	0.53
1:B:94:VAL:O	1:B:133:ILE:HA	2.09	0.53
1:B:57:ASN:ND2	1:B:239:ARG:HH21	2.06	0.53
1:A:94:VAL:O	1:A:133:ILE:HA	2.09	0.53
1:A:294:ILE:HD13	1:A:300:VAL:HG21	1.90	0.53
1:B:294:ILE:HD13	1:B:300:VAL:HG21	1.90	0.53
1:C:349:MSE:HE3	1:D:225:ILE:HD12	1.88	0.53
1:D:260:ASP:OD2	1:D:262:VAL:HG22	2.09	0.53
1:A:218[B]:GLU:OE2	1:B:221:HIS:CE1	2.61	0.52
1:B:176:ALA:HA	1:B:181:ASN:O	2.09	0.52
1:C:55:VAL:CG1	1:C:56:ASP:N	2.71	0.52
1:A:53:ALA:CB	1:A:83:PHE:CD2	2.91	0.52
1:A:205:GLU:HA	1:A:231:VAL:O	2.10	0.52
1:C:420:PRO:HA	2:C:611:HOH:O	2.09	0.52
1:A:124:THR:HG22	1:A:126:VAL:N	2.24	0.52
1:A:176:ALA:HA	1:A:181:ASN:O	2.08	0.52
1:B:260:ASP:O	1:B:264:GLU:HB2	2.09	0.52
1:B:357:LEU:HD11	1:B:399:VAL:HG13	1.91	0.52
1:B:9:GLU:HG3	2:B:678:HOH:O	2.09	0.52
1:D:226:TYR:HA	2:D:639:HOH:O	2.08	0.52
1:B:281:ASN:HD21	1:B:305[B]:GLU:CD	2.17	0.52
1:C:225:ILE:HD12	1:D:349:MSE:HE3	1.87	0.52
1:D:383:GLY:O	1:D:384:MSE:HB3	2.10	0.52
1:D:406:ALA:HA	1:D:412:LYS:HE3	1.91	0.52
1:B:363:MSE:HE3	1:B:373:ASN:HA	1.92	0.52
1:C:238:LYS:HD3	2:C:617:HOH:O	2.09	0.52
1:C:357:LEU:HD11	1:C:399:VAL:HG13	1.92	0.52
1:B:57:ASN:HD21	1:B:239:ARG:HH21	1.56	0.52
1:D:294:ILE:HD13	1:D:300:VAL:HG21	1.91	0.52
1:B:272:LEU:CD2	1:B:479:VAL:HG11	2.33	0.51
1:B:326:ASN:HB2	2:B:553:HOH:O	2.08	0.51
1:D:333:THR:HG23	1:D:334:VAL:N	2.26	0.51
1:C:435:ALA:CA	1:C:476:MSE:HE1	2.41	0.51
1:D:57:ASN:O	1:D:57:ASN:ND2	2.43	0.51
1:D:357:LEU:HD11	1:D:399:VAL:HG13	1.91	0.51
1:B:176:ALA:HB1	1:B:230:LEU:HD21	1.92	0.51
1:D:260:ASP:O	1:D:264:GLU:HB2	2.10	0.51
1:A:260:ASP:O	1:A:264:GLU:HB2	2.09	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:294:ILE:HD13	1:C:300:VAL:HG21	1.92	0.51
1:D:30:ILE:HD11	1:D:58:PHE:HE2	1.75	0.51
1:B:177:ASP:HA	1:B:210:VAL:O	2.11	0.51
1:B:124:THR:HG22	1:B:126:VAL:N	2.25	0.51
1:B:305[A]:GLU:HG2	1:B:327:ALA:HB2	1.93	0.51
1:C:55:VAL:HG12	1:C:56:ASP:N	2.24	0.51
1:C:124:THR:HG21	1:C:388:MSE:SE	2.61	0.51
1:B:347:PHE:O	1:B:351:ARG:HB2	2.11	0.51
1:B:435:ALA:CA	1:B:476:MSE:HE1	2.41	0.51
1:C:124:THR:HG22	1:C:126:VAL:N	2.24	0.51
1:B:211:ASP:OD1	1:B:211:ASP:N	2.45	0.50
1:D:138:ASP:CG	1:D:139:GLY:H	2.19	0.50
1:B:333:THR:HG23	1:B:334:VAL:N	2.27	0.50
1:B:384:MSE:HE2	1:B:384:MSE:H	1.76	0.50
1:D:375:MSE:HE2	1:D:420:PRO:CG	2.34	0.50
1:A:450:LEU:HD21	1:A:454:LEU:HB2	1.94	0.50
1:A:27:LEU:HD11	1:A:55:VAL:CG2	2.41	0.50
1:C:445:LEU:N	1:C:445:LEU:CD2	2.74	0.50
1:D:312:GLY:HA3	1:D:333:THR:HG22	1.94	0.50
1:A:302:LEU:O	1:A:311:LEU:HD23	2.11	0.50
1:C:204:VAL:CG1	1:C:227:VAL:HG13	2.41	0.50
1:A:30:ILE:HD11	1:A:58:PHE:HE2	1.76	0.50
1:B:148:ARG:NH2	2:B:688:HOH:O	2.38	0.49
1:C:460:LYS:HB2	1:C:460:LYS:HZ2	1.76	0.49
1:D:172:LYS:HE3	1:D:236:TYR:CE1	2.47	0.49
1:D:393:SER:O	1:D:394:ALA:CB	2.60	0.49
1:A:333:THR:HG23	1:A:334:VAL:N	2.26	0.49
1:B:55:VAL:O	1:B:61:GLY:HA3	2.13	0.49
1:C:333:THR:HG23	1:C:334:VAL:N	2.28	0.49
1:C:347:PHE:O	1:C:351:ARG:HB2	2.12	0.49
1:A:312:GLY:HA3	1:A:333:THR:HG22	1.94	0.49
1:A:347:PHE:O	1:A:351:ARG:HB2	2.11	0.49
1:C:374:TRP:CE3	1:C:384:MSE:HG3	2.48	0.49
1:A:402:MSE:O	1:A:432:THR:HA	2.13	0.49
1:A:435:ALA:HB1	1:A:447:LEU:CD1	2.42	0.49
1:D:402:MSE:O	1:D:432:THR:HA	2.12	0.49
1:A:83:PHE:C	1:A:85:ARG:N	2.69	0.49
1:A:333:THR:CG2	1:A:334:VAL:N	2.75	0.49
1:C:67:LYS:HD3	1:C:67:LYS:N	2.28	0.49
1:C:435:ALA:HB1	1:C:447:LEU:CD1	2.43	0.49
1:D:450:LEU:HD21	1:D:454:LEU:HB2	1.94	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:375:MSE:HE3	1:A:377:PRO:HG3	1.94	0.49
1:C:23:GLY:HA3	1:C:192:ASN:OD1	2.13	0.49
1:D:84:GLU:HG3	1:D:85:ARG:N	2.27	0.49
1:D:347:PHE:O	1:D:351:ARG:HB2	2.13	0.49
1:A:121:GLY:O	1:A:124:THR:HB	2.13	0.49
1:C:205:GLU:HA	1:C:231:VAL:O	2.13	0.49
1:C:275:GLU:HG2	2:C:520:HOH:O	2.13	0.49
1:D:333:THR:CG2	1:D:334:VAL:N	2.75	0.49
1:B:294:ILE:CD1	1:B:300:VAL:HG21	2.43	0.48
1:B:366:SER:OG	2:B:634:HOH:O	2.20	0.48
1:C:136:ASN:HD22	1:C:136:ASN:N	1.97	0.48
1:D:363:MSE:HE3	1:D:373:ASN:HA	1.95	0.48
1:D:478:GLN:O	1:D:479:VAL:HG13	2.13	0.48
1:D:23:GLY:HA3	1:D:192:ASN:OD1	2.14	0.48
1:A:3:PHE:CE2	1:A:230:LEU:HD23	2.49	0.48
1:C:478:GLN:O	1:C:479:VAL:HG13	2.14	0.48
1:D:205:GLU:HA	1:D:231:VAL:O	2.12	0.48
1:A:375:MSE:HE2	1:A:420:PRO:CG	2.37	0.48
1:B:124:THR:CG2	1:B:125:LEU:N	2.77	0.48
1:C:30:ILE:HD11	1:C:58:PHE:HE2	1.76	0.48
1:C:124:THR:CG2	1:C:125:LEU:N	2.77	0.48
1:D:435:ALA:HB1	1:D:447:LEU:CD1	2.43	0.48
1:A:100:GLY:HA2	1:A:347:PHE:CG	2.49	0.48
1:B:402:MSE:O	1:B:432:THR:HA	2.13	0.48
1:B:407:LYS:NZ	2:B:532:HOH:O	2.47	0.48
1:C:245:VAL:HG12	1:C:246:ARG:N	2.29	0.48
1:C:333:THR:CG2	1:C:334:VAL:N	2.76	0.48
1:A:294:ILE:CD1	1:A:300:VAL:HG21	2.44	0.48
1:B:23:GLY:HA3	1:B:192:ASN:OD1	2.13	0.48
1:B:121:GLY:O	1:B:124:THR:HB	2.14	0.48
1:B:205:GLU:HA	1:B:231:VAL:O	2.13	0.48
1:C:21:LEU:HD23	1:C:49:VAL:HG13	1.96	0.48
1:C:98:PRO:HD3	1:C:384:MSE:CE	2.43	0.48
1:A:21:LEU:HD23	1:A:49:VAL:HG13	1.96	0.48
1:A:55:VAL:O	1:A:61:GLY:HA3	2.14	0.48
1:B:333:THR:CG2	1:B:334:VAL:N	2.76	0.48
1:C:57:ASN:O	1:C:57:ASN:ND2	2.47	0.48
1:C:414:MSE:HE2	1:C:416:LYS:O	2.14	0.48
1:D:457:ASP:OD2	1:D:461:LYS:HE3	2.14	0.48
1:B:30:ILE:HD11	1:B:58:PHE:HE2	1.75	0.48
1:B:6:ASP:OD1	1:B:8:VAL:HB	2.14	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:121:GLY:O	1:C:124:THR:HB	2.14	0.47
1:C:367:LYS:HG3	1:C:445:LEU:HD21	1.94	0.47
1:D:77:VAL:HG11	1:D:83:PHE:CZ	2.49	0.47
1:A:124:THR:CG2	1:A:125:LEU:N	2.77	0.47
1:C:196:CYS:SG	1:C:202:THR:HG21	2.54	0.47
1:D:100:GLY:HA2	1:D:347:PHE:CG	2.49	0.47
1:C:435:ALA:C	1:C:476:MSE:CE	2.87	0.47
1:D:435:ALA:C	1:D:476:MSE:CE	2.87	0.47
1:A:478:GLN:O	1:A:479:VAL:HG13	2.14	0.47
1:B:245:VAL:HG12	1:B:246:ARG:N	2.29	0.47
1:B:450:LEU:HD21	1:B:454:LEU:HB2	1.97	0.47
1:D:124:THR:HG22	1:D:126:VAL:N	2.29	0.47
1:D:211:ASP:OD1	1:D:211:ASP:N	2.48	0.47
1:D:428:ASN:C	1:D:439:VAL:HG13	2.39	0.47
1:D:435:ALA:CA	1:D:476:MSE:HE1	2.44	0.47
1:A:245:VAL:HG12	1:A:246:ARG:N	2.29	0.47
1:A:328:GLY:O	1:A:329:LYS:HB2	2.15	0.47
1:A:435:ALA:CA	1:A:476:MSE:HE1	2.45	0.47
1:B:441:ARG:HD2	2:B:740:HOH:O	2.13	0.47
1:C:441:ARG:HG3	2:C:697:HOH:O	2.13	0.47
1:D:210:VAL:HG22	1:D:214:SER:OG	2.14	0.47
1:D:374:TRP:CZ3	1:D:384:MSE:HE2	2.49	0.47
1:B:435:ALA:C	1:B:476:MSE:CE	2.87	0.47
1:D:294:ILE:CD1	1:D:300:VAL:HG21	2.45	0.47
1:B:21:LEU:HD23	1:B:49:VAL:HG13	1.96	0.47
1:C:98:PRO:HD3	1:C:384:MSE:HE1	1.97	0.47
1:C:450:LEU:HD21	1:C:454:LEU:HB2	1.97	0.47
1:A:406:ALA:O	1:A:407:LYS:C	2.58	0.47
1:A:428:ASN:C	1:A:439:VAL:HG13	2.40	0.47
1:D:268:LYS:O	1:D:479:VAL:HG22	2.15	0.47
1:C:100:GLY:HA2	1:C:347:PHE:CG	2.50	0.46
1:C:402:MSE:O	1:C:432:THR:HA	2.15	0.46
1:C:441:ARG:HB3	1:C:441:ARG:NH1	2.30	0.46
1:D:21:LEU:HD23	1:D:49:VAL:HG13	1.98	0.46
1:A:349:MSE:HE3	1:B:225:ILE:HD12	1.96	0.46
1:A:357:LEU:HD12	1:A:397:LYS:O	2.15	0.46
1:B:237:GLU:OE1	1:B:239:ARG:NH1	2.49	0.46
1:D:284:ILE:HG22	2:D:610:HOH:O	2.15	0.46
1:B:355:VAL:HB	2:B:715:HOH:O	2.14	0.46
1:D:355:VAL:HB	2:D:612:HOH:O	2.15	0.46
1:B:435:ALA:HB1	1:B:447:LEU:CD1	2.45	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:441:ARG:CB	1:C:441:ARG:HH11	2.29	0.46
1:A:304:SER:HB2	1:A:311:LEU:HD22	1.96	0.46
1:B:124:THR:HG21	1:B:388:MSE:SE	2.65	0.46
1:B:268:LYS:O	1:B:479:VAL:HG22	2.16	0.46
1:B:375:MSE:HE2	1:B:420:PRO:CG	2.34	0.46
1:B:478:GLN:O	1:B:479:VAL:HG13	2.15	0.46
1:C:237:GLU:OE1	1:C:239:ARG:NH1	2.49	0.46
1:D:138:ASP:CG	1:D:139:GLY:N	2.74	0.46
1:D:245:VAL:HG12	1:D:246:ARG:N	2.31	0.46
1:D:263:ARG:O	1:D:267:ILE:HG13	2.16	0.46
1:A:65:GLN:HG2	2:A:528:HOH:O	2.16	0.46
1:C:272:LEU:CD2	1:C:479:VAL:HG11	2.35	0.46
1:C:294:ILE:CD1	1:C:300:VAL:HG21	2.45	0.46
1:D:124:THR:CG2	1:D:125:LEU:N	2.79	0.46
1:A:60:LEU:CD2	1:A:72:MSE:SE	3.15	0.45
1:C:55:VAL:O	1:C:61:GLY:HA3	2.16	0.45
1:C:428:ASN:C	1:C:439:VAL:HG13	2.41	0.45
1:A:6:ASP:OD1	1:A:8:VAL:HB	2.16	0.45
1:A:218[B]:GLU:OE2	1:B:184:PHE:O	2.35	0.45
1:A:435:ALA:C	1:A:476:MSE:CE	2.88	0.45
1:C:268:LYS:O	1:C:479:VAL:HG22	2.15	0.45
1:A:124:THR:HG21	1:A:388:MSE:SE	2.65	0.45
1:B:414:MSE:HE2	1:B:416:LYS:O	2.16	0.45
1:B:440:ASP:CG	1:B:443:LYS:HG2	2.41	0.45
1:C:172:LYS:HE3	1:C:236:TYR:CE1	2.51	0.45
1:A:124:THR:HG23	1:A:126:VAL:H	1.82	0.45
1:B:104:GLU:O	1:B:107[A]:ARG:NH1	2.50	0.45
1:C:42:GLY:O	1:C:44:LYS:HG3	2.16	0.45
1:C:124:THR:HG23	1:C:126:VAL:H	1.81	0.45
1:D:196:CYS:SG	1:D:202:THR:HG21	2.57	0.45
1:A:237:GLU:OE1	1:A:239:ARG:NH1	2.50	0.45
1:C:272:LEU:HD11	1:C:479:VAL:HG13	1.99	0.45
1:A:397:LYS:HD2	2:A:592:HOH:O	2.16	0.45
1:D:450:LEU:HD23	1:D:451:TRP:N	2.32	0.45
1:D:57:ASN:O	1:D:57:ASN:CG	2.60	0.45
1:B:100:GLY:HA2	1:B:347:PHE:CG	2.52	0.45
1:A:353:GLY:HA2	2:A:559:HOH:O	2.17	0.44
1:B:365:VAL:HG21	1:B:400:VAL:HG21	2.00	0.44
1:D:72:MSE:HE2	1:D:83:PHE:CE2	2.52	0.44
1:B:176:ALA:CB	1:B:230:LEU:HD21	2.48	0.44
1:C:477:GLN:NE2	2:C:515:HOH:O	2.49	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:172:LYS:HE3	1:A:236:TYR:CE1	2.52	0.44
1:A:196:CYS:SG	1:A:202:THR:HG21	2.57	0.44
1:C:38:LEU:HD12	1:C:63:LEU:HD21	1.99	0.44
1:D:237:GLU:OE1	1:D:239:ARG:NH1	2.50	0.44
1:A:14:ILE:HD12	1:A:38:LEU:HD21	1.99	0.44
1:A:450:LEU:HD23	1:A:451:TRP:N	2.32	0.44
1:B:137:LYS:CD	1:B:137:LYS:N	2.77	0.44
1:D:414:MSE:HE2	1:D:416:LYS:O	2.17	0.44
1:D:446:THR:HG22	2:D:628:HOH:O	2.17	0.44
1:B:60:LEU:HB2	2:B:544:HOH:O	2.17	0.44
1:B:196:CYS:SG	1:B:202:THR:HG21	2.58	0.44
1:C:104:GLU:HG2	1:C:351:ARG:HH22	1.82	0.44
1:C:224:LYS:NZ	2:C:510:HOH:O	2.48	0.44
1:C:237:GLU:O	1:C:238:LYS:C	2.61	0.44
1:C:357:LEU:HD12	1:C:397:LYS:O	2.17	0.44
1:D:237:GLU:O	1:D:238:LYS:C	2.59	0.44
1:D:450:LEU:O	1:D:475:PRO:HA	2.18	0.44
1:A:268:LYS:O	1:A:479:VAL:HG22	2.17	0.44
1:A:360:LEU:O	1:A:400:VAL:HA	2.17	0.44
1:A:414:MSE:HE2	1:A:416:LYS:O	2.17	0.44
1:C:450:LEU:O	1:C:475:PRO:HA	2.17	0.44
1:B:124:THR:HG23	1:B:126:VAL:H	1.81	0.44
1:C:362:ALA:HB2	1:C:371:LEU:HD11	2.00	0.44
1:D:326:ASN:CB	1:D:332:VAL:HG21	2.47	0.44
1:D:362:ALA:HB2	1:D:371:LEU:HD11	2.00	0.44
1:B:38:LEU:HD12	1:B:63:LEU:HD21	1.99	0.44
1:B:325:ILE:HG22	1:B:331:THR:HA	2.00	0.44
1:B:360:LEU:O	1:B:400:VAL:HA	2.18	0.44
1:B:384:MSE:H	1:B:384:MSE:SE	2.50	0.44
1:A:460:LYS:HB2	1:A:460:LYS:HZ3	1.81	0.43
1:A:38:LEU:HD12	1:A:63:LEU:HD21	2.00	0.43
1:B:428:ASN:C	1:B:439:VAL:HG13	2.43	0.43
1:C:441:ARG:NH1	1:C:441:ARG:CB	2.81	0.43
1:D:6:ASP:OD1	1:D:8:VAL:HB	2.17	0.43
1:D:360:LEU:O	1:D:400:VAL:HA	2.18	0.43
1:A:77:VAL:CG1	1:A:83:PHE:CE2	3.01	0.43
1:B:47:THR:HG23	1:B:71:ARG:HB3	2.00	0.43
1:B:362:ALA:HB2	1:B:371:LEU:HD11	2.01	0.43
1:D:272:LEU:CD2	1:D:479:VAL:HG11	2.35	0.43
1:A:60:LEU:HD23	1:A:72:MSE:SE	2.68	0.43
1:A:237:GLU:O	1:A:238:LYS:C	2.60	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:450:LEU:O	1:B:475:PRO:HA	2.19	0.43
1:C:6:ASP:OD1	1:C:8:VAL:HB	2.18	0.43
1:D:374:TRP:HB2	1:D:384:MSE:HA	2.00	0.43
1:A:362:ALA:HB2	1:A:371:LEU:HD11	2.00	0.43
1:A:450:LEU:O	1:A:475:PRO:HA	2.19	0.43
1:B:286:ILE:N	1:B:287:PRO:HD2	2.33	0.43
1:D:121:GLY:O	1:D:124:THR:HB	2.18	0.43
1:D:172:LYS:HD2	1:D:173:ALA:N	2.33	0.43
1:A:448:ILE:HG13	1:A:449:GLU:HG3	2.00	0.43
1:D:172:LYS:CE	1:D:236:TYR:CE1	3.02	0.43
1:B:272:LEU:HD11	1:B:479:VAL:HG13	2.01	0.43
1:C:41:THR:HG22	1:C:42:GLY:N	2.34	0.43
1:C:286:ILE:N	1:C:287:PRO:HD2	2.34	0.43
1:D:149:GLU:O	1:D:159:ILE:HA	2.18	0.43
1:A:218[B]:GLU:HG2	1:B:340:TYR:HB2	2.01	0.43
1:A:272:LEU:HD11	1:A:479:VAL:HG13	2.00	0.43
1:B:14:ILE:HD12	1:B:38:LEU:HD21	2.00	0.43
1:B:294:ILE:HD13	1:B:300:VAL:CG2	2.48	0.43
1:D:304:SER:HB2	1:D:311:LEU:HD22	2.00	0.43
1:A:79:GLU:CD	1:A:79:GLU:N	2.77	0.42
1:A:172:LYS:HD2	1:A:173:ALA:N	2.34	0.42
1:B:477:GLN:NE2	2:B:536:HOH:O	2.51	0.42
1:C:83:PHE:CZ	1:C:94:VAL:HG21	2.53	0.42
1:C:360:LEU:O	1:C:400:VAL:HA	2.19	0.42
1:D:272:LEU:HD11	1:D:479:VAL:HG13	2.01	0.42
1:B:237:GLU:O	1:B:238:LYS:C	2.62	0.42
1:C:294:ILE:HD13	1:C:300:VAL:CG2	2.49	0.42
1:C:365:VAL:HG21	1:C:400:VAL:HG21	2.00	0.42
1:A:136:ASN:C	1:A:138:ASP:H	2.26	0.42
1:B:107[A]:ARG:NH1	1:B:108:ALA:CA	2.82	0.42
1:B:384:MSE:HE2	1:B:384:MSE:N	2.34	0.42
1:D:305:GLU:H	1:D:305:GLU:HG3	1.38	0.42
1:B:136:ASN:O	1:B:137:LYS:C	2.62	0.42
1:B:172:LYS:HE3	1:B:236:TYR:CE1	2.54	0.42
1:D:124:THR:HG23	1:D:126:VAL:H	1.84	0.42
1:B:98:PRO:HG2	1:B:101:THR:OG1	2.20	0.42
1:B:217:PRO:HG2	1:B:218:GLU:OE1	2.19	0.42
1:D:325:ILE:HG22	1:D:331:THR:HA	2.01	0.42
1:D:326:ASN:HD21	1:D:330:GLU:HB2	1.84	0.42
1:A:82:GLU:CD	1:A:86:GLN:HE21	2.26	0.42
1:A:205:GLU:O	1:A:205:GLU:HG3	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:294:ILE:HD13	1:A:300:VAL:CG2	2.49	0.42
1:B:41:THR:HG22	1:B:42:GLY:N	2.34	0.42
1:B:91:GLU:HB3	1:C:407:LYS:HD2	2.01	0.42
1:A:149:GLU:O	1:A:159:ILE:HA	2.19	0.42
1:B:181:ASN:CG	1:B:220:ILE:HD13	2.45	0.42
1:C:345:GLU:HG2	2:C:504:HOH:O	2.19	0.42
1:D:205:GLU:O	1:D:205:GLU:HG3	2.18	0.42
1:A:23:GLY:HA3	1:A:192:ASN:OD1	2.19	0.42
1:A:83:PHE:O	1:A:84:GLU:C	2.63	0.42
1:C:65:GLN:HG2	2:C:536:HOH:O	2.20	0.42
1:C:172:LYS:HD2	1:C:173:ALA:N	2.34	0.42
1:C:325:ILE:HG22	1:C:331:THR:HA	2.01	0.42
1:D:14:ILE:HD12	1:D:38:LEU:HD21	2.01	0.42
1:A:325:ILE:HG22	1:A:331:THR:HA	2.02	0.41
1:B:149:GLU:O	1:B:159:ILE:HA	2.20	0.41
1:C:60:LEU:HB2	2:C:544:HOH:O	2.20	0.41
1:D:269:ARG:NH1	1:D:449:GLU:OE2	2.53	0.41
1:B:463:THR:HG22	1:B:465:CYS:H	1.86	0.41
1:D:42:GLY:O	1:D:44:LYS:HG2	2.20	0.41
1:A:286:ILE:N	1:A:287:PRO:HD2	2.34	0.41
1:A:440:ASP:OD2	1:A:443:LYS:HG2	2.20	0.41
1:B:104:GLU:HG2	1:B:351:ARG:HH22	1.85	0.41
1:C:71:ARG:HG3	2:C:579:HOH:O	2.19	0.41
1:C:367:LYS:HE3	1:C:466[A]:ASP:OD1	2.19	0.41
1:A:136:ASN:ND2	1:A:140:SER:OG	2.51	0.41
1:A:425:GLN:O	1:A:441:ARG:NH1	2.54	0.41
1:B:335:LEU:HB3	1:B:336:PRO:HD2	2.02	0.41
1:B:448:ILE:HG13	1:B:449:GLU:HG3	2.02	0.41
1:D:38:LEU:HD12	1:D:63:LEU:HD21	2.01	0.41
1:B:172:LYS:HD2	1:B:173:ALA:N	2.35	0.41
1:C:172:LYS:CE	1:C:236:TYR:CE1	3.04	0.41
1:D:448:ILE:HG13	1:D:449:GLU:HG3	2.02	0.41
1:B:35:ILE:HG23	1:B:63:LEU:CD1	2.49	0.41
1:B:450:LEU:HD23	1:B:451:TRP:N	2.36	0.41
1:C:14:ILE:HD12	1:C:38:LEU:HD21	2.03	0.41
1:C:77:VAL:HG21	1:C:83:PHE:CE2	2.56	0.41
1:C:282:LEU:CD1	1:C:291:SER:HB3	2.50	0.41
1:D:55:VAL:O	1:D:61:GLY:HA3	2.20	0.41
1:A:460:LYS:HE3	2:A:588:HOH:O	2.20	0.41
1:C:2:LYS:HE3	2:C:680:HOH:O	2.19	0.41
1:C:149:GLU:O	1:C:159:ILE:HA	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:60:LEU:CD2	1:D:72:MSE:SE	3.19	0.41
1:D:262:VAL:O	1:D:266:ILE:HG13	2.20	0.41
1:D:294:ILE:HD13	1:D:300:VAL:CG2	2.51	0.41
1:A:181:ASN:CG	1:A:220:ILE:HD13	2.46	0.41
1:B:375:MSE:CE	1:B:420:PRO:HG3	2.36	0.41
1:B:441:ARG:HG3	2:B:600:HOH:O	2.20	0.41
1:C:57:ASN:O	1:C:57:ASN:CG	2.64	0.41
1:C:247:LYS:HE2	1:C:247:LYS:HB2	1.98	0.41
1:D:440:ASP:HB3	1:D:443:LYS:HG2	2.03	0.41
1:D:47:THR:HG23	1:D:47:THR:O	2.20	0.41
1:D:79:GLU:N	1:D:79:GLU:CD	2.79	0.41
1:D:286:ILE:N	1:D:287:PRO:HD2	2.36	0.41
1:A:282:LEU:CD1	1:A:291:SER:HB3	2.50	0.40
1:A:326:ASN:HD21	1:A:330:GLU:HB2	1.86	0.40
1:B:205:GLU:O	1:B:205:GLU:HG3	2.21	0.40
1:C:375:MSE:HE2	1:C:420:PRO:CG	2.35	0.40
1:D:282:LEU:CD1	1:D:291:SER:HB3	2.51	0.40
1:D:383:GLY:O	1:D:384:MSE:CB	2.68	0.40
1:C:189:ARG:O	1:C:190:ASN:C	2.64	0.40
1:A:330:GLU:O	1:A:332:VAL:HG23	2.22	0.40
1:B:403:GLU:O	1:B:412:LYS:HD2	2.21	0.40
1:C:181:ASN:CG	1:C:220:ILE:HD13	2.47	0.40
1:C:205:GLU:O	1:C:205:GLU:HG3	2.20	0.40
1:A:136:ASN:C	1:A:138:ASP:N	2.79	0.40
1:B:107[A]:ARG:HH11	1:B:108:ALA:N	2.18	0.40
1:B:189:ARG:O	1:B:190:ASN:C	2.64	0.40
1:C:104:GLU:HG2	1:C:351:ARG:NH2	2.36	0.40
1:D:49:VAL:O	1:D:49:VAL:HG22	2.21	0.40
1:D:70:LYS:HE3	1:D:70:LYS:HB2	1.95	0.40
1:A:245:VAL:HG13	1:A:315:PRO:O	2.21	0.40
1:C:441:ARG:HH11	1:C:441:ARG:HB2	1.86	0.40
1:D:72:MSE:HE2	1:D:83:PHE:HE2	1.87	0.40
1:D:241:GLU:CD	1:D:329:LYS:HE3	2.46	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	469/481 (98%)	441 (94%)	25 (5%)	3 (1%)	21	38
1	B	471/481 (98%)	451 (96%)	14 (3%)	6 (1%)	9	18
1	C	472/481 (98%)	450 (95%)	17 (4%)	5 (1%)	11	22
1	D	469/481 (98%)	440 (94%)	21 (4%)	8 (2%)	7	13
All	All	1881/1924 (98%)	1782 (95%)	77 (4%)	22 (1%)	10	20

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	137	LYS
1	D	384	MSE
1	D	393	SER
1	D	406	ALA
1	D	138	ASP
1	D	394	ALA
1	A	190	ASN
1	A	249	GLU
1	B	137	LYS
1	B	138	ASP
1	B	249	GLU
1	C	190	ASN
1	C	249	GLU
1	D	249	GLU
1	B	190	ASN
1	B	260	ASP
1	C	260	ASP
1	D	190	ASN
1	A	479	VAL
1	B	479	VAL
1	C	479	VAL
1	D	479	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	387/380 (102%)	360 (93%)	27 (7%)	14	29
1	B	388/380 (102%)	363 (94%)	25 (6%)	16	33
1	C	389/380 (102%)	361 (93%)	28 (7%)	13	28
1	D	387/380 (102%)	363 (94%)	24 (6%)	16	34
All	All	1551/1520 (102%)	1447 (93%)	104 (7%)	15	31

All (104) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	THR
1	A	47	THR
1	A	49	VAL
1	A	67	LYS
1	A	74	SER
1	A	85	ARG
1	A	124	THR
1	A	136	ASN
1	A	171	VAL
1	A	218[A]	GLU
1	A	218[B]	GLU
1	A	239	ARG
1	A	297	ASN
1	A	305	GLU
1	A	311	LEU
1	A	324	LEU
1	A	333	THR
1	A	334	VAL
1	A	345	GLU
1	A	360	LEU
1	A	398	VAL
1	A	399	VAL
1	A	409	ASN
1	A	429	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	439	VAL
1	A	450	LEU
1	A	460	LYS
1	B	41	THR
1	B	49	VAL
1	B	67	LYS
1	B	71	ARG
1	B	74	SER
1	B	107[A]	ARG
1	B	107[B]	ARG
1	B	124	THR
1	B	148	ARG
1	B	171	VAL
1	B	218	GLU
1	B	239	ARG
1	B	262	VAL
1	B	324	LEU
1	B	333	THR
1	B	334	VAL
1	B	345	GLU
1	B	360	LEU
1	B	384	MSE
1	B	398	VAL
1	B	399	VAL
1	B	439	VAL
1	B	450	LEU
1	B	457	ASP
1	B	460	LYS
1	C	41	THR
1	C	49	VAL
1	C	67	LYS
1	C	71	ARG
1	C	74	SER
1	C	85	ARG
1	C	124	THR
1	C	136	ASN
1	C	171	VAL
1	C	204	VAL
1	C	208	GLU
1	C	218	GLU
1	C	239	ARG
1	C	263[A]	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	263[B]	ARG
1	C	297	ASN
1	C	324	LEU
1	C	333	THR
1	C	334	VAL
1	C	360	LEU
1	C	384	MSE
1	C	398	VAL
1	C	399	VAL
1	C	439	VAL
1	C	445	LEU
1	C	450	LEU
1	C	457	ASP
1	C	460	LYS
1	D	41	THR
1	D	49	VAL
1	D	55	VAL
1	D	71	ARG
1	D	74	SER
1	D	124	THR
1	D	128	GLU
1	D	137	LYS
1	D	171	VAL
1	D	218	GLU
1	D	239	ARG
1	D	261	ASN
1	D	305	GLU
1	D	311	LEU
1	D	324	LEU
1	D	333	THR
1	D	334	VAL
1	D	360	LEU
1	D	398	VAL
1	D	399	VAL
1	D	409	ASN
1	D	439	VAL
1	D	450	LEU
1	D	460	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	ASN
1	A	86	GLN
1	A	99	GLN
1	A	136	ASN
1	A	154	ASN
1	A	228	HIS
1	A	261	ASN
1	A	477	GLN
1	B	57	ASN
1	B	65	GLN
1	B	99	GLN
1	B	154	ASN
1	B	228	HIS
1	B	261	ASN
1	B	425	GLN
1	B	477	GLN
1	C	86	GLN
1	C	99	GLN
1	C	136	ASN
1	C	154	ASN
1	C	228	HIS
1	C	261	ASN
1	C	297	ASN
1	C	477	GLN
1	D	57	ASN
1	D	99	GLN
1	D	154	ASN
1	D	228	HIS
1	D	261	ASN
1	D	477	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	459/481 (95%)	0.48	30 (6%) 25 22	7, 27, 60, 104	1 (0%)
1	B	460/481 (95%)	0.31	20 (4%) 40 35	3, 24, 50, 104	2 (0%)
1	C	460/481 (95%)	0.25	15 (3%) 49 45	4, 25, 50, 105	3 (0%)
1	D	459/481 (95%)	0.43	22 (4%) 35 31	6, 28, 53, 105	1 (0%)
All	All	1838/1924 (95%)	0.37	87 (4%) 36 32	3, 26, 53, 105	7 (0%)

All (87) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	479	VAL	7.1
1	C	479	VAL	6.3
1	A	479	VAL	5.6
1	D	480	THR	4.6
1	A	480	THR	4.4
1	C	259	GLY	4.4
1	D	479	VAL	4.4
1	C	480	THR	4.2
1	B	480	THR	4.1
1	B	259	GLY	4.0
1	A	139	GLY	3.9
1	B	442	LYS	3.9
1	B	238	LYS	3.9
1	C	481	THR	3.8
1	C	250	ASP	3.8
1	A	481	THR	3.7
1	D	250	ASP	3.6
1	B	247	LYS	3.5
1	B	481	THR	3.4
1	A	138	ASP	3.3
1	A	451	TRP	3.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	260	ASP	3.2
1	A	136	ASN	3.2
1	D	249	GLU	3.0
1	D	57	ASN	3.0
1	B	317	GLN	3.0
1	A	83	PHE	3.0
1	B	250	ASP	3.0
1	C	238	LYS	3.0
1	C	451	TRP	3.0
1	A	53	ALA	3.0
1	B	211	ASP	3.0
1	D	481	THR	2.9
1	D	383	GLY	2.9
1	B	368	TYR	2.8
1	D	239	ARG	2.7
1	B	248	GLU	2.7
1	A	250	ASP	2.7
1	A	441	ARG	2.7
1	A	88	LEU	2.6
1	B	451	TRP	2.6
1	D	248	GLU	2.6
1	A	262	VAL	2.6
1	A	317	GLN	2.6
1	A	465	CYS	2.6
1	A	77	VAL	2.5
1	A	57	ASN	2.5
1	D	238	LYS	2.5
1	B	261	ASN	2.5
1	A	81	ALA	2.5
1	A	92	LEU	2.5
1	A	78	GLY	2.4
1	C	260	ASP	2.4
1	A	80	ASN	2.4
1	A	84	GLU	2.4
1	B	441	ARG	2.4
1	D	247	LYS	2.4
1	C	247	LYS	2.3
1	C	246	ARG	2.3
1	D	139	GLY	2.3
1	D	262	VAL	2.3
1	D	380	LEU	2.3
1	B	262	VAL	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	381	VAL	2.3
1	C	57	ASN	2.3
1	B	249	GLU	2.3
1	A	260	ASP	2.2
1	C	453	GLY	2.2
1	C	248	GLU	2.2
1	A	135	TYR	2.1
1	A	459	ILE	2.1
1	D	442	LYS	2.1
1	D	451	TRP	2.1
1	A	380	LEU	2.1
1	D	376	ILE	2.1
1	D	460	LYS	2.1
1	D	58	PHE	2.1
1	C	466[A]	ASP	2.1
1	D	77	VAL	2.1
1	D	410	ALA	2.1
1	A	297	ASN	2.1
1	C	136	ASN	2.1
1	A	54	GLY	2.1
1	B	439	VAL	2.0
1	A	453	GLY	2.0
1	A	455	THR	2.0
1	B	459	ILE	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.