



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:30 AM UTC

PDB ID : 9R3Z / pdb_00009r3z
Title : Exploiting ALDH1A2 and ALDH1A3 Isoform Variability for Crystallization Screening
Authors : Garaavglia, S.; Mazzorana, M.
Deposited on : 2025-05-06
Resolution : 2.80 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

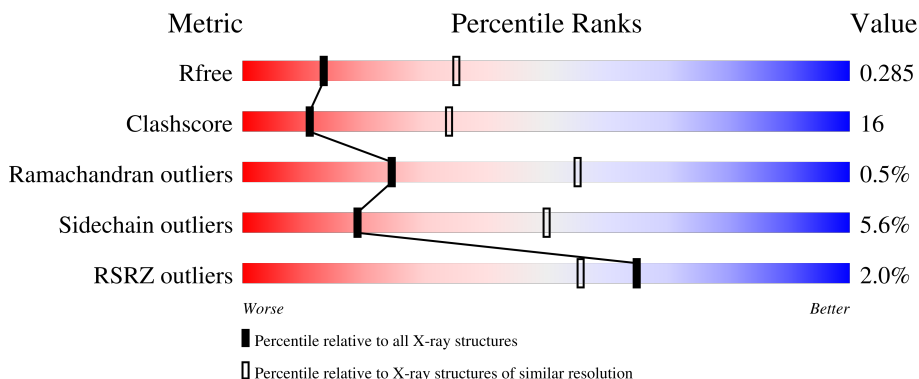
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	518	 2% 59% 31% 9%
1	B	518	 2% 61% 28% 9%
1	C	518	 2% 56% 32% 8%
1	D	518	 % 57% 33% 8%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 14710 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 Retinal dehydrogenase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	472	Total	C	N	O	S	0	0	0
			3657	2333	623	685	16			
1	B	472	Total	C	N	O	S	0	0	0
			3658	2333	623	686	16			
1	C	474	Total	C	N	O	S	0	0	0
			3671	2340	626	689	16			
1	D	474	Total	C	N	O	S	0	0	0
			3671	2340	626	689	16			

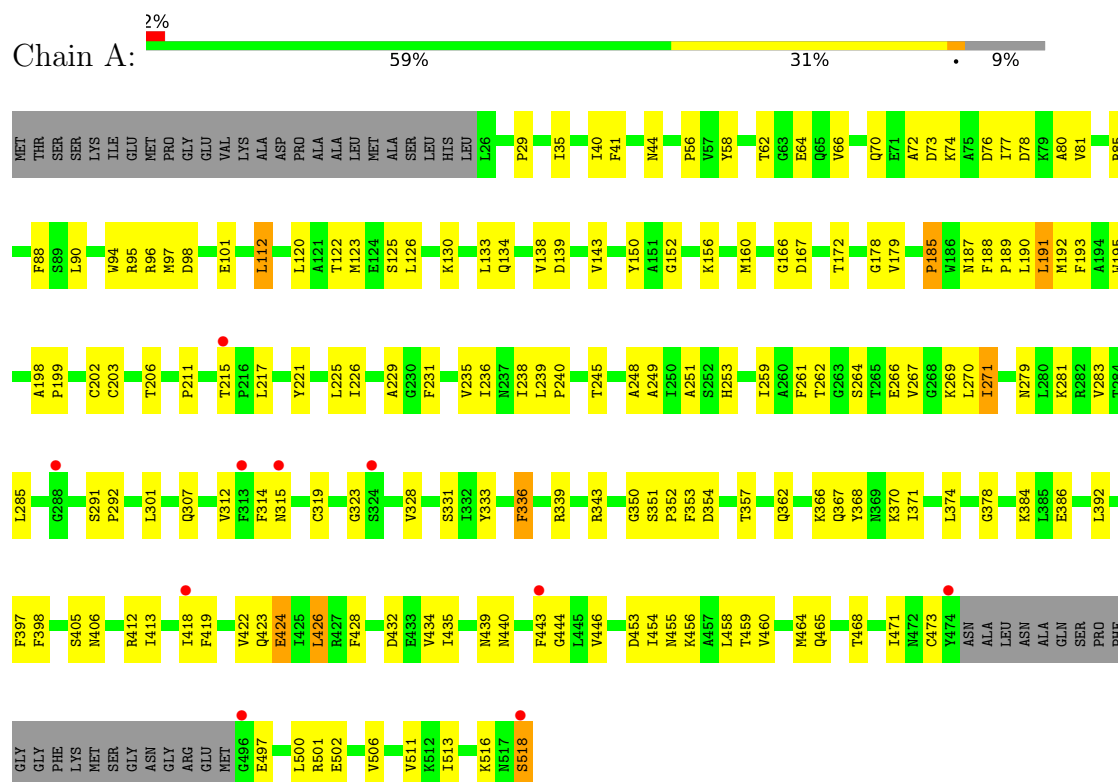
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	4	Total	O	0	0
			4	4		
2	B	17	Total	O	0	0
			17	17		
2	C	9	Total	O	0	0
			9	9		
2	D	23	Total	O	0	0
			23	23		

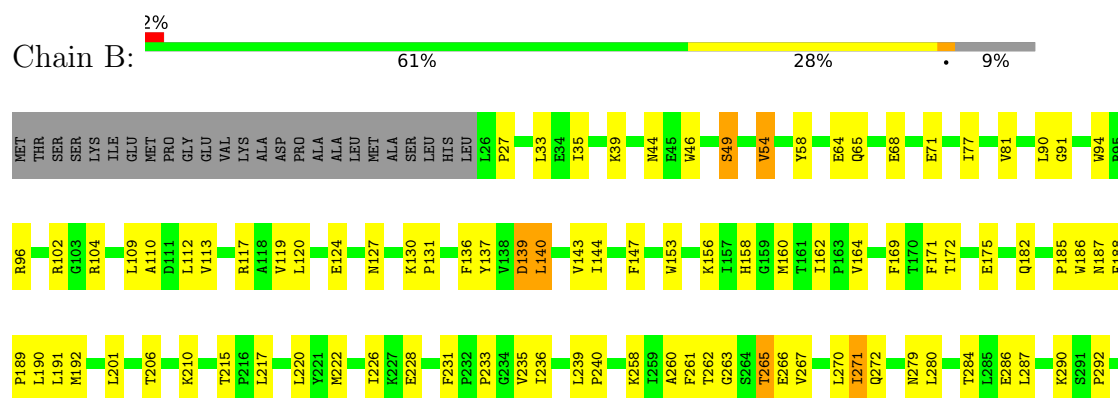
3 Residue-property plots [i](#)

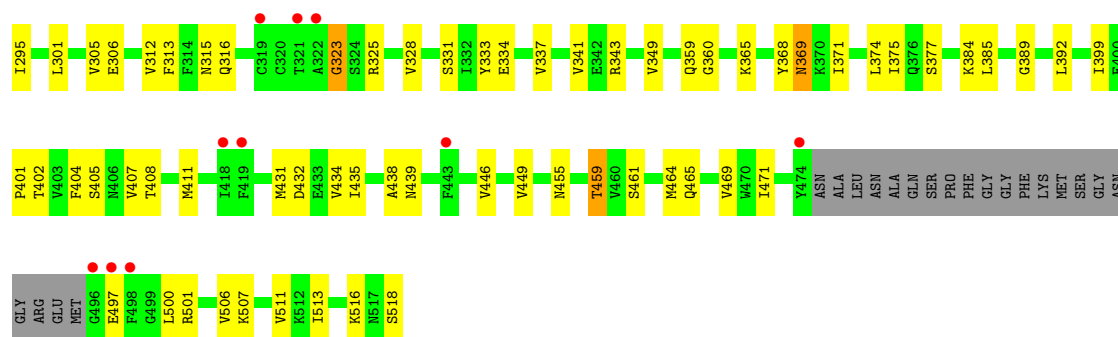
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Retinal dehydrogenase 2

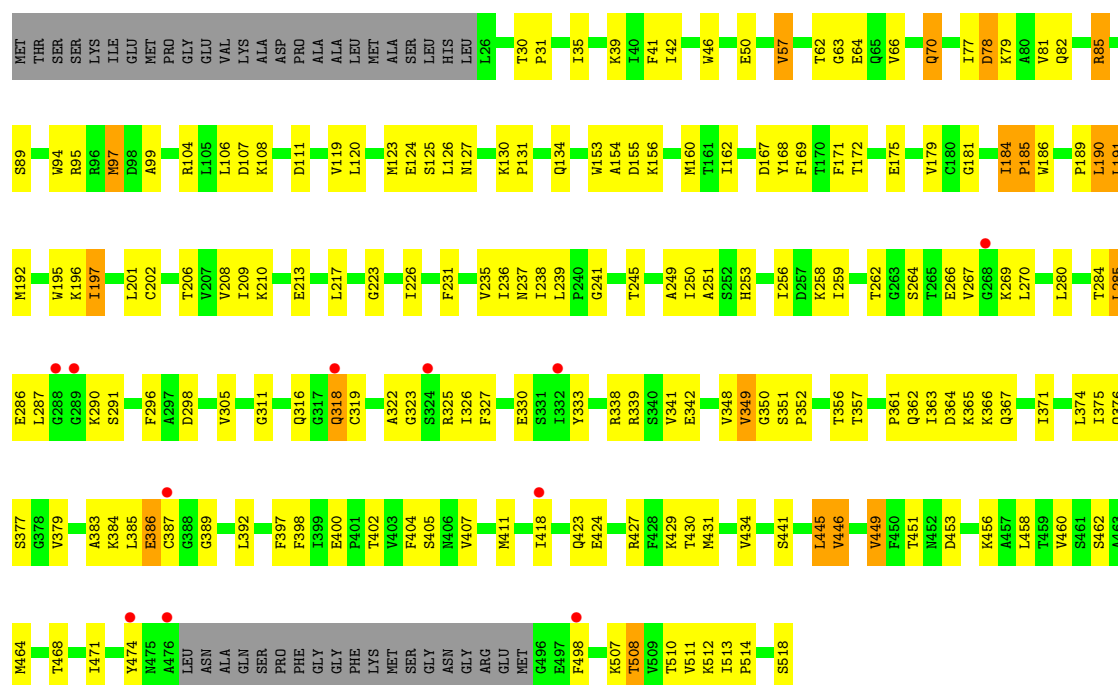


• Molecule 1: Retinal dehydrogenase 2

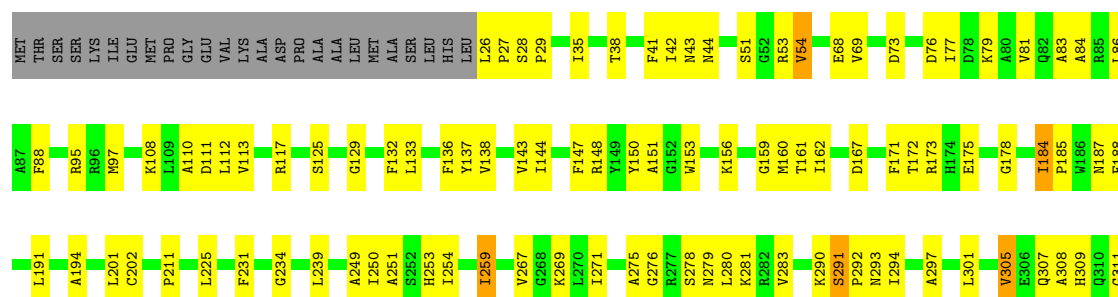




• Molecule 1: Retinal dehydrogenase 2



• Molecule 1: Retinal dehydrogenase 2





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	82.84Å 139.48Å 85.17Å 90.00° 93.93° 90.00°	Depositor
Resolution (Å)	72.57 – 2.80 72.57 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (72.57-2.80) 99.9 (72.57-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.13 (at 2.77Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419	Depositor
R, R_{free}	0.208 , 0.285 0.208 , 0.285	Depositor DCC
R_{free} test set	2244 reflections (4.66%)	wwPDB-VP
Wilson B-factor (Å ²)	62.1	Xtriage
Anisotropy	0.099	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 64.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.000 for l,-k,h	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	14710	wwPDB-VP
Average B, all atoms (Å ²)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.70% 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	0.36	0/3734	0.57	0/5054
1	B	0.44	0/3735	0.65	2/5056 (0.0%)
1	C	0.36	0/3748	0.56	0/5074
1	D	0.44	0/3748	0.62	0/5074
All	All	0.40	0/14965	0.60	2/20258 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	90	LEU	CA-C-N	-6.91	107.87	121.41
1	B	90	LEU	C-N-CA	-6.91	107.87	121.41

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3657	0	3644	121	0
1	B	3658	0	3644	109	0
1	C	3671	0	3655	140	0
1	D	3671	0	3655	140	0
2	A	4	0	0	2	0
2	B	17	0	0	1	0
2	C	9	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	23	0	0	1	0
All	All	14710	0	14598	480	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 16.

All (480) 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:113:VAL:HG22	1:B:222:MET:HE1	1.51	0.90
1:C:77:ILE:HD13	1:C:239:LEU:HD22	1.56	0.87
1:A:98:ASP:HB2	1:A:101:GLU:HG3	1.60	0.83
1:C:333:TYR:HE2	1:C:427:ARG:HA	1.43	0.82
1:B:77:ILE:HD13	1:B:239:LEU:HD22	1.61	0.82
1:D:77:ILE:HD13	1:D:239:LEU:HD22	1.62	0.81
1:A:518:SER:HB2	1:D:95:ARG:HE	1.45	0.80
1:B:439:ASN:HD22	1:B:465:GLN:HG3	1.46	0.79
1:C:471:ILE:HD12	1:D:511:VAL:HG22	1.64	0.79
1:B:172:THR:HG23	1:B:506:VAL:HG13	1.66	0.78
1:C:407:VAL:HG13	1:C:411:MET:HE2	1.66	0.77
1:D:429:LYS:HG3	1:D:430:THR:HG22	1.67	0.75
1:A:143:VAL:HG21	1:A:190:LEU:HG	1.69	0.75
1:C:186:TRP:HZ3	1:C:318:GLN:HG2	1.52	0.74
1:C:341:VAL:HG21	1:C:386:GLU:HG2	1.69	0.73
1:C:185:PRO:HD2	1:C:192:MET:HG2	1.70	0.73
1:B:316:GLN:HE21	1:B:360:GLY:H	1.35	0.73
1:A:187:ASN:HD21	1:A:419:PHE:HZ	1.37	0.72
1:D:449:VAL:HG11	1:D:460:VAL:HG11	1.72	0.72
1:B:375:ILE:HG21	1:B:389:GLY:HA2	1.72	0.71
1:C:262:THR:HG23	1:C:286:GLU:HB3	1.72	0.71
1:C:471:ILE:HB	1:D:511:VAL:HG13	1.73	0.71
1:A:123:MET:HE2	1:A:217:LEU:HB3	1.71	0.71
1:C:185:PRO:HD3	1:C:262:THR:HB	1.73	0.71
1:B:455:ASN:O	1:B:459:THR:HG22	1.91	0.70
1:B:201:LEU:HD11	1:B:236:ILE:HD11	1.71	0.70
1:D:117:ARG:HD3	1:D:136:PHE:CZ	2.27	0.69
1:B:226:ILE:HD13	1:B:236:ILE:HG21	1.75	0.69
1:B:265:THR:HG22	1:B:287:LEU:HB3	1.73	0.69
1:C:384:LYS:HB3	1:C:405:SER:HB3	1.75	0.67
1:C:305:VAL:HG21	1:C:339:ARG:HB2	1.75	0.67
1:A:307:GLN:HE21	1:A:473:CYS:HA	1.60	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:172:THR:HG21	1:D:498:PHE:HE2	1.59	0.66
1:B:384:LYS:HB3	1:B:405:SER:HB2	1.78	0.66
1:A:40:ILE:HG13	1:A:70:GLN:HB2	1.77	0.66
1:B:33:LEU:HD11	1:B:119:VAL:HG13	1.78	0.66
1:D:400:GLU:O	1:D:402:THR:HG22	1.96	0.65
1:A:367:GLN:O	1:A:371:ILE:HG13	1.96	0.65
1:C:291:SER:HB2	1:C:323:GLY:HA3	1.78	0.65
1:D:312:VAL:HG23	1:D:313:PHE:CD1	2.31	0.65
1:C:290:LYS:HD2	1:C:441:SER:HB2	1.78	0.65
1:B:117:ARG:HD3	1:B:136:PHE:CZ	2.32	0.64
1:B:153:TRP:CE2	1:D:156:LYS:HD3	2.32	0.64
1:D:251:ALA:HA	1:D:259:ILE:HD13	1.77	0.64
1:C:392:LEU:HD12	1:C:400:GLU:HG2	1.80	0.64
1:C:451:THR:HG22	1:C:453:ASP:H	1.61	0.64
1:B:54:VAL:CG2	1:B:68:GLU:HB3	2.28	0.64
1:D:305:VAL:HG21	1:D:339:ARG:HB2	1.80	0.64
1:A:120:LEU:HD11	1:A:221:TYR:CD2	2.32	0.64
1:A:120:LEU:HD11	1:A:221:TYR:CE2	2.33	0.64
1:B:49:SER:HB3	1:B:71:GLU:O	1.97	0.63
1:D:413:ILE:HG23	1:D:418:ILE:HD11	1.80	0.63
1:A:453:ASP:HB3	1:A:456:LYS:HB2	1.78	0.63
1:C:160:MET:HG3	1:C:162:ILE:HD11	1.80	0.63
1:C:267:VAL:HA	1:C:270:LEU:HD12	1.80	0.63
1:A:62:THR:HB	1:A:64:GLU:HG2	1.80	0.63
1:D:375:ILE:HG21	1:D:389:GLY:HA2	1.79	0.63
1:C:85:ARG:HG2	1:C:179:VAL:HG21	1.80	0.63
1:D:250:ILE:HG22	1:D:259:ILE:HD12	1.80	0.62
1:C:123:MET:HE2	1:C:217:LEU:HB3	1.81	0.62
1:A:122:THR:HG23	1:A:353:PHE:HE2	1.64	0.62
1:A:185:PRO:HD2	1:A:192:MET:HG2	1.79	0.62
1:C:498:PHE:HE2	1:D:172:THR:HG21	1.64	0.61
1:C:175:GLU:OE1	1:C:507:LYS:HE3	2.00	0.61
1:B:39:LYS:HD2	1:B:46:TRP:HB3	1.82	0.61
1:A:187:ASN:ND2	1:A:419:PHE:HZ	1.99	0.61
1:B:44:ASN:OD1	1:B:233:PRO:HA	2.00	0.61
1:D:374:LEU:O	1:D:413:ILE:HD11	2.00	0.61
1:B:206:THR:HG22	1:B:235:VAL:HG13	1.82	0.60
1:C:462:SER:HA	1:D:173:ARG:HH22	1.66	0.60
1:C:290:LYS:O	1:C:445:LEU:HB3	2.01	0.60
1:B:518:SER:OXT	1:C:175:GLU:HG2	2.00	0.60
1:B:120:LEU:HB2	1:B:140:LEU:HD21	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:184:ILE:HD13	1:C:209:ILE:HD11	1.84	0.60
1:A:291:SER:HA	1:A:446:VAL:O	2.02	0.60
1:C:456:LYS:O	1:C:460:VAL:HG12	2.02	0.60
1:C:57:VAL:HG11	1:C:217:LEU:HD11	1.84	0.59
1:A:455:ASN:O	1:A:459:THR:HG22	2.02	0.59
1:C:451:THR:HG22	1:C:453:ASP:N	2.17	0.59
1:A:439:ASN:HD21	1:A:464:MET:HA	1.67	0.59
1:B:349:VAL:HG21	1:B:401:PRO:HD3	1.85	0.59
1:C:169:PHE:CE2	1:C:171:PHE:HD2	2.21	0.58
1:A:112:LEU:HD11	1:A:229:ALA:HB2	1.85	0.58
1:B:226:ILE:HD13	1:B:236:ILE:HD13	1.84	0.58
1:D:308:ALA:O	1:D:312:VAL:HG22	2.03	0.58
1:D:313:PHE:CE2	1:D:401:PRO:HB3	2.38	0.58
1:C:285:LEU:HB3	1:C:287:LEU:HD21	1.86	0.58
1:A:418:ILE:HG21	1:A:422:VAL:HB	1.86	0.58
1:D:408:THR:HG22	1:D:411:MET:HG3	1.85	0.57
1:A:94:TRP:HA	1:A:97:MET:HE3	1.86	0.57
1:C:290:LYS:HD3	1:C:325:ARG:NH2	2.20	0.57
1:D:327:PHE:CE1	1:D:426:LEU:HD13	2.39	0.57
1:C:374:LEU:HB3	1:C:418:ILE:HD12	1.86	0.57
1:C:125:SER:OG	1:C:352:PRO:HB2	2.05	0.57
1:C:77:ILE:HD12	1:C:250:ILE:HG13	1.87	0.57
1:D:407:VAL:HA	1:D:411:MET:SD	2.45	0.56
1:D:364:ASP:HA	1:D:397:PHE:CE2	2.41	0.56
1:A:80:ALA:HB2	2:A:603:HOH:O	2.05	0.56
1:A:435:ILE:HD11	1:A:460:VAL:HG22	1.88	0.56
1:B:124:GLU:OE2	1:B:189:PRO:HB2	2.05	0.56
1:C:325:ARG:HB3	1:C:327:PHE:HE1	1.71	0.56
1:A:291:SER:HB2	1:A:323:GLY:N	2.21	0.56
1:A:501:ARG:HD2	1:B:501:ARG:HE	1.71	0.56
1:C:338:ARG:O	1:C:342:GLU:HG3	2.06	0.56
1:C:375:ILE:HD13	1:C:389:GLY:HA2	1.88	0.56
1:A:40:ILE:HG12	1:A:240:PRO:HD2	1.86	0.55
1:A:66:VAL:HG11	1:A:126:LEU:HD21	1.87	0.55
1:D:112:LEU:HB3	1:D:225:LEU:HG	1.87	0.55
1:A:156:LYS:HD3	1:C:153:TRP:CE2	2.41	0.55
1:B:130:LYS:HE3	1:B:315:ASN:OD1	2.06	0.55
1:B:513:ILE:HD11	1:B:516:LYS:HB2	1.89	0.55
1:C:498:PHE:CE2	1:D:172:THR:HG21	2.42	0.55
1:D:297:ALA:HA	1:D:332:ILE:HD13	1.88	0.55
1:B:109:LEU:O	1:B:113:VAL:HG23	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:66:VAL:HG11	1:C:126:LEU:HD21	1.88	0.55
1:A:333:TYR:HE1	1:A:426:LEU:O	1.90	0.55
1:B:156:LYS:HE2	1:D:153:TRP:CD1	2.41	0.55
1:A:56:PRO:HB2	1:A:58:TYR:CE1	2.42	0.54
1:A:187:ASN:ND2	1:A:419:PHE:CZ	2.75	0.54
1:B:439:ASN:HB2	1:B:465:GLN:HB2	1.89	0.54
1:A:354:ASP:O	1:A:357:THR:HG22	2.08	0.54
1:A:428:PHE:CD2	1:A:434:VAL:HB	2.41	0.54
1:D:41:PHE:CZ	1:D:44:ASN:HA	2.43	0.54
1:B:35:ILE:HG12	1:B:217:LEU:HD13	1.90	0.54
1:C:290:LYS:HG3	1:C:445:LEU:HD13	1.89	0.54
1:D:327:PHE:HE1	1:D:426:LEU:HD13	1.72	0.54
1:C:290:LYS:HD3	1:C:325:ARG:HH21	1.71	0.54
1:D:327:PHE:HD2	1:D:434:VAL:HG23	1.73	0.54
1:A:374:LEU:HD13	1:A:418:ILE:HG12	1.88	0.54
1:C:208:VAL:HG13	1:C:239:LEU:HD13	1.89	0.54
1:B:153:TRP:CG	1:B:500:LEU:HD11	2.43	0.54
1:C:197:ILE:HD11	1:C:236:ILE:HG21	1.89	0.54
1:C:383:ALA:HB2	1:C:411:MET:HE1	1.89	0.54
1:B:266:GLU:HG3	1:B:267:VAL:H	1.73	0.54
1:C:210:LYS:HG3	1:C:239:LEU:O	2.06	0.54
1:C:441:SER:HB3	1:C:445:LEU:HD11	1.90	0.54
1:A:221:TYR:CE2	1:A:225:LEU:HD11	2.43	0.53
1:A:471:ILE:HD12	1:B:511:VAL:HG22	1.90	0.53
1:B:497:GLU:HA	1:B:500:LEU:HD12	1.90	0.53
1:A:291:SER:HB2	1:A:323:GLY:HA3	1.90	0.53
1:C:226:ILE:HG23	1:C:231:PHE:CD1	2.43	0.53
1:D:201:LEU:HD13	1:D:231:PHE:CE2	2.44	0.53
1:A:189:PRO:HG3	1:A:215:THR:HG21	1.89	0.53
1:A:418:ILE:HD12	1:A:422:VAL:HG11	1.91	0.53
1:B:292:PRO:HD2	1:B:446:VAL:O	2.08	0.53
1:B:316:GLN:HE21	1:B:360:GLY:N	2.05	0.53
1:D:312:VAL:HG12	1:D:324:SER:HA	1.91	0.53
1:A:328:VAL:HG21	1:A:336:PHE:CD2	2.44	0.53
1:D:188:PHE:HB3	1:D:191:LEU:HB3	1.90	0.52
1:B:292:PRO:HD3	1:B:325:ARG:NH2	2.23	0.52
1:B:333:TYR:O	1:B:337:VAL:HG13	2.09	0.52
1:D:366:LYS:HD3	2:D:622:HOH:O	2.09	0.52
1:A:269:LYS:HA	1:B:280:LEU:HD21	1.90	0.52
1:A:460:VAL:O	1:A:464:MET:HG2	2.10	0.52
1:C:325:ARG:NH1	1:C:327:PHE:HZ	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:235:VAL:HG12	1:A:236:ILE:HD12	1.92	0.52
1:B:431:MET:O	1:B:435:ILE:HG13	2.09	0.52
1:B:461:SER:HB2	1:B:469:VAL:HG11	1.91	0.52
1:A:291:SER:HB2	1:A:323:GLY:CA	2.40	0.52
1:C:385:LEU:HD23	1:C:387:CYS:H	1.75	0.52
1:D:172:THR:HG23	1:D:506:VAL:HG13	1.92	0.51
1:A:239:LEU:HD11	2:A:603:HOH:O	2.10	0.51
1:B:127:ASN:HD22	1:B:217:LEU:HB2	1.74	0.51
1:B:156:LYS:HD3	1:D:153:TRP:CE2	2.46	0.51
1:C:333:TYR:CE2	1:C:427:ARG:HA	2.34	0.51
1:B:143:VAL:HG21	1:B:190:LEU:HG	1.92	0.51
1:D:27:PRO:HD3	1:D:137:TYR:OH	2.10	0.51
1:D:175:GLU:CD	1:D:507:LYS:HG3	2.36	0.51
1:A:446:VAL:HG22	1:A:468:THR:HB	1.93	0.51
1:C:365:LYS:HG3	1:C:366:LYS:N	2.25	0.51
1:A:72:ALA:HA	1:A:76:ASP:OD2	2.10	0.51
1:C:168:TYR:CE1	1:C:512:LYS:HD2	2.45	0.51
1:C:197:ILE:HD11	1:C:236:ILE:HG12	1.93	0.51
1:A:191:LEU:HG	1:A:195:TRP:CZ2	2.46	0.51
1:D:84:ALA:HA	1:D:234:GLY:O	2.10	0.51
1:D:313:PHE:HE2	1:D:401:PRO:HB3	1.75	0.51
1:C:498:PHE:CD2	1:D:506:VAL:HG11	2.46	0.51
1:B:267:VAL:HA	1:B:270:LEU:CD1	2.41	0.51
1:B:175:GLU:OE1	1:B:507:LYS:HE2	2.10	0.50
1:A:41:PHE:CZ	1:A:44:ASN:HA	2.45	0.50
1:A:366:LYS:O	1:A:370:LYS:HG3	2.10	0.50
1:B:262:THR:HG23	1:B:286:GLU:HB3	1.94	0.50
1:C:468:THR:HA	1:D:508:THR:O	2.11	0.50
1:A:85:ARG:HD3	1:A:179:VAL:HG21	1.94	0.50
1:A:152:GLY:C	1:C:156:LYS:HE2	2.36	0.50
1:B:27:PRO:HG3	1:B:136:PHE:CD2	2.47	0.50
1:B:131:PRO:HD3	1:B:316:GLN:HE22	1.77	0.50
1:C:186:TRP:CZ3	1:C:318:GLN:HG2	2.40	0.50
1:C:206:THR:HG22	1:C:235:VAL:HA	1.94	0.50
1:D:51:SER:OG	1:D:53:ARG:HB2	2.11	0.50
1:D:447:ALA:HB3	1:D:469:VAL:HG22	1.92	0.50
1:A:443:PHE:HD2	1:A:444:GLY:H	1.59	0.50
1:C:251:ALA:HA	1:C:259:ILE:HD12	1.93	0.50
1:D:309:HIS:NE2	1:D:347:ARG:HD2	2.27	0.50
1:B:313:PHE:CE2	1:B:401:PRO:HB3	2.46	0.49
1:C:184:ILE:HG22	1:C:196:LYS:HD2	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:ILE:O	1:A:81:VAL:HG23	2.11	0.49
1:B:127:ASN:ND2	1:B:215:THR:HA	2.27	0.49
1:A:454:ILE:O	1:A:458:LEU:HG	2.12	0.49
1:D:384:LYS:HB3	1:D:405:SER:HB2	1.93	0.49
1:B:306:GLU:OE1	1:B:343:ARG:HD3	2.12	0.49
1:D:439:ASN:OD1	1:D:465:GLN:HG2	2.13	0.49
1:D:455:ASN:O	1:D:459:THR:HG23	2.13	0.49
1:D:138:VAL:HG11	1:D:314:PHE:HZ	1.77	0.49
1:D:292:PRO:HD3	1:D:325:ARG:HH21	1.78	0.49
1:D:351:SER:O	1:D:357:THR:HG21	2.12	0.49
1:D:349:VAL:HG21	1:D:401:PRO:HD3	1.94	0.49
1:D:449:VAL:HG11	1:D:460:VAL:CG1	2.40	0.49
1:C:127:ASN:HB2	1:C:217:LEU:HD12	1.94	0.49
1:C:341:VAL:HG13	1:C:387:CYS:HB2	1.95	0.49
1:B:131:PRO:HD3	1:B:316:GLN:NE2	2.27	0.49
1:C:371:ILE:HG23	1:C:418:ILE:HD11	1.95	0.49
1:A:458:LEU:HD12	1:C:514:PRO:HD3	1.94	0.48
1:C:326:ILE:HD12	1:C:423:GLN:HG3	1.94	0.48
1:D:129:GLY:O	1:D:361:PRO:HD2	2.11	0.48
1:C:89:SER:O	1:C:95:ARG:HG3	2.13	0.48
1:D:88:PHE:CE1	1:D:178:GLY:HA2	2.47	0.48
1:A:301:LEU:HD23	1:A:339:ARG:NE	2.28	0.48
1:A:374:LEU:HD23	1:A:412:ARG:HH21	1.78	0.48
1:D:453:ASP:HB3	1:D:456:LYS:HB2	1.95	0.48
1:A:88:PHE:CE2	1:A:178:GLY:HA2	2.49	0.48
1:B:182:GLN:HG2	1:B:260:ALA:HB3	1.95	0.48
1:A:166:GLY:O	1:A:516:LYS:HD3	2.13	0.48
1:A:206:THR:HG22	1:A:235:VAL:HA	1.94	0.48
1:B:226:ILE:CD1	1:B:236:ILE:HG21	2.42	0.48
1:B:130:LYS:HE2	1:B:139:ASP:OD2	2.13	0.48
1:B:337:VAL:O	1:B:341:VAL:HG23	2.13	0.48
1:A:261:PHE:HB3	1:A:285:LEU:HD23	1.96	0.48
1:D:77:ILE:HG13	1:D:249:ALA:HB3	1.95	0.48
1:C:78:ASP:O	1:C:82:GLN:HG2	2.14	0.48
1:C:94:TRP:CE3	1:C:97:MET:HE2	2.48	0.48
1:D:113:VAL:CG1	1:D:144:ILE:HG12	2.44	0.48
1:D:125:SER:HB3	1:D:353:PHE:CZ	2.49	0.48
1:D:375:ILE:HD13	1:D:389:GLY:HA2	1.95	0.48
1:B:267:VAL:HA	1:B:270:LEU:HG	1.96	0.47
1:D:311:GLY:O	1:D:322:ALA:HB1	2.14	0.47
1:B:160:MET:HB3	1:B:162:ILE:HD11	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:291:SER:HB2	1:D:323:GLY:HA3	1.95	0.47
1:C:167:ASP:C	1:C:513:ILE:HG12	2.40	0.47
1:B:158:HIS:CD2	1:C:162:ILE:HG13	2.49	0.47
1:B:405:SER:O	1:B:407:VAL:HG23	2.14	0.47
1:C:35:ILE:HD13	1:C:217:LEU:HD13	1.95	0.47
1:A:138:VAL:HG21	1:A:314:PHE:HZ	1.80	0.47
1:B:265:THR:HG22	1:B:287:LEU:CB	2.42	0.47
1:C:374:LEU:HD23	1:C:418:ILE:HB	1.97	0.47
1:A:72:ALA:CB	1:A:239:LEU:HD12	2.45	0.47
1:A:350:GLY:O	1:A:398:PHE:HE2	1.98	0.47
1:B:365:LYS:NZ	1:B:369:ASN:HD22	2.12	0.47
1:C:120:LEU:HD12	1:C:190:LEU:HD11	1.96	0.47
1:C:258:LYS:HG2	1:C:259:ILE:N	2.29	0.47
1:D:43:ASN:HA	1:D:234:GLY:H	1.78	0.47
1:B:175:GLU:HB2	1:B:507:LYS:HD3	1.97	0.47
1:B:374:LEU:HD23	1:B:374:LEU:HA	1.61	0.47
1:D:148:ARG:O	1:D:151:ALA:HB3	2.15	0.47
1:C:316:GLN:HB2	1:C:318:GLN:OE1	2.14	0.46
1:D:254:ILE:HD12	1:D:254:ILE:H	1.79	0.46
1:D:450:PHE:HA	1:D:472:ASN:OD1	2.15	0.46
1:C:130:LYS:HG2	1:C:131:PRO:HD2	1.97	0.46
1:D:279:ASN:OD1	1:D:281:LYS:HE2	2.15	0.46
1:A:513:ILE:HG22	1:C:458:LEU:HD13	1.97	0.46
1:C:169:PHE:CE2	1:C:171:PHE:CD2	3.03	0.46
1:C:298:ASP:OD1	1:C:451:THR:HA	2.16	0.46
1:C:449:VAL:HG21	1:C:460:VAL:HG11	1.97	0.46
1:C:62:THR:O	1:C:64:GLU:HG3	2.16	0.46
1:D:97:MET:HE3	1:D:97:MET:HB2	1.78	0.46
1:D:290:LYS:HB2	1:D:290:LYS:HE3	1.52	0.46
1:C:374:LEU:HD12	1:C:374:LEU:HA	1.61	0.46
1:C:39:LYS:HB2	1:C:46:TRP:HB3	1.96	0.46
1:D:167:ASP:C	1:D:513:ILE:HG12	2.40	0.46
1:D:54:VAL:HG13	1:D:68:GLU:HB3	1.98	0.46
1:D:143:VAL:HG13	1:D:194:ALA:HB2	1.96	0.46
1:C:213:GLU:HB3	1:C:241:GLY:O	2.16	0.46
1:A:185:PRO:HD3	1:A:262:THR:HB	1.98	0.46
1:D:26:LEU:HD23	1:D:26:LEU:HA	1.72	0.46
1:A:199:PRO:O	1:A:202:CYS:HB3	2.16	0.46
1:B:94:TRP:CZ2	1:B:102:ARG:HD2	2.51	0.46
1:B:127:ASN:HD21	1:B:215:THR:HA	1.81	0.46
1:C:39:LYS:HA	1:C:70:GLN:HG2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:291:SER:HA	1:C:446:VAL:O	2.15	0.46
1:A:270:LEU:HD12	1:A:270:LEU:H	1.80	0.45
1:B:104:ARG:HD2	1:B:104:ARG:HA	1.76	0.45
1:A:211:PRO:HD2	1:A:239:LEU:O	2.16	0.45
1:D:153:TRP:CG	1:D:500:LEU:HD11	2.52	0.45
1:D:293:ASN:HB3	1:D:326:ILE:HA	1.99	0.45
1:A:35:ILE:HG23	1:A:123:MET:CE	2.47	0.45
1:D:388:GLY:HA2	1:D:400:GLU:HB3	1.98	0.45
1:A:259:ILE:CG2	1:A:283:VAL:HG22	2.47	0.45
1:C:106:LEU:HD23	1:C:106:LEU:HA	1.76	0.45
1:D:29:PRO:HG3	1:D:132:PHE:CD2	2.52	0.45
1:A:362:GLN:HG3	1:A:371:ILE:HD12	1.98	0.45
1:B:185:PRO:HD2	1:B:192:MET:HG2	1.97	0.45
1:A:266:GLU:O	1:A:270:LEU:HD12	2.17	0.45
1:B:385:LEU:HB2	1:B:404:PHE:CE1	2.51	0.45
1:C:108:LYS:HB2	1:C:108:LYS:HE3	1.66	0.45
1:C:511:VAL:HG13	1:D:471:ILE:HB	1.98	0.45
1:A:406:ASN:O	1:A:406:ASN:CG	2.60	0.45
1:C:131:PRO:HD3	1:C:316:GLN:NE2	2.32	0.45
1:D:307:GLN:C	1:D:474:TYR:HE1	2.24	0.45
1:C:269:LYS:HA	1:D:280:LEU:HD21	1.99	0.45
1:A:95:ARG:NE	1:D:518:SER:HB2	2.31	0.45
1:A:96:ARG:HD2	1:D:516:LYS:O	2.17	0.45
1:C:197:ILE:HD11	1:C:236:ILE:CG2	2.45	0.45
1:C:291:SER:HB2	1:C:323:GLY:CA	2.47	0.44
1:D:159:GLY:HA3	1:D:172:THR:O	2.18	0.44
1:D:361:PRO:HB3	1:D:398:PHE:CE1	2.52	0.44
1:A:72:ALA:HB1	1:A:239:LEU:HD12	1.98	0.44
1:A:267:VAL:HA	1:A:270:LEU:HD13	2.00	0.44
1:A:465:GLN:O	1:A:465:GLN:HG3	2.17	0.44
1:D:319:CYS:HB3	1:D:322:ALA:HB3	1.99	0.44
1:B:160:MET:H	1:B:172:THR:HB	1.82	0.44
1:C:201:LEU:HD13	1:C:231:PHE:CE2	2.53	0.44
1:D:184:ILE:HG12	1:D:211:PRO:HA	1.98	0.44
1:B:140:LEU:O	1:B:144:ILE:HG13	2.18	0.44
1:B:438:ALA:HB3	1:B:464:MET:HE1	1.98	0.44
1:A:134:GLN:O	1:A:138:VAL:HG22	2.18	0.44
1:B:312:VAL:HG22	1:B:323:GLY:O	2.17	0.44
1:C:77:ILE:HG13	1:C:249:ALA:HB3	2.00	0.44
1:A:249:ALA:O	1:A:253:HIS:HB2	2.18	0.44
1:B:220:LEU:HD11	1:B:240:PRO:HG3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:261:PHE:CD2	1:B:271:ILE:HD12	2.53	0.44
1:C:130:LYS:HE3	1:C:134:GLN:HB3	1.98	0.44
1:A:443:PHE:HE1	1:B:280:LEU:HB2	1.82	0.44
1:B:112:LEU:HD13	1:B:228:GLU:HB3	1.99	0.44
1:C:81:VAL:HG11	1:C:253:HIS:CE1	2.52	0.44
1:C:510:THR:HB	1:D:470:TRP:CE3	2.53	0.44
1:B:58:TYR:HA	1:B:65:GLN:HA	1.99	0.44
1:C:441:SER:OG	1:C:445:LEU:HD21	2.18	0.44
1:D:294:ILE:HG23	1:D:434:VAL:HG21	2.00	0.44
1:B:188:PHE:HB3	1:B:191:LEU:HB3	2.00	0.43
1:B:365:LYS:HA	1:B:368:TYR:HB3	2.00	0.43
1:B:392:LEU:HD12	1:B:392:LEU:HA	1.77	0.43
1:B:408:THR:OG1	1:B:411:MET:HG3	2.18	0.43
1:C:41:PHE:HB3	1:C:238:ILE:H	1.82	0.43
1:C:349:VAL:HG12	1:C:350:GLY:H	1.82	0.43
1:C:376:GLN:HA	1:C:379:VAL:HG12	1.99	0.43
1:B:295:ILE:N	1:B:295:ILE:HD12	2.33	0.43
1:D:337:VAL:O	1:D:341:VAL:HG13	2.18	0.43
1:D:413:ILE:HD13	1:D:413:ILE:HA	1.73	0.43
1:A:259:ILE:HG22	1:A:283:VAL:HG22	2.00	0.43
1:B:110:ALA:HB2	1:B:147:PHE:HB2	1.99	0.43
1:B:374:LEU:O	1:B:377:SER:HB3	2.18	0.43
1:C:296:PHE:CZ	1:C:431:MET:HG3	2.53	0.43
1:D:113:VAL:HG12	1:D:144:ILE:HG12	2.01	0.43
1:D:160:MET:HG3	1:D:162:ILE:HD11	2.00	0.43
1:D:431:MET:O	1:D:434:VAL:HG12	2.19	0.43
1:B:137:TYR:HA	2:B:606:HOH:O	2.18	0.43
1:B:153:TRP:CZ2	1:B:497:GLU:HB3	2.53	0.43
1:D:88:PHE:CZ	1:D:178:GLY:HA2	2.53	0.43
1:D:171:PHE:CZ	1:D:509:VAL:HB	2.53	0.43
1:B:27:PRO:HG3	1:B:136:PHE:CE2	2.53	0.43
1:B:127:ASN:ND2	1:B:217:LEU:H	2.16	0.43
1:D:42:ILE:HD13	1:D:79:LYS:HB3	2.00	0.43
1:B:169:PHE:CE2	1:B:171:PHE:CD2	3.06	0.43
1:D:150:TYR:CD2	1:D:500:LEU:HD21	2.54	0.43
1:A:29:PRO:CG	1:A:353:PHE:HD2	2.31	0.43
1:A:251:ALA:HB2	1:A:271:ILE:HD13	2.00	0.43
1:A:307:GLN:NE2	1:A:473:CYS:HA	2.30	0.43
1:D:323:GLY:HA2	1:D:417:GLU:OE2	2.18	0.43
1:D:374:LEU:HD23	1:D:374:LEU:HA	1.87	0.43
1:A:279:ASN:HB3	1:A:281:LYS:HG3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:312:VAL:HG21	1:A:423:GLN:HG3	2.01	0.43
1:B:153:TRP:CZ2	1:D:156:LYS:HD3	2.53	0.43
1:C:50:GLU:OE1	1:C:79:LYS:HE3	2.18	0.43
1:D:333:TYR:CD2	1:D:427:ARG:HG3	2.54	0.43
1:D:374:LEU:HA	1:D:377:SER:HB3	2.01	0.43
1:D:392:LEU:HD23	1:D:392:LEU:HA	1.92	0.43
1:A:150:TYR:HB2	1:A:198:ALA:HB1	2.01	0.42
1:C:108:LYS:O	1:C:111:ASP:HB2	2.19	0.42
1:C:245:THR:HG22	2:C:602:HOH:O	2.19	0.42
1:D:408:THR:CG2	1:D:411:MET:HG3	2.49	0.42
1:A:130:LYS:NZ	1:A:188:PHE:HA	2.34	0.42
1:A:160:MET:HE3	1:A:160:MET:HB2	1.57	0.42
1:D:301:LEU:HA	1:D:301:LEU:HD12	1.74	0.42
1:A:81:VAL:O	1:A:85:ARG:HB2	2.19	0.42
1:A:85:ARG:HH11	1:A:179:VAL:HG23	1.84	0.42
1:A:150:TYR:CB	1:A:198:ALA:HB1	2.48	0.42
1:A:292:PRO:HD2	1:A:446:VAL:O	2.18	0.42
1:C:375:ILE:CD1	1:C:402:THR:HG21	2.49	0.42
1:D:275:ALA:HA	1:D:278:SER:HB3	2.01	0.42
1:A:138:VAL:HG23	1:A:139:ASP:N	2.34	0.42
1:A:167:ASP:C	1:A:513:ILE:HG12	2.44	0.42
1:A:203:CYS:SG	1:A:500:LEU:HD22	2.60	0.42
1:B:371:ILE:HG21	1:B:399:ILE:HD13	2.01	0.42
1:D:470:TRP:CZ3	1:D:475:ASN:HB2	2.54	0.42
1:A:190:LEU:O	1:A:193:PHE:HB3	2.20	0.42
1:C:349:VAL:HG12	1:C:398:PHE:HD2	1.83	0.42
1:D:43:ASN:OD1	1:D:83:ALA:HB1	2.19	0.42
1:D:375:ILE:HG23	1:D:404:PHE:CZ	2.55	0.42
1:A:248:ALA:HA	1:A:251:ALA:HB3	2.00	0.42
1:C:186:TRP:HZ3	1:C:318:GLN:CG	2.29	0.42
1:B:186:TRP:O	1:B:189:PRO:HD3	2.20	0.42
1:C:42:ILE:HA	1:C:237:ASN:HD22	1.85	0.42
1:C:330:GLU:CD	1:C:429:LYS:HG2	2.45	0.42
1:D:276:GLY:HA2	1:D:280:LEU:HD23	2.00	0.42
1:D:428:PHE:CD2	1:D:434:VAL:HB	2.55	0.42
1:A:238:ILE:C	1:A:239:LEU:HD22	2.45	0.42
1:B:77:ILE:O	1:B:81:VAL:HG23	2.20	0.42
1:C:364:ASP:OD1	1:C:367:GLN:HG2	2.20	0.42
1:D:392:LEU:HD21	1:D:400:GLU:HG3	2.01	0.42
1:A:133:LEU:HD23	1:A:133:LEU:HA	1.72	0.42
1:C:325:ARG:NH1	1:C:327:PHE:CZ	2.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:125:SER:OG	1:A:352:PRO:HB2	2.20	0.42
1:A:368:TYR:HD2	1:A:397:PHE:HB3	1.85	0.42
1:D:470:TRP:CH2	1:D:475:ASN:HB2	2.54	0.42
1:A:511:VAL:HG22	1:B:471:ILE:HD12	2.02	0.41
1:B:235:VAL:C	1:B:236:ILE:HG13	2.45	0.41
1:A:424:GLU:H	1:A:424:GLU:HG3	1.74	0.41
1:B:91:GLY:O	1:B:96:ARG:HD3	2.21	0.41
1:C:162:ILE:N	1:C:162:ILE:HD12	2.34	0.41
1:D:35:ILE:HG22	1:D:38:THR:HG22	2.02	0.41
1:D:110:ALA:HB2	1:D:147:PHE:HB2	2.02	0.41
1:D:309:HIS:O	1:D:313:PHE:HB2	2.20	0.41
1:A:343:ARG:HD2	1:A:343:ARG:HA	1.88	0.41
1:A:502:GLU:O	1:A:502:GLU:HG2	2.21	0.41
1:B:210:LYS:HG3	1:B:239:LEU:O	2.20	0.41
1:C:124:GLU:OE2	1:C:189:PRO:HD2	2.21	0.41
1:C:160:MET:HE2	1:C:160:MET:HB3	1.72	0.41
1:C:191:LEU:HG	1:C:195:TRP:CH2	2.55	0.41
1:C:208:VAL:HG13	1:C:239:LEU:CD1	2.51	0.41
1:D:43:ASN:HA	1:D:234:GLY:N	2.35	0.41
1:B:263:GLY:O	1:B:287:LEU:HA	2.20	0.41
1:C:311:GLY:O	1:C:322:ALA:HB1	2.21	0.41
1:C:453:ASP:OD2	1:C:456:LYS:HG3	2.19	0.41
1:B:127:ASN:ND2	1:B:217:LEU:HB2	2.36	0.41
1:C:104:ARG:HD2	1:C:104:ARG:HA	1.90	0.41
1:C:280:LEU:HD11	1:D:269:LYS:HG3	2.02	0.41
1:D:73:ASP:H	1:D:76:ASP:HB2	1.84	0.41
1:D:81:VAL:HG21	1:D:253:HIS:CD2	2.56	0.41
1:D:160:MET:HE2	1:D:160:MET:HB3	1.77	0.41
1:D:161:THR:HG22	1:D:171:PHE:CB	2.50	0.41
1:D:375:ILE:HG23	1:D:404:PHE:HZ	1.85	0.41
1:B:334:GLU:O	1:B:337:VAL:HG22	2.21	0.41
1:C:160:MET:HG3	1:C:162:ILE:CD1	2.50	0.41
1:D:150:TYR:HD2	1:D:500:LEU:HD21	1.85	0.41
1:D:305:VAL:HG21	1:D:339:ARG:CB	2.49	0.41
1:A:130:LYS:HZ1	1:A:188:PHE:HA	1.84	0.41
1:A:378:GLY:HA3	1:A:413:ILE:HD13	2.03	0.41
1:C:223:GLY:HA2	1:C:226:ILE:HD12	2.03	0.41
1:D:327:PHE:HD2	1:D:434:VAL:CG2	2.33	0.41
1:B:201:LEU:HD13	1:B:231:PHE:CE2	2.56	0.41
1:B:301:LEU:HD12	1:B:301:LEU:HA	1.89	0.41
1:C:363:ILE:CG2	1:C:367:GLN:HG3	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:86:LEU:HA	1:D:86:LEU:HD12	1.82	0.41
1:D:161:THR:HG22	1:D:171:PHE:HB3	2.02	0.41
1:A:112:LEU:H	1:A:112:LEU:HG	1.61	0.41
1:A:130:LYS:HE2	1:A:315:ASN:OD1	2.21	0.41
1:A:301:LEU:HD12	1:A:301:LEU:HA	1.92	0.41
1:B:365:LYS:HZ3	1:B:365:LYS:HG2	1.49	0.41
1:B:431:MET:O	1:B:434:VAL:HG12	2.21	0.41
1:C:181:GLY:O	1:C:259:ILE:HA	2.21	0.41
1:C:348:VAL:HG12	1:C:357:THR:HA	2.02	0.41
1:C:404:PHE:HD1	1:C:404:PHE:HA	1.81	0.41
1:D:312:VAL:HG23	1:D:313:PHE:HD1	1.83	0.41
1:A:439:ASN:OD1	1:A:465:GLN:HG2	2.21	0.41
1:C:30:THR:HA	1:C:31:PRO:HD3	1.93	0.41
1:D:138:VAL:HG11	1:D:314:PHE:CZ	2.55	0.41
1:D:294:ILE:O	1:D:449:VAL:HA	2.21	0.41
1:D:334:GLU:H	1:D:334:GLU:HG2	1.70	0.41
1:A:384:LYS:HG2	1:A:386:GLU:OE2	2.21	0.40
1:B:328:VAL:HG11	1:B:333:TYR:HA	2.03	0.40
1:C:39:LYS:HA	1:C:70:GLN:CG	2.51	0.40
1:C:172:THR:HG22	1:C:508:THR:HG23	2.04	0.40
1:D:281:LYS:O	1:D:283:VAL:HG23	2.21	0.40
1:D:500:LEU:HA	1:D:500:LEU:HD23	1.87	0.40
1:A:97:MET:HE3	1:A:97:MET:HB2	1.61	0.40
1:A:264:SER:OG	1:A:267:VAL:HG23	2.20	0.40
1:C:250:ILE:HG23	1:C:256:ILE:HD13	2.03	0.40
1:C:361:PRO:HB3	1:C:398:PHE:CE1	2.56	0.40
1:A:73:ASP:CG	1:A:74:LYS:H	2.29	0.40
1:A:226:ILE:HG23	1:A:231:PHE:CD1	2.56	0.40
1:A:351:SER:O	1:A:357:THR:HG21	2.21	0.40
1:B:349:VAL:HG22	1:B:359:GLN:HB3	2.04	0.40
1:C:99:ALA:HB1	1:C:154:ALA:O	2.22	0.40
1:D:110:ALA:HB2	1:D:147:PHE:CB	2.51	0.40
1:C:97:MET:HE3	1:C:97:MET:HB3	1.81	0.40
1:C:362:GLN:HG2	1:C:397:PHE:O	2.21	0.40
1:D:108:LYS:O	1:D:111:ASP:HB2	2.20	0.40
1:C:460:VAL:O	1:C:464:MET:HG2	2.22	0.40
1:D:267:VAL:O	1:D:271:ILE:HG12	2.22	0.40
1:D:374:LEU:O	1:D:377:SER:HB3	2.22	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	468/518 (90%)	430 (92%)	35 (8%)	3 (1%)	21	51
1	B	468/518 (90%)	434 (93%)	32 (7%)	2 (0%)	30	60
1	C	470/518 (91%)	436 (93%)	30 (6%)	4 (1%)	14	41
1	D	470/518 (91%)	439 (93%)	30 (6%)	1 (0%)	43	72
All	All	1876/2072 (90%)	1739 (93%)	127 (7%)	10 (0%)	24	55

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	279	ASN
1	C	63	GLY
1	A	185	PRO
1	A	440	ASN
1	C	70	GLN
1	C	97	MET
1	A	336	PHE
1	D	185	PRO
1	C	185	PRO
1	B	323	GLY

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	387/422 (92%)	370 (96%)	17 (4%)	25	59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	387/422 (92%)	367 (95%)	20 (5%)	21	53
1	C	388/422 (92%)	357 (92%)	31 (8%)	11	34
1	D	388/422 (92%)	369 (95%)	19 (5%)	22	55
All	All	1550/1688 (92%)	1463 (94%)	87 (6%)	19	50

All (87) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	78	ASP
1	A	90	LEU
1	A	112	LEU
1	A	172	THR
1	A	191	LEU
1	A	245	THR
1	A	271	ILE
1	A	319	CYS
1	A	331	SER
1	A	392	LEU
1	A	405	SER
1	A	424	GLU
1	A	426	LEU
1	A	432	ASP
1	A	497	GLU
1	A	506	VAL
1	A	518	SER
1	B	49	SER
1	B	54	VAL
1	B	64	GLU
1	B	139	ASP
1	B	140	LEU
1	B	164	VAL
1	B	187	ASN
1	B	258	LYS
1	B	265	THR
1	B	271	ILE
1	B	272	GLN
1	B	284	THR
1	B	290	LYS
1	B	305	VAL
1	B	331	SER
1	B	369	ASN

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Mol	Chain	Res	Type
1	B	402	THR
1	B	432	ASP
1	B	449	VAL
1	B	459	THR
1	C	57	VAL
1	C	78	ASP
1	C	85	ARG
1	C	107	ASP
1	C	119	VAL
1	C	155	ASP
1	C	184	ILE
1	C	190	LEU
1	C	191	LEU
1	C	197	ILE
1	C	202	CYS
1	C	264	SER
1	C	266	GLU
1	C	284	THR
1	C	285	LEU
1	C	318	GLN
1	C	319	CYS
1	C	349	VAL
1	C	351	SER
1	C	356	THR
1	C	377	SER
1	C	386	GLU
1	C	424	GLU
1	C	430	THR
1	C	434	VAL
1	C	445	LEU
1	C	446	VAL
1	C	449	VAL
1	C	474	TYR
1	C	508	THR
1	C	518	SER
1	D	28	SER
1	D	54	VAL
1	D	69	VAL
1	D	133	LEU
1	D	184	ILE
1	D	187	ASN
1	D	202	CYS

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Mol	Chain	Res	Type
1	D	259	ILE
1	D	291	SER
1	D	305	VAL
1	D	399	ILE
1	D	402	THR
1	D	424	GLU
1	D	425	ILE
1	D	430	THR
1	D	442	ASP
1	D	474	TYR
1	D	497	GLU
1	D	511	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	182	GLN
1	A	362	GLN
1	A	369	ASN
1	A	515	GLN
1	A	517	ASN
1	B	127	ASN
1	B	293	ASN
1	B	316	GLN
1	B	369	ASN
1	B	440	ASN
1	B	455	ASN
1	C	47	GLN
1	C	48	ASN
1	C	70	GLN
1	C	158	HIS
1	C	174	HIS
1	C	237	ASN
1	C	272	GLN
1	C	359	GLN
1	C	362	GLN
1	D	32	ASN
1	D	48	ASN
1	D	310	GLN
1	D	362	GLN
1	D	367	GLN
1	D	455	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

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	472/518 (91%)	0.25	10 (2%) 63 54	38, 76, 118, 160	0
1	B	472/518 (91%)	-0.01	10 (2%) 63 54	30, 55, 87, 167	0
1	C	474/518 (91%)	0.31	11 (2%) 61 51	41, 76, 124, 168	0
1	D	474/518 (91%)	0.05	7 (1%) 72 63	32, 55, 98, 179	0
All	All	1892/2072 (91%)	0.15	38 (2%) 65 56	30, 65, 112, 179	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	476	ALA	5.2
1	D	321	THR	4.6
1	C	476	ALA	4.5
1	D	474	TYR	4.1
1	D	320	CYS	3.8
1	B	419	PHE	3.6
1	C	474	TYR	3.4
1	A	313	PHE	3.4
1	A	418	ILE	3.2
1	A	496	GLY	3.0
1	B	496	GLY	2.8
1	A	324	SER	2.7
1	B	497	GLU	2.7
1	B	498	PHE	2.7
1	A	518	SER	2.7
1	B	443	PHE	2.6
1	D	443	PHE	2.6
1	C	418	ILE	2.6
1	C	324	SER	2.6
1	A	315	ASN	2.6
1	C	498	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	289	GLY	2.5
1	B	474	TYR	2.5
1	C	318	GLN	2.5
1	A	288	GLY	2.4
1	D	498	PHE	2.3
1	B	322	ALA	2.3
1	A	443	PHE	2.3
1	C	387	CYS	2.3
1	B	319	CYS	2.3
1	B	321	THR	2.3
1	A	474	TYR	2.1
1	B	418	ILE	2.1
1	C	268	GLY	2.1
1	C	288	GLY	2.0
1	C	332	ILE	2.0
1	A	215	THR	2.0
1	D	417	GLU	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.