



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2014 – 04:02 AM GMT

PDB ID : 4I3X
Title : Structure of phosphonoacetaldehydedehydrogenase in complex with phosphonoacetate and cofactor NAD⁺
Authors : Nair, S.K.; Agarwal, V.
Deposited on : 2012-11-26
Resolution : 2.07 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

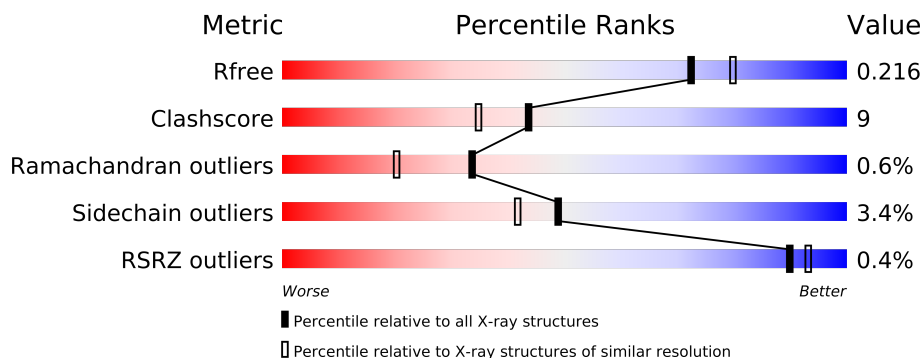
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.07 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}	66092	1224 (2.08-2.04)
Clashscore	79885	1390 (2.08-2.04)
Ramachandran outliers	78287	1381 (2.08-2.04)
Sidechain outliers	78261	1381 (2.08-2.04)
RSRZ outliers	66119	1225 (2.08-2.04)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	488	
1	B	488	
1	C	488	
1	D	488	
1	E	488	
1	F	488	
1	G	488	
1	H	488	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 32452 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Aldehyde dehydrogenase (NAD+).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	476	Total	C	N	O	S	0	0	0
			3651	2310	636	686	19			
1	B	474	Total	C	N	O	S	0	0	0
			3633	2299	631	684	19			
1	C	475	Total	C	N	O	S	0	0	0
			3644	2305	635	685	19			
1	D	476	Total	C	N	O	S	0	0	0
			3651	2310	636	686	19			
1	E	476	Total	C	N	O	S	0	0	0
			3649	2308	636	686	19			
1	F	476	Total	C	N	O	S	0	0	0
			3651	2310	636	686	19			
1	G	474	Total	C	N	O	S	0	0	0
			3633	2299	631	684	19			
1	H	476	Total	C	N	O	S	0	0	0
			3651	2310	636	686	19			

There are 24 discrepancies between the modelled and reference sequences:

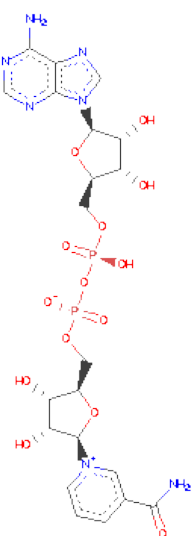
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	EXPRESSION TAG	UNP Q92UV7
A	-1	SER	-	EXPRESSION TAG	UNP Q92UV7
A	0	HIS	-	EXPRESSION TAG	UNP Q92UV7
B	-2	GLY	-	EXPRESSION TAG	UNP Q92UV7
B	-1	SER	-	EXPRESSION TAG	UNP Q92UV7
B	0	HIS	-	EXPRESSION TAG	UNP Q92UV7
C	-2	GLY	-	EXPRESSION TAG	UNP Q92UV7
C	-1	SER	-	EXPRESSION TAG	UNP Q92UV7
C	0	HIS	-	EXPRESSION TAG	UNP Q92UV7
D	-2	GLY	-	EXPRESSION TAG	UNP Q92UV7
D	-1	SER	-	EXPRESSION TAG	UNP Q92UV7
D	0	HIS	-	EXPRESSION TAG	UNP Q92UV7
E	-2	GLY	-	EXPRESSION TAG	UNP Q92UV7

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
E	-1	SER	-	EXPRESSION TAG	UNP Q92UV7
E	0	HIS	-	EXPRESSION TAG	UNP Q92UV7
F	-2	GLY	-	EXPRESSION TAG	UNP Q92UV7
F	-1	SER	-	EXPRESSION TAG	UNP Q92UV7
F	0	HIS	-	EXPRESSION TAG	UNP Q92UV7
G	-2	GLY	-	EXPRESSION TAG	UNP Q92UV7
G	-1	SER	-	EXPRESSION TAG	UNP Q92UV7
G	0	HIS	-	EXPRESSION TAG	UNP Q92UV7
H	-2	GLY	-	EXPRESSION TAG	UNP Q92UV7
H	-1	SER	-	EXPRESSION TAG	UNP Q92UV7
H	0	HIS	-	EXPRESSION TAG	UNP Q92UV7

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



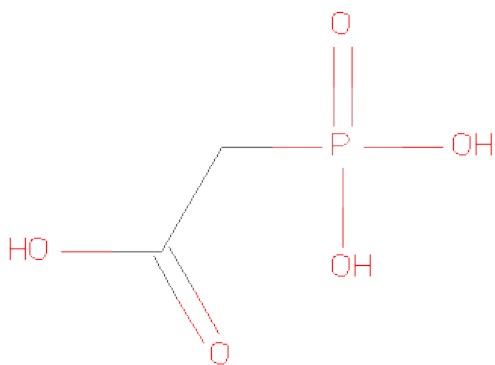
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	B	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	C	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	D	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	E	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	F	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	G	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	H	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 3 is PHOSPHONOACETIC ACID (three-letter code: PAE) (formula: C₂H₅O₅P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	P	0	0
			8	2	5	1		
3	B	1	Total	C	O	P	0	0
			8	2	5	1		
3	C	1	Total	C	O	P	0	0
			8	2	5	1		
3	D	1	Total	C	O	P	0	0
			8	2	5	1		
3	E	1	Total	C	O	P	0	0
			8	2	5	1		
3	F	1	Total	C	O	P	0	0
			8	2	5	1		
3	G	1	Total	C	O	P	0	0
			8	2	5	1		
3	H	1	Total	C	O	P	0	0
			8	2	5	1		

- Molecule 4 is water.

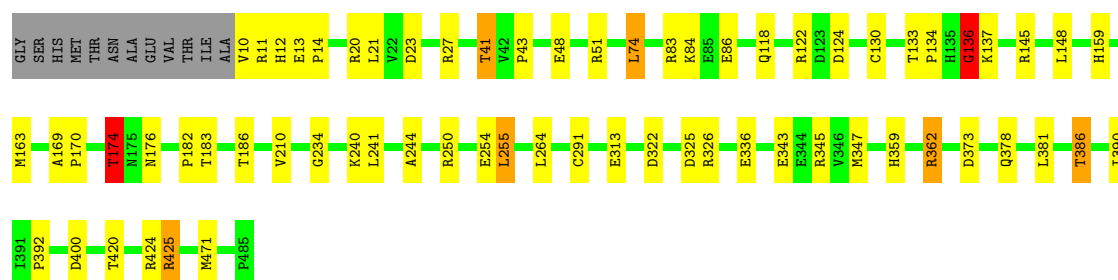
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	497	Total 497	O 497	0	0
4	B	380	Total 380	O 380	0	0
4	C	337	Total 337	O 337	0	0
4	D	302	Total 302	O 302	0	0
4	E	376	Total 376	O 376	0	0
4	F	325	Total 325	O 325	0	0
4	G	358	Total 358	O 358	0	0
4	H	298	Total 298	O 298	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

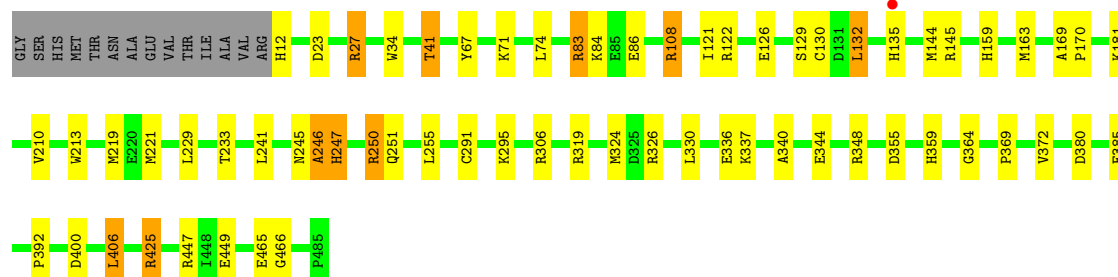
- Molecule 1: Aldehyde dehydrogenase (NAD+)

Chain A: 



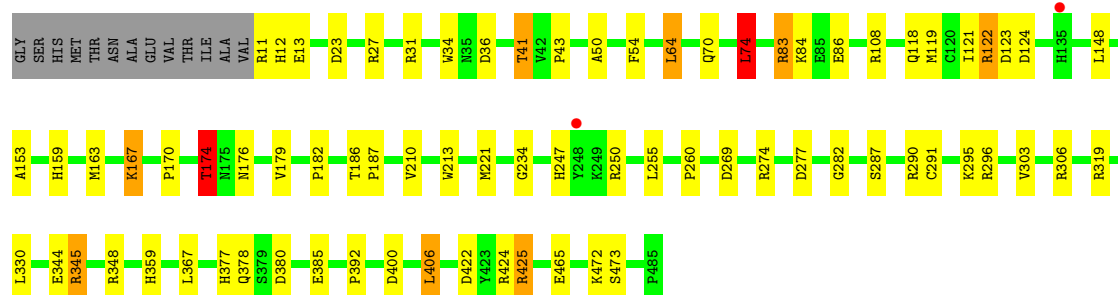
- Molecule 1: Aldehyde dehydrogenase (NAD+)

Chain B: 



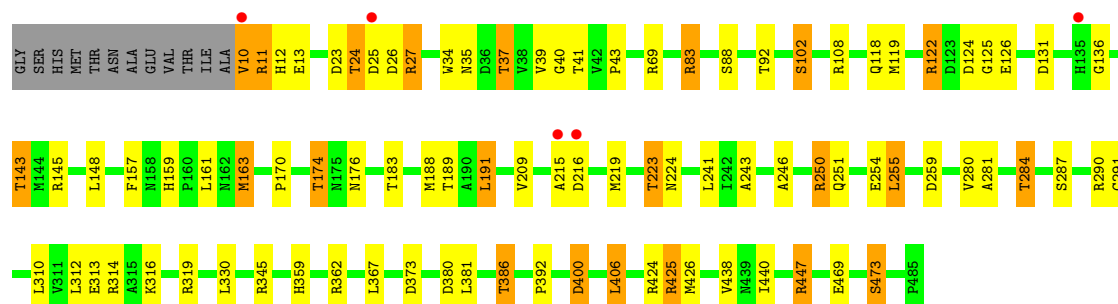
- Molecule 1: Aldehyde dehydrogenase (NAD+)

Chain C: 



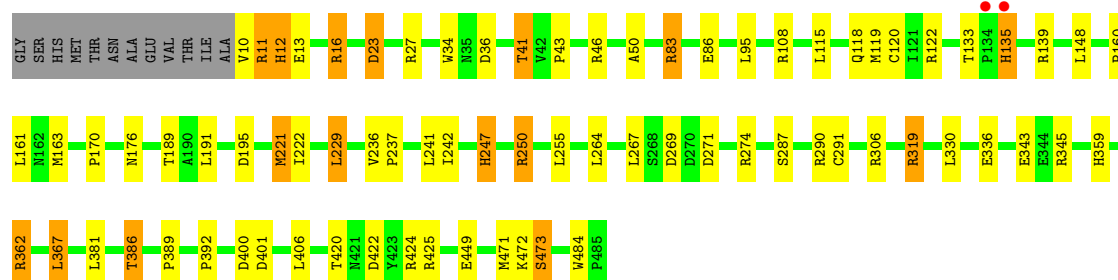
- Molecule 1: Aldehyde dehydrogenase (NAD+)

Chain D:



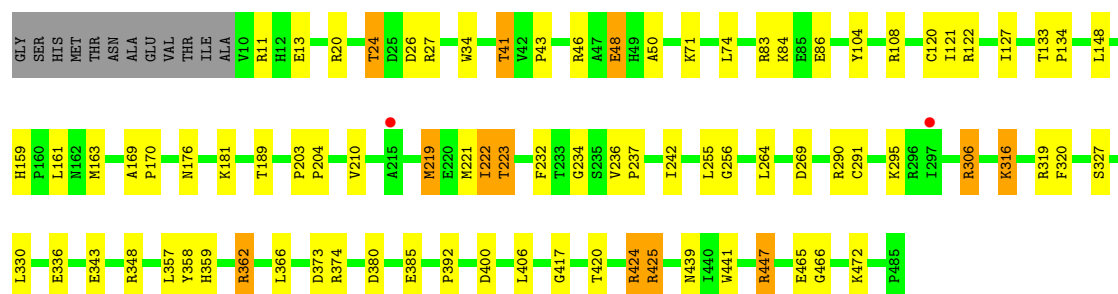
- Molecule 1: Aldehyde dehydrogenase (NAD+)

Chain E:



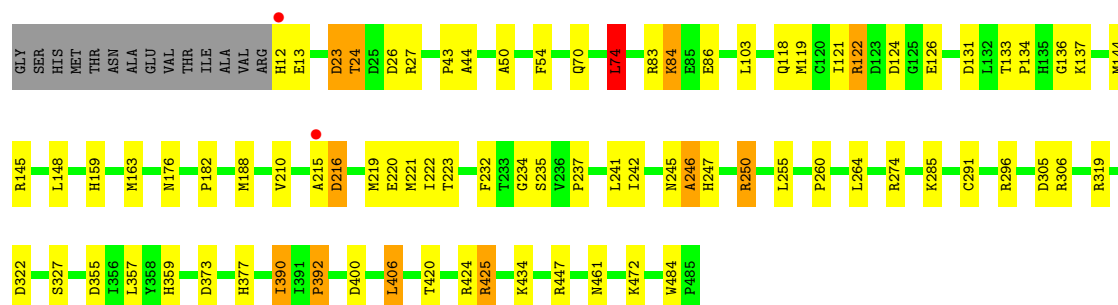
- Molecule 1: Aldehyde dehydrogenase (NAD+)

Chain F:



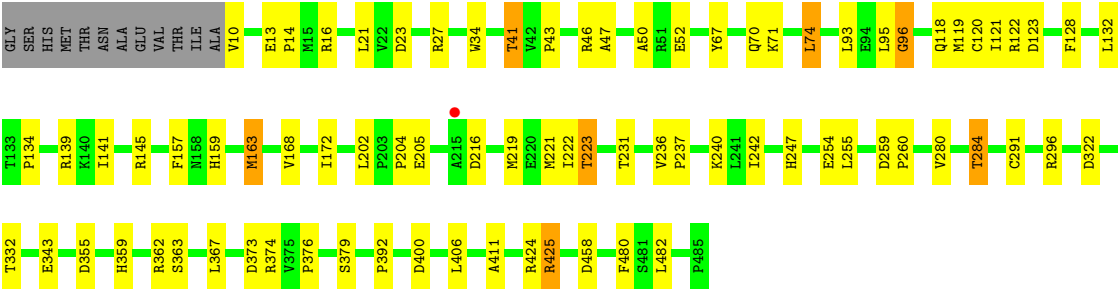
- Molecule 1: Aldehyde dehydrogenase (NAD+)

Chain G:



- Molecule 1: Aldehyde dehydrogenase (NAD+)

Chain H: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	95.16Å 172.76Å 142.60Å 90.00° 107.28° 90.00°	Depositor
Resolution (Å)	50.00 – 2.07 29.47 – 2.07	Depositor EDS
% Data completeness (in resolution range)	94.0 (50.00-2.07) 94.0 (29.47-2.07)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.57 (at 2.08Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.162 , 0.217 0.161 , 0.216	Depositor DCC
R_{free} test set	12509 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	25.3	Xtriage
Anisotropy	0.035	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 35.1	EDS
Estimated twinning fraction	0.013 for h,-k,-h-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	2 of 250226 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	32452	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.79% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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

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	1.08	3/3724 (0.1%)	1.12	19/5066 (0.4%)
1	B	0.94	3/3706 (0.1%)	1.05	18/5042 (0.4%)
1	C	0.98	3/3717 (0.1%)	1.06	18/5056 (0.4%)
1	D	0.94	3/3724 (0.1%)	1.03	16/5066 (0.3%)
1	E	0.98	3/3722 (0.1%)	1.07	19/5063 (0.4%)
1	F	0.90	2/3724 (0.1%)	1.02	11/5066 (0.2%)
1	G	0.91	2/3706 (0.1%)	1.03	17/5042 (0.3%)
1	H	0.88	3/3724 (0.1%)	0.99	15/5066 (0.3%)
All	All	0.95	22/29747 (0.1%)	1.05	133/40467 (0.3%)

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	F	0	1
1	G	0	1
All	All	0	2

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	126	GLU	CD-OE1	8.83	1.35	1.25
1	G	126	GLU	CD-OE1	6.68	1.33	1.25
1	E	34	TRP	CD2-CE2	6.50	1.49	1.41
1	D	34	TRP	CD2-CE2	6.13	1.48	1.41
1	G	484	TRP	CD2-CE2	6.07	1.48	1.41
1	A	362	ARG	CD-NE	-5.95	1.36	1.46
1	C	34	TRP	CD2-CE2	5.66	1.48	1.41
1	C	213	TRP	CD2-CE2	5.63	1.48	1.41

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	120	CYS	CB-SG	-5.52	1.72	1.81
1	D	254	GLU	CG-CD	5.50	1.60	1.51
1	H	96	GLY	N-CA	5.49	1.54	1.46
1	F	441	TRP	CD2-CE2	5.49	1.48	1.41
1	A	254	GLU	CG-CD	5.46	1.60	1.51
1	B	34	TRP	CD2-CE2	5.43	1.47	1.41
1	H	254	GLU	CG-CD	5.43	1.60	1.51
1	D	102	SER	CB-OG	-5.38	1.35	1.42
1	E	473	SER	CB-OG	-5.34	1.35	1.42
1	H	34	TRP	CD2-CE2	5.28	1.47	1.41
1	B	213	TRP	CD2-CE2	5.22	1.47	1.41
1	C	282	GLY	N-CA	5.18	1.53	1.46
1	E	484	TRP	CD2-CE2	5.14	1.47	1.41
1	A	313	GLU	CG-CD	5.04	1.59	1.51

All (133) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	362	ARG	NE-CZ-NH2	-17.34	111.63	120.30
1	G	425	ARG	NE-CZ-NH2	-16.84	111.88	120.30
1	G	425	ARG	NE-CZ-NH1	14.97	127.79	120.30
1	C	425	ARG	NE-CZ-NH1	13.95	127.28	120.30
1	E	83	ARG	NE-CZ-NH2	-13.70	113.45	120.30
1	C	425	ARG	NE-CZ-NH2	-11.89	114.35	120.30
1	E	83	ARG	NE-CZ-NH1	11.74	126.17	120.30
1	A	425	ARG	NE-CZ-NH2	-11.69	114.46	120.30
1	F	425	ARG	NE-CZ-NH1	11.45	126.03	120.30
1	D	425	ARG	NE-CZ-NH2	-11.34	114.63	120.30
1	F	425	ARG	NE-CZ-NH2	-10.79	114.90	120.30
1	B	83	ARG	NE-CZ-NH2	-10.40	115.10	120.30
1	H	425	ARG	NE-CZ-NH2	-10.08	115.26	120.30
1	A	362	ARG	NE-CZ-NH1	10.03	125.31	120.30
1	B	425	ARG	NE-CZ-NH1	9.93	125.26	120.30
1	A	424	ARG	NE-CZ-NH1	9.89	125.25	120.30
1	A	145	ARG	NE-CZ-NH2	-9.77	115.41	120.30
1	E	362	ARG	NE-CZ-NH2	-9.43	115.59	120.30
1	B	132	LEU	CB-CG-CD1	-9.29	95.21	111.00
1	B	250	ARG	NE-CZ-NH1	9.11	124.86	120.30
1	D	425	ARG	NE-CZ-NH1	8.60	124.60	120.30
1	B	425	ARG	NE-CZ-NH2	-8.48	116.06	120.30
1	G	74	LEU	CB-CG-CD1	8.18	124.91	111.00
1	C	345	ARG	NE-CZ-NH1	8.15	124.37	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	83	ARG	NE-CZ-NH1	8.09	124.34	120.30
1	D	447	ARG	NE-CZ-NH1	7.86	124.23	120.30
1	C	424	ARG	NE-CZ-NH1	7.69	124.14	120.30
1	D	447	ARG	NE-CZ-NH2	-7.60	116.50	120.30
1	B	250	ARG	NE-CZ-NH2	-7.55	116.52	120.30
1	G	250	ARG	NE-CZ-NH1	7.51	124.06	120.30
1	H	95	LEU	C-N-CA	-7.41	106.74	122.30
1	A	250	ARG	NE-CZ-NH2	-7.37	116.62	120.30
1	F	447	ARG	NE-CZ-NH1	7.36	123.98	120.30
1	E	250	ARG	NE-CZ-NH1	7.25	123.93	120.30
1	F	120	CYS	CB-CA-C	-7.22	95.96	110.40
1	B	108	ARG	NE-CZ-NH2	-7.21	116.69	120.30
1	H	424	ARG	NE-CZ-NH1	7.21	123.90	120.30
1	A	136	GLY	N-CA-C	7.15	130.98	113.10
1	A	74	LEU	CB-CG-CD1	7.14	123.14	111.00
1	B	406	LEU	CA-CB-CG	7.13	131.71	115.30
1	C	83	ARG	NE-CZ-NH2	-7.13	116.74	120.30
1	D	400	ASP	CB-CG-OD1	7.04	124.63	118.30
1	H	425	ARG	NE-CZ-NH1	7.00	123.80	120.30
1	D	145	ARG	NE-CZ-NH2	-6.96	116.82	120.30
1	B	145	ARG	NE-CZ-NH1	6.85	123.72	120.30
1	A	425	ARG	NE-CZ-NH1	6.83	123.72	120.30
1	E	250	ARG	NE-CZ-NH2	-6.81	116.89	120.30
1	H	322	ASP	CB-CG-OD1	6.78	124.40	118.30
1	C	424	ARG	NE-CZ-NH2	-6.75	116.92	120.30
1	B	108	ARG	NE-CZ-NH1	6.74	123.67	120.30
1	G	305	ASP	CB-CG-OD1	6.71	124.34	118.30
1	B	326	ARG	NE-CZ-NH1	-6.67	116.96	120.30
1	D	83	ARG	NE-CZ-NH2	-6.66	116.97	120.30
1	A	373	ASP	CB-CG-OD1	6.63	124.26	118.30
1	E	46	ARG	NE-CZ-NH1	6.59	123.60	120.30
1	C	345	ARG	NE-CZ-NH2	-6.56	117.02	120.30
1	A	145	ARG	NE-CZ-NH1	6.53	123.57	120.30
1	G	390	ILE	CG1-CB-CG2	-6.52	97.05	111.40
1	H	120	CYS	CB-CA-C	-6.49	97.42	110.40
1	A	362	ARG	CG-CD-NE	-6.47	98.20	111.80
1	A	322	ASP	CB-CG-OD1	6.45	124.10	118.30
1	G	472	LYS	CD-CE-NZ	-6.44	96.89	111.70
1	B	145	ARG	NE-CZ-NH2	-6.30	117.15	120.30
1	D	373	ASP	CB-CG-OD1	6.28	123.95	118.30
1	G	322	ASP	CB-CG-OD1	6.25	123.92	118.30
1	H	145	ARG	NE-CZ-NH2	-6.20	117.20	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	306	ARG	NE-CZ-NH1	6.16	123.38	120.30
1	E	362	ARG	CG-CD-NE	-6.13	98.92	111.80
1	F	472	LYS	CD-CE-NZ	-6.09	97.69	111.70
1	C	83	ARG	NE-CZ-NH1	6.08	123.34	120.30
1	H	119	MET	CG-SD-CE	5.93	109.70	100.20
1	A	424	ARG	NE-CZ-NH2	-5.89	117.36	120.30
1	A	174	THR	N-CA-CB	-5.88	99.12	110.30
1	G	145	ARG	NE-CZ-NH1	5.83	123.22	120.30
1	A	326	ARG	NE-CZ-NH1	5.80	123.20	120.30
1	G	250	ARG	NE-CZ-NH2	-5.76	117.42	120.30
1	B	306	ARG	NE-CZ-NH2	-5.74	117.43	120.30
1	C	367	LEU	CA-CB-CG	5.70	128.41	115.30
1	A	325	ASP	CB-CG-OD2	-5.70	113.17	118.30
1	F	306	ARG	NE-CZ-NH1	5.69	123.15	120.30
1	C	124	ASP	CB-CG-OD1	5.67	123.40	118.30
1	D	250	ARG	NE-CZ-NH2	-5.66	117.47	120.30
1	C	274	ARG	NE-CZ-NH1	5.65	123.13	120.30
1	E	221	MET	CG-SD-CE	5.64	109.22	100.20
1	H	139	ARG	NE-CZ-NH2	-5.55	117.53	120.30
1	E	401	ASP	CB-CG-OD1	5.47	123.22	118.30
1	H	254	GLU	OE1-CD-OE2	-5.45	116.76	123.30
1	G	322	ASP	CB-CG-OD2	-5.45	113.40	118.30
1	F	424	ARG	NE-CZ-NH2	-5.44	117.58	120.30
1	G	145	ARG	NE-CZ-NH2	-5.41	117.60	120.30
1	D	102	SER	CB-CA-C	-5.40	99.85	110.10
1	B	246	ALA	N-CA-CB	5.37	117.62	110.10
1	E	472	LYS	CD-CE-NZ	-5.37	99.36	111.70
1	B	245	ASN	CB-CA-C	-5.36	99.67	110.40
1	E	274	ARG	NE-CZ-NH1	5.36	122.98	120.30
1	E	367	LEU	CA-CB-CG	5.35	127.61	115.30
1	C	274	ARG	NE-CZ-NH2	-5.32	117.64	120.30
1	D	290	ARG	NE-CZ-NH2	-5.31	117.64	120.30
1	D	69	ARG	NE-CZ-NH2	-5.31	117.65	120.30
1	B	355	ASP	N-CA-CB	-5.27	101.11	110.60
1	A	322	ASP	CB-CG-OD2	-5.25	113.57	118.30
1	C	119	MET	CG-SD-CE	5.25	108.60	100.20
1	G	84	LYS	CD-CE-NZ	5.25	123.77	111.70
1	E	139	ARG	NE-CZ-NH2	-5.24	117.68	120.30
1	H	367	LEU	CA-CB-CG	5.23	127.34	115.30
1	C	74	LEU	CB-CG-CD1	5.23	119.89	111.00
1	C	174	THR	N-CA-CB	-5.21	100.41	110.30
1	E	36	ASP	CB-CG-OD2	-5.21	113.61	118.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	124	ASP	CB-CG-OD1	5.20	122.98	118.30
1	H	93	LEU	CB-CG-CD1	-5.19	102.18	111.00
1	E	16	ARG	NE-CZ-NH1	5.18	122.89	120.30
1	H	139	ARG	NE-CZ-NH1	5.18	122.89	120.30
1	C	473	SER	CB-CA-C	-5.17	100.29	110.10
1	F	306	ARG	NE-CZ-NH2	-5.15	117.72	120.30
1	H	145	ARG	NE-CZ-NH1	5.12	122.86	120.30
1	G	447	ARG	NE-CZ-NH2	-5.10	117.75	120.30
1	E	229	LEU	CB-CG-CD2	-5.10	102.33	111.00
1	D	362	ARG	NE-CZ-NH1	5.10	122.85	120.30
1	E	422	ASP	CB-CG-OD1	5.08	122.88	118.30
1	C	122	ARG	NE-CZ-NH1	5.08	122.84	120.30
1	F	362	ARG	NE-CZ-NH2	-5.08	117.76	120.30
1	G	425	ARG	CD-NE-CZ	5.07	130.70	123.60
1	F	74	LEU	CB-CG-CD2	5.07	119.61	111.00
1	C	422	ASP	CB-CG-OD1	5.06	122.85	118.30
1	G	373	ASP	CB-CG-OD1	5.05	122.85	118.30
1	D	259	ASP	CB-CG-OD1	5.04	122.83	118.30
1	G	124	ASP	CB-CG-OD2	-5.03	113.77	118.30
1	F	362	ARG	CG-CD-NE	-5.03	101.23	111.80
1	A	124	ASP	CB-CG-OD1	5.02	122.82	118.30
1	H	259	ASP	CB-CG-OD1	5.02	122.82	118.30
1	E	46	ARG	NE-CZ-NH2	-5.02	117.79	120.30
1	E	120	CYS	CA-CB-SG	-5.01	104.97	114.00
1	B	83	ARG	NE-CZ-NH1	5.01	122.81	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	F	222	ILE	Peptide
1	G	246	ALA	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3651	0	3684	52	0
1	B	3633	0	3662	61	0
1	C	3644	0	3675	76	0
1	D	3651	0	3684	83	0
1	E	3649	0	3677	67	0
1	F	3651	0	3684	77	0
1	G	3633	0	3662	79	0
1	H	3651	0	3684	47	0
2	A	44	0	26	4	0
2	B	44	0	26	2	0
2	C	44	0	26	5	0
2	D	44	0	26	6	0
2	E	44	0	26	3	0
2	F	44	0	26	4	0
2	G	44	0	26	4	0
2	H	44	0	26	3	0
3	A	8	0	2	0	0
3	B	8	0	2	1	0
3	C	8	0	2	5	0
3	D	8	0	2	3	0
3	E	8	0	2	2	0
3	F	8	0	2	2	0
3	G	8	0	2	0	0
3	H	8	0	2	0	0
4	A	497	0	0	5	0
4	B	380	0	0	7	0
4	C	337	0	0	12	1
4	D	302	0	0	14	0
4	E	376	0	0	8	2
4	F	325	0	0	10	1
4	G	358	0	0	14	0
4	H	298	0	0	5	0
All	All	32452	0	29636	516	2

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 9.

All (516) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:12:HIS:CE1	1:C:27:ARG:NH2	1.82	1.44
1:C:221:MET:SD	4:C:911:HOH:O	2.00	1.18
1:C:12:HIS:CE1	1:C:27:ARG:HH22	1.51	1.16
1:C:291:CYS:SG	2:C:501:NAD:C4N	2.35	1.15

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:290:ARG:HE	3:C:502:PAE:H12	1.04	1.11
1:B:246:ALA:HB3	1:B:251:GLN:NE2	1.64	1.10
1:D:426:MET:SD	4:D:836:HOH:O	2.10	1.09
1:B:122:ARG:HB2	1:D:122:ARG:HH22	0.92	1.08
1:B:132:LEU:HD12	1:B:132:LEU:N	1.63	1.07
1:B:221:MET:SD	4:B:945:HOH:O	2.12	1.07
1:C:12:HIS:ND1	1:C:27:ARG:NH2	2.03	1.06
1:A:345:ARG:HH11	1:A:386:THR:HG22	1.18	1.05
1:E:122:ARG:HD2	1:G:122:ARG:NE	1.69	1.04
1:E:122:ARG:NH2	4:E:854:HOH:O	1.92	1.02
1:B:246:ALA:HB3	1:B:251:GLN:HE21	1.19	1.01
1:E:122:ARG:HD2	1:G:122:ARG:HE	0.85	1.01
1:D:345:ARG:CZ	4:D:877:HOH:O	2.06	1.00
1:A:291:CYS:SG	2:A:501:NAD:C4N	2.50	1.00
1:B:12:HIS:HE1	1:B:27:ARG:NH2	1.59	0.99
1:E:122:ARG:CD	1:G:122:ARG:HE	1.75	0.99
1:B:12:HIS:CE1	1:B:27:ARG:NH2	2.31	0.99
1:B:122:ARG:HB2	1:D:122:ARG:NH2	1.77	0.98
1:C:319:ARG:HH12	1:E:269:ASP:HB3	1.27	0.97
1:B:122:ARG:CB	1:D:122:ARG:HH22	1.76	0.97
1:F:148:LEU:H	1:F:176:ASN:HD21	1.10	0.94
1:C:50:ALA:HB1	1:C:221:MET:CE	1.97	0.94
1:G:54:PHE:HE2	1:G:221:MET:HE2	1.32	0.92
1:B:12:HIS:ND1	1:B:41:THR:HG22	1.84	0.92
1:B:210:VAL:HG21	1:B:221:MET:HE1	1.51	0.92
1:H:400:ASP:OD2	1:H:425:ARG:HD3	1.69	0.92
1:G:50:ALA:HB1	1:G:221:MET:HE1	1.52	0.91
1:A:400:ASP:OD2	1:A:425:ARG:HD3	1.70	0.91
1:C:159:HIS:NE2	3:C:502:PAE:H11	1.84	0.91
1:F:221:MET:SD	4:F:645:HOH:O	2.28	0.91
1:B:246:ALA:CB	1:B:251:GLN:HE21	1.82	0.91
1:E:122:ARG:HG2	1:G:122:ARG:HH21	1.35	0.91
1:G:50:ALA:HB1	1:G:221:MET:CE	1.99	0.91
1:A:400:ASP:OD2	1:A:425:ARG:CD	2.19	0.91
1:D:291:CYS:SG	2:D:501:NAD:C4N	2.58	0.90
1:C:290:ARG:NE	3:C:502:PAE:H12	1.87	0.90
1:B:132:LEU:HD12	1:B:132:LEU:H	1.34	0.90
1:A:122:ARG:NH2	1:H:122:ARG:HB2	1.86	0.90
1:G:221:MET:SD	4:G:889:HOH:O	2.29	0.89
1:F:27:ARG:HD3	1:F:41:THR:HG21	1.53	0.89
1:C:50:ALA:HB1	1:C:221:MET:HE1	1.55	0.88
1:F:319:ARG:CD	4:F:849:HOH:O	2.21	0.88

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:174:THR:CG2	1:C:176:ASN:OD1	2.22	0.88
1:H:291:CYS:SG	2:H:501:NAD:C4N	2.61	0.88
1:G:291:CYS:SG	2:G:501:NAD:C4N	2.62	0.88
1:B:291:CYS:SG	2:B:501:NAD:C4N	2.61	0.88
1:A:27:ARG:HE	1:A:41:THR:CG2	1.89	0.85
1:F:319:ARG:HD3	4:F:849:HOH:O	1.75	0.85
1:D:345:ARG:NE	4:D:877:HOH:O	2.07	0.84
1:G:148:LEU:H	1:G:176:ASN:HD21	1.25	0.83
1:C:54:PHE:HE2	1:C:221:MET:HE2	1.40	0.83
1:A:345:ARG:NH1	1:A:386:THR:HG22	1.92	0.83
1:A:27:ARG:HH21	1:A:41:THR:HG22	1.40	0.83
1:A:148:LEU:H	1:A:176:ASN:HD21	1.28	0.82
1:G:23:ASP:OD1	1:G:27:ARG:NH1	2.13	0.82
1:C:122:ARG:HE	1:F:122:ARG:NH2	1.78	0.82
1:F:319:ARG:NE	4:F:849:HOH:O	2.12	0.81
1:B:210:VAL:HG21	1:B:221:MET:CE	2.10	0.81
1:E:148:LEU:H	1:E:176:ASN:HD21	1.26	0.81
1:C:174:THR:HG23	1:C:176:ASN:OD1	1.79	0.81
1:E:291:CYS:SG	2:E:501:NAD:C4N	2.69	0.81
1:C:291:CYS:SG	2:C:501:NAD:C3N	2.69	0.80
1:F:159:HIS:HB2	1:F:163:MET:HG2	1.64	0.80
1:C:148:LEU:H	1:C:176:ASN:HD21	1.29	0.80
1:G:133:THR:O	4:G:822:HOH:O	2.00	0.80
1:C:11:ARG:N	4:C:752:HOH:O	2.15	0.79
1:F:291:CYS:SG	2:F:501:NAD:C4N	2.71	0.79
1:E:381:LEU:O	1:E:386:THR:HG23	1.83	0.78
1:B:246:ALA:CB	1:B:251:GLN:NE2	2.40	0.78
1:G:27:ARG:NH2	4:G:868:HOH:O	2.12	0.78
1:E:50:ALA:HB1	1:E:221:MET:HE2	1.64	0.78
1:F:50:ALA:HB2	1:F:221:MET:CE	2.14	0.77
1:G:159:HIS:HB2	1:G:163:MET:HG2	1.66	0.77
1:D:174:THR:CG2	1:D:176:ASN:OD1	2.32	0.77
1:D:148:LEU:H	1:D:176:ASN:HD21	1.29	0.77
1:D:11:ARG:HH11	1:D:188:MET:HE1	1.50	0.77
1:C:12:HIS:HE1	1:C:27:ARG:HH22	0.83	0.76
1:G:54:PHE:CE2	1:G:221:MET:HE2	2.19	0.76
1:F:27:ARG:HH11	1:F:41:THR:HG21	1.50	0.76
1:D:88:SER:HB2	1:D:102:SER:HB2	1.66	0.76
1:B:159:HIS:HB2	1:B:163:MET:HG2	1.67	0.76
1:B:84:LYS:HD2	4:B:764:HOH:O	1.85	0.76
1:A:174:THR:HG23	1:A:176:ASN:OD1	1.85	0.75
1:H:96:GLY:HA3	1:H:332:THR:OG1	1.87	0.74

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:12:HIS:HE1	1:C:27:ARG:NH2	1.45	0.74
1:D:280:VAL:O	1:D:284:THR:HB	1.87	0.74
1:H:219:MET:O	1:H:223:THR:HB	1.88	0.73
1:B:135:HIS:NE2	4:B:946:HOH:O	2.18	0.73
1:G:216:ASP:OD2	1:G:216:ASP:N	2.20	0.73
1:G:54:PHE:HE2	1:G:221:MET:CE	2.02	0.73
1:A:27:ARG:HE	1:A:41:THR:HG23	1.51	0.73
1:H:280:VAL:O	1:H:284:THR:HB	1.88	0.73
1:C:319:ARG:NH1	1:E:269:ASP:HB3	2.02	0.72
1:D:11:ARG:HH11	1:D:188:MET:CE	2.02	0.72
1:F:148:LEU:H	1:F:176:ASN:ND2	1.85	0.72
1:B:291:CYS:SG	2:B:501:NAD:C3N	2.77	0.72
1:C:12:HIS:CE1	1:C:27:ARG:CZ	2.72	0.72
1:D:406:LEU:HD13	4:D:661:HOH:O	1.90	0.71
1:F:27:ARG:HH11	1:F:41:THR:CG2	2.03	0.71
1:H:13:GLU:HG3	1:H:16:ARG:HH12	1.55	0.71
1:D:12:HIS:HB3	1:D:27:ARG:HH21	1.54	0.71
1:H:291:CYS:SG	2:H:501:NAD:C3N	2.79	0.70
1:C:277:ASP:OD1	4:C:877:HOH:O	2.08	0.70
1:C:54:PHE:CE2	1:C:221:MET:HE2	2.23	0.70
1:A:400:ASP:OD2	1:A:425:ARG:HD2	1.90	0.70
1:G:319:ARG:NH2	1:G:327:SER:HB2	2.06	0.70
1:G:222:ILE:CD1	1:G:242:ILE:HG12	2.22	0.70
1:C:400:ASP:OD2	1:C:425:ARG:HD3	1.92	0.69
1:F:219:MET:O	1:F:223:THR:HB	1.92	0.69
1:E:381:LEU:O	1:E:386:THR:CG2	2.41	0.69
1:B:132:LEU:CD1	1:B:132:LEU:N	2.49	0.69
1:F:50:ALA:HB2	1:F:221:MET:HE2	1.75	0.69
1:B:12:HIS:CE1	1:B:27:ARG:CZ	2.75	0.69
1:D:125:GLY:HA2	1:D:143:THR:HG22	1.74	0.69
1:B:210:VAL:CG2	1:B:221:MET:CE	2.71	0.68
1:G:221:MET:HA	1:G:221:MET:HE2	1.75	0.68
1:C:182:PRO:HD2	1:C:210:VAL:O	1.93	0.68
1:C:291:CYS:SG	2:C:501:NAD:H4N	2.31	0.68
1:G:122:ARG:HH11	1:G:122:ARG:HB2	1.58	0.68
1:H:50:ALA:HB1	1:H:221:MET:CE	2.24	0.68
1:E:12:HIS:HB3	4:E:769:HOH:O	1.93	0.68
1:G:131:ASP:OD2	4:G:931:HOH:O	2.11	0.67
1:A:244:ALA:HA	1:B:247:HIS:ND1	2.09	0.67
1:G:188:MET:HE3	4:G:928:HOH:O	1.92	0.67
1:F:400:ASP:OD2	1:F:425:ARG:HD3	1.94	0.67
1:G:223:THR:HG22	4:G:740:HOH:O	1.92	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:H:163:MET:CE	1:H:163:MET:HA	2.24	0.67
1:E:247:HIS:N	4:E:853:HOH:O	2.26	0.67
1:C:221:MET:HA	1:C:221:MET:HE2	1.75	0.67
1:D:291:CYS:SG	2:D:501:NAD:C3N	2.83	0.67
1:D:174:THR:HG23	1:D:176:ASN:OD1	1.95	0.67
1:E:319:ARG:HB3	1:E:319:ARG:HH11	1.60	0.67
1:B:129:SER:O	1:B:132:LEU:HD11	1.95	0.66
1:A:174:THR:CG2	1:A:176:ASN:OD1	2.43	0.66
1:D:131:ASP:OD2	4:D:797:HOH:O	2.12	0.66
1:C:27:ARG:HH21	1:C:41:THR:HG22	1.61	0.66
1:E:345:ARG:HH11	1:E:386:THR:HG22	1.61	0.66
1:G:274:ARG:NH1	4:G:856:HOH:O	2.29	0.65
1:C:50:ALA:HB1	1:C:221:MET:HE3	1.78	0.65
1:D:400:ASP:OD2	1:D:425:ARG:CD	2.44	0.65
1:G:24:THR:HB	1:G:43:PRO:HB3	1.79	0.65
1:C:170:PRO:O	1:C:174:THR:HB	1.97	0.65
1:G:50:ALA:CB	1:G:221:MET:HE1	2.26	0.64
1:A:27:ARG:HH21	1:A:41:THR:CG2	2.10	0.64
1:F:83:ARG:HD3	1:F:86:GLU:OE1	1.98	0.64
1:G:70:GLN:HG2	1:G:74:LEU:HD22	1.79	0.64
1:D:345:ARG:NH2	4:D:877:HOH:O	2.25	0.64
1:D:381:LEU:O	1:D:386:THR:CG2	2.45	0.64
1:D:426:MET:HE1	1:H:482:LEU:HD22	1.78	0.64
1:A:170:PRO:O	1:A:174:THR:HB	1.97	0.64
1:E:122:ARG:CG	1:G:122:ARG:HH21	2.09	0.64
1:G:222:ILE:HD12	1:G:242:ILE:HG12	1.79	0.64
1:G:182:PRO:HD2	1:G:210:VAL:O	1.98	0.64
1:C:345:ARG:HD3	4:C:910:HOH:O	1.97	0.64
1:D:345:ARG:HH11	1:D:380:ASP:HB3	1.63	0.63
1:E:269:ASP:OD1	1:E:306:ARG:HD2	1.97	0.63
1:D:400:ASP:OD2	1:D:425:ARG:HD3	1.99	0.63
1:G:219:MET:HE1	1:G:245:ASN:HB3	1.79	0.63
1:A:130:CYS:O	1:A:136:GLY:O	2.17	0.63
1:B:400:ASP:OD2	1:B:425:ARG:HD2	1.99	0.63
1:G:50:ALA:CB	1:G:221:MET:CE	2.75	0.63
1:D:424:ARG:NH2	4:D:685:HOH:O	2.31	0.63
1:D:35:ASN:OD1	1:D:37:THR:HG23	1.99	0.63
1:C:290:ARG:HE	3:C:502:PAE:C1P	1.97	0.63
1:A:291:CYS:SG	2:A:501:NAD:C3N	2.87	0.62
1:E:291:CYS:SG	2:E:501:NAD:C3N	2.87	0.62
1:B:135:HIS:CE1	4:B:946:HOH:O	2.52	0.62
1:F:50:ALA:CB	1:F:221:MET:CE	2.78	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:G:24:THR:CG2	1:G:26:ASP:O	2.48	0.62
1:F:27:ARG:HD3	1:F:41:THR:CG2	2.28	0.62
1:F:400:ASP:OD2	1:F:425:ARG:CD	2.46	0.62
1:F:50:ALA:CB	1:F:221:MET:HE2	2.30	0.62
1:E:237:PRO:O	1:E:241:LEU:HD13	2.00	0.62
1:A:159:HIS:HB2	1:A:163:MET:HG2	1.82	0.61
1:F:319:ARG:NH2	1:F:327:SER:OG	2.32	0.61
1:A:381:LEU:O	1:A:386:THR:HG23	2.00	0.61
1:H:400:ASP:OD2	1:H:425:ARG:CD	2.47	0.61
1:A:244:ALA:HA	1:B:247:HIS:HD1	1.65	0.61
1:G:119:MET:SD	1:G:122:ARG:NH1	2.71	0.61
1:C:400:ASP:OD2	1:C:425:ARG:CD	2.49	0.61
1:G:148:LEU:H	1:G:176:ASN:ND2	1.95	0.61
1:F:348:ARG:NH1	1:F:380:ASP:OD2	2.34	0.61
1:E:27:ARG:HE	1:E:41:THR:HG23	1.65	0.60
1:F:222:ILE:CD1	1:F:242:ILE:HG12	2.31	0.60
1:B:400:ASP:OD2	1:B:425:ARG:CD	2.50	0.60
1:A:122:ARG:HH22	1:H:122:ARG:HB2	1.65	0.60
1:D:13:GLU:O	1:D:43:PRO:HD3	2.02	0.60
1:B:210:VAL:CG2	1:B:221:MET:HE3	2.32	0.59
1:F:11:ARG:NH1	4:F:855:HOH:O	2.36	0.59
1:A:10:VAL:N	4:A:957:HOH:O	2.35	0.59
1:E:122:ARG:NH1	1:E:122:ARG:HB3	2.16	0.59
1:E:424:ARG:HB3	4:E:955:HOH:O	2.03	0.59
1:H:172:ILE:HD12	1:H:202:LEU:CD1	2.33	0.59
1:G:222:ILE:HG23	1:G:246:ALA:HB2	1.85	0.59
1:F:24:THR:HG22	1:F:26:ASP:O	2.03	0.59
1:E:10:VAL:O	1:E:11:ARG:HB2	2.03	0.58
1:F:316:LYS:HD3	1:F:358:TYR:CD1	2.37	0.58
1:F:222:ILE:HD12	1:F:242:ILE:HG23	1.84	0.58
1:A:20:ARG:HD3	4:A:1067:HOH:O	2.03	0.58
1:G:50:ALA:HB1	1:G:221:MET:HE3	1.85	0.58
1:F:27:ARG:NH1	1:F:41:THR:HG21	2.17	0.58
1:C:84:LYS:NZ	4:C:836:HOH:O	2.36	0.58
1:D:88:SER:HB2	1:D:102:SER:CB	2.34	0.58
1:D:23:ASP:OD1	1:D:27:ARG:NH1	2.36	0.58
1:D:12:HIS:HB3	1:D:27:ARG:NH2	2.18	0.58
1:B:108:ARG:HD2	1:B:449:GLU:OE1	2.03	0.58
1:F:163:MET:HE3	1:F:163:MET:HA	1.84	0.57
1:E:381:LEU:HD12	1:E:386:THR:HG21	1.87	0.57
1:E:13:GLU:O	1:E:43:PRO:HD3	2.05	0.57
1:D:108:ARG:HH12	3:D:502:PAE:P	2.28	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:E:23:ASP:OD1	1:E:27:ARG:NH1	2.38	0.57
1:D:35:ASN:CG	1:D:37:THR:HG23	2.25	0.57
1:A:343:GLU:OE1	1:A:362:ARG:HD3	2.04	0.57
1:D:161:LEU:HB2	1:D:189:THR:HG21	1.86	0.57
1:B:163:MET:HE1	1:B:233:THR:HG21	1.87	0.57
1:F:210:VAL:HG21	1:F:221:MET:CE	2.35	0.56
1:F:236:VAL:HB	1:F:237:PRO:HD3	1.87	0.56
1:G:400:ASP:OD2	1:G:425:ARG:CD	2.53	0.56
1:C:27:ARG:HB3	1:C:41:THR:HG23	1.87	0.56
1:B:122:ARG:CB	1:D:122:ARG:NH2	2.52	0.56
1:B:121:ILE:HD11	1:D:119:MET:CE	2.35	0.56
1:G:54:PHE:CE2	1:G:221:MET:CE	2.83	0.56
1:D:400:ASP:OD2	1:D:425:ARG:HD2	2.05	0.56
1:C:83:ARG:HD3	1:C:86:GLU:OE1	2.06	0.56
1:D:10:VAL:HG12	1:D:11:ARG:HE	1.71	0.55
1:C:50:ALA:CB	1:C:221:MET:CE	2.77	0.55
1:B:132:LEU:H	1:B:132:LEU:CD1	2.15	0.55
1:E:27:ARG:HH21	1:E:41:THR:HG23	1.71	0.55
1:A:163:MET:HE2	1:A:163:MET:HA	1.88	0.55
1:C:118:GLN:O	1:C:121:ILE:HG12	2.07	0.55
1:F:222:ILE:HD12	1:F:242:ILE:HG12	1.87	0.55
1:D:92:THR:OG1	1:D:102:SER:OG	2.24	0.55
1:F:424:ARG:NH2	4:F:819:HOH:O	2.30	0.55
1:F:50:ALA:HB2	1:F:221:MET:HE1	1.89	0.55
1:D:381:LEU:O	1:D:386:THR:HG23	2.07	0.55
1:C:50:ALA:CB	1:C:221:MET:HE3	2.37	0.55
1:C:54:PHE:CE2	1:C:221:MET:CE	2.90	0.55
1:A:345:ARG:HH11	1:A:386:THR:CG2	2.07	0.55
1:A:291:CYS:HB3	2:A:501:NAD:C2N	2.36	0.55
1:H:50:ALA:CB	1:H:221:MET:CE	2.85	0.55
1:G:133:THR:HB	1:G:134:PRO:HD2	1.88	0.55
1:C:64:LEU:HD13	4:C:889:HOH:O	2.07	0.55
1:C:250:ARG:NH1	4:C:754:HOH:O	2.41	0.54
1:E:50:ALA:HB1	1:E:221:MET:CE	2.35	0.54
1:D:24:THR:HB	1:D:43:PRO:HB3	1.88	0.54
1:G:24:THR:HG22	1:G:26:ASP:O	2.07	0.54
1:H:172:ILE:HD12	1:H:202:LEU:HD13	1.88	0.54
1:B:121:ILE:HD11	1:D:119:MET:HE3	1.89	0.54
1:G:188:MET:CE	4:G:928:HOH:O	2.52	0.54
1:G:136:GLY:HA2	4:G:815:HOH:O	2.08	0.54
1:E:290:ARG:HH21	3:E:502:PAE:P	2.31	0.54
1:H:118:GLN:O	1:H:121:ILE:HG12	2.08	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:E:16:ARG:NH2	1:E:195:ASP:OD2	2.28	0.53
1:D:170:PRO:O	1:D:174:THR:HB	2.08	0.53
1:E:291:CYS:HB3	2:E:501:NAD:C2N	2.36	0.53
1:H:14:PRO:HG2	1:H:21:LEU:HD22	1.91	0.53
1:E:267:LEU:HD22	1:E:271:ASP:HB3	1.90	0.53
1:D:426:MET:HE3	1:D:440:ILE:HG13	1.91	0.53
1:C:269:ASP:OD1	1:C:306:ARG:HD2	2.09	0.53
1:G:222:ILE:HD11	1:G:242:ILE:HG12	1.90	0.53
1:H:163:MET:HE2	1:H:163:MET:HA	1.91	0.53
1:G:306:ARG:HG3	1:G:306:ARG:HH11	1.74	0.53
1:F:13:GLU:O	1:F:43:PRO:HD3	2.08	0.53
1:D:312:LEU:HG	1:D:316:LYS:HE3	1.91	0.53
1:C:122:ARG:HE	1:F:122:ARG:HH22	1.52	0.52
1:G:13:GLU:O	1:G:43:PRO:HD3	2.09	0.52
1:H:222:ILE:HD12	1:H:242:ILE:HG23	1.90	0.52
1:A:264:LEU:HD12	1:A:420:THR:HB	1.92	0.52
1:G:424:ARG:NE	4:G:792:HOH:O	2.42	0.52
1:B:210:VAL:CG2	1:B:221:MET:HE1	2.29	0.52
1:F:24:THR:CG2	1:F:26:ASP:O	2.58	0.52
1:A:291:CYS:SG	2:A:501:NAD:H4N	2.48	0.52
1:E:222:ILE:CD1	1:E:242:ILE:HG12	2.40	0.52
1:D:291:CYS:HB3	2:D:501:NAD:C2N	2.40	0.52
1:G:400:ASP:OD2	1:G:425:ARG:HD2	2.10	0.52
1:C:465:GLU:HB2	4:C:703:HOH:O	2.10	0.52
1:G:24:THR:HG21	1:G:44:ALA:H	1.73	0.51
1:A:234:GLY:O	1:A:255:LEU:HA	2.11	0.51
1:E:400:ASP:OD2	1:E:425:ARG:CD	2.58	0.51
1:G:255:LEU:O	2:G:501:NAD:H2N	2.10	0.51
1:A:133:THR:HB	1:A:134:PRO:HD2	1.92	0.51
1:F:269:ASP:OD1	1:F:306:ARG:HD2	2.10	0.51
1:F:50:ALA:CB	1:F:221:MET:HE1	2.41	0.51
1:D:406:LEU:HD12	4:D:771:HOH:O	2.11	0.51
1:C:377:HIS:CD2	1:C:406:LEU:HD11	2.45	0.51
1:C:159:HIS:HB2	1:C:163:MET:HG2	1.93	0.51
1:C:378:GLN:NE2	4:C:773:HOH:O	2.22	0.51
1:E:122:ARG:CZ	1:E:122:ARG:HB3	2.42	0.50
2:D:501:NAD:H5N	3:D:502:PAE:O2	2.11	0.50
1:F:291:CYS:SG	2:F:501:NAD:C3N	2.99	0.50
1:H:50:ALA:HB1	1:H:221:MET:HE2	1.93	0.50
1:G:12:HIS:HB3	4:G:868:HOH:O	2.11	0.50
1:B:330:LEU:HD23	1:B:369:PRO:HD3	1.93	0.50
1:C:50:ALA:CB	1:C:221:MET:HE1	2.34	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:G:222:ILE:CG2	1:G:246:ALA:HB2	2.42	0.50
1:G:50:ALA:CB	1:G:221:MET:HE3	2.41	0.50
1:C:122:ARG:HD3	1:C:123:ASP:N	2.27	0.50
1:H:291:CYS:HB3	2:H:501:NAD:C2N	2.42	0.50
1:D:11:ARG:N	4:D:842:HOH:O	2.45	0.50
1:D:83:ARG:NH2	4:D:834:HOH:O	2.41	0.50
1:B:295:LYS:HE2	1:B:385:GLU:HG3	1.94	0.50
1:D:255:LEU:O	2:D:501:NAD:H2N	2.12	0.49
1:B:447:ARG:HD2	4:B:607:HOH:O	2.12	0.49
1:B:12:HIS:CE1	1:B:27:ARG:HH22	2.24	0.49
1:G:291:CYS:SG	2:G:501:NAD:C3N	3.00	0.49
1:C:122:ARG:HD3	1:C:123:ASP:H	1.76	0.49
1:E:115:LEU:HD12	1:E:449:GLU:HB2	1.93	0.49
1:F:161:LEU:HB2	1:F:189:THR:HG21	1.94	0.49
1:A:381:LEU:HD11	1:A:390:ILE:HG21	1.93	0.49
1:C:291:CYS:HB3	2:C:501:NAD:C2N	2.42	0.49
1:G:219:MET:O	1:G:223:THR:HB	2.12	0.49
1:A:51:ARG:HD2	4:A:1076:HOH:O	2.12	0.49
1:A:183:THR:HG23	1:A:186:THR:H	1.77	0.49
1:G:119:MET:HE1	1:G:122:ARG:HH22	1.77	0.49
1:D:250:ARG:NH1	4:D:757:HOH:O	2.45	0.49
1:D:10:VAL:HG12	1:D:11:ARG:NE	2.27	0.49
1:E:319:ARG:HH11	1:E:319:ARG:CB	2.25	0.49
1:E:367:LEU:HD23	1:E:389:PRO:HD2	1.94	0.49
1:C:27:ARG:HE	1:C:41:THR:CG2	2.26	0.48
1:D:126:GLU:H	1:D:143:THR:HG22	1.78	0.48
1:G:24:THR:HG21	1:G:44:ALA:N	2.28	0.48
1:F:83:ARG:NH2	4:F:816:HOH:O	2.45	0.48
1:G:400:ASP:OD2	1:G:425:ARG:HD3	2.12	0.48
1:E:400:ASP:OD2	1:E:425:ARG:HD3	2.13	0.48
1:E:287:SER:HA	1:E:330:LEU:CD1	2.43	0.48
1:E:424:ARG:HD2	4:E:955:HOH:O	2.12	0.48
1:D:219:MET:O	1:D:223:THR:HB	2.14	0.48
1:F:343:GLU:OE1	1:F:362:ARG:HD3	2.12	0.48
1:A:27:ARG:NE	1:A:41:THR:HG23	2.25	0.48
1:F:320:PHE:HA	1:F:330:LEU:O	2.13	0.48
1:D:281:ALA:HB3	4:D:838:HOH:O	2.12	0.48
1:F:316:LYS:HD3	1:F:358:TYR:CE1	2.47	0.48
1:C:148:LEU:H	1:C:176:ASN:ND2	2.05	0.48
1:D:11:ARG:O	1:D:40:GLY:HA2	2.14	0.48
1:D:126:GLU:H	1:D:143:THR:CG2	2.25	0.48
1:D:159:HIS:HB2	1:D:163:MET:HG2	1.96	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:E:264:LEU:HD12	1:E:420:THR:HB	1.96	0.48
1:E:50:ALA:CB	1:E:221:MET:CE	2.92	0.48
1:H:236:VAL:O	1:H:240:LYS:HG2	2.14	0.48
1:F:169:ALA:HB3	1:F:170:PRO:HD3	1.95	0.48
1:H:411:ALA:O	1:H:458:ASP:HB2	2.14	0.48
1:H:122:ARG:NH2	4:H:879:HOH:O	2.46	0.48
1:A:27:ARG:HE	1:A:41:THR:HG21	1.74	0.48
1:A:381:LEU:O	1:A:386:THR:CG2	2.62	0.47
1:D:125:GLY:CA	1:D:143:THR:HG22	2.41	0.47
1:F:210:VAL:HG21	1:F:221:MET:HE1	1.96	0.47
1:A:343:GLU:O	1:A:347:MET:HG2	2.14	0.47
1:H:204:PRO:HD2	1:H:205:GLU:OE1	2.15	0.47
1:B:108:ARG:HH22	3:B:502:PAE:P	2.37	0.47
1:C:108:ARG:HH12	3:C:502:PAE:P	2.38	0.47
1:E:27:ARG:NH2	4:E:769:HOH:O	2.47	0.47
1:D:319:ARG:HD3	4:D:839:HOH:O	2.14	0.47
1:D:246:ALA:HB3	1:D:251:GLN:NE2	2.29	0.47
1:E:229:LEU:C	1:E:229:LEU:HD23	2.36	0.47
1:F:210:VAL:HG21	1:F:221:MET:HE3	1.97	0.47
1:D:12:HIS:HD1	1:D:41:THR:HG1	1.63	0.47
1:H:168:VAL:O	1:H:172:ILE:HG12	2.15	0.47
1:E:319:ARG:HH11	1:E:319:ARG:CG	2.28	0.46
1:F:108:ARG:HH12	3:F:502:PAE:P	2.38	0.46
1:B:130:CYS:C	1:B:132:LEU:CD1	2.84	0.46
1:E:236:VAL:HB	1:E:237:PRO:HD3	1.96	0.46
1:E:12:HIS:HA	1:E:41:THR:HG22	1.97	0.46
1:G:235:SER:HB2	1:G:237:PRO:HD2	1.97	0.46
1:E:148:LEU:H	1:E:176:ASN:ND2	2.04	0.46
1:H:159:HIS:HB2	1:H:163:MET:HG2	1.97	0.46
1:E:343:GLU:OE1	1:E:362:ARG:HD3	2.16	0.46
1:G:50:ALA:HB3	1:G:220:GLU:HG2	1.97	0.46
1:F:121:ILE:HG13	1:F:122:ARG:HG3	1.97	0.46
1:A:27:ARG:NE	1:A:41:THR:CG2	2.69	0.46
4:A:814:HOH:O	1:B:247:HIS:HB3	2.16	0.46
1:H:343:GLU:OE1	1:H:362:ARG:HD3	2.15	0.46
1:H:237:PRO:HG2	4:H:718:HOH:O	2.15	0.46
1:C:287:SER:HA	1:C:330:LEU:CD1	2.46	0.45
1:D:191:LEU:HD13	1:D:209:VAL:CG1	2.46	0.45
1:C:122:ARG:HE	1:F:122:ARG:HH21	1.58	0.45
1:C:348:ARG:NH1	1:C:380:ASP:OD2	2.48	0.45
1:F:222:ILE:HD11	1:F:242:ILE:HG12	1.98	0.45
1:A:336:GLU:OE2	1:A:362:ARG:NH2	2.45	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:E:163:MET:CE	1:E:163:MET:HA	2.46	0.45
1:D:10:VAL:HA	1:D:11:ARG:HB3	1.98	0.45
1:F:400:ASP:OD2	1:F:425:ARG:HD2	2.15	0.45
1:F:34:TRP:HZ3	1:F:366:LEU:HD22	1.81	0.45
1:G:390:ILE:O	1:G:392:PRO:HD3	2.17	0.45
1:F:264:LEU:HD12	1:F:420:THR:HB	1.98	0.45
1:B:181:LYS:HB2	1:B:221:MET:HE3	1.98	0.45
1:F:71:LYS:HD2	4:F:833:HOH:O	2.17	0.45
1:E:133:THR:OG1	1:E:135:HIS:HB2	2.16	0.45
1:F:290:ARG:HH21	3:F:502:PAE:P	2.40	0.45
1:E:83:ARG:HD3	1:E:86:GLU:OE1	2.17	0.45
1:H:70:GLN:HG3	1:H:74:LEU:HD22	1.98	0.45
1:C:345:ARG:HD2	1:C:380:ASP:HB3	1.98	0.44
1:G:247:HIS:N	4:G:748:HOH:O	2.49	0.44
1:C:13:GLU:O	1:C:43:PRO:HD3	2.17	0.44
1:H:260:PRO:HA	1:H:296:ARG:O	2.17	0.44
1:B:400:ASP:OD2	1:B:425:ARG:HD3	2.16	0.44
1:G:291:CYS:HB3	2:G:501:NAD:C2N	2.47	0.44
1:F:163:MET:CA	1:F:163:MET:HE3	2.46	0.44
1:F:163:MET:HB3	1:F:163:MET:HE2	1.70	0.44
1:F:104:TYR:HE2	1:F:108:ARG:HD2	1.82	0.44
1:B:324:MET:HE3	4:B:906:HOH:O	2.17	0.44
1:A:11:ARG:HG3	4:A:904:HOH:O	2.18	0.44
1:F:373:ASP:OD1	1:F:374:ARG:N	2.45	0.44
1:G:83:ARG:HD2	1:G:86:GLU:OE1	2.17	0.44
1:D:10:VAL:HG12	1:D:11:ARG:HH21	1.81	0.44
1:C:303:VAL:HG12	1:C:306:ARG:NH2	2.32	0.44
1:D:243:ALA:HA	1:D:251:GLN:HE22	1.82	0.44
1:F:133:THR:HB	1:F:134:PRO:HD2	2.00	0.44
1:D:11:ARG:NH1	1:D:188:MET:CE	2.76	0.44
1:D:386:THR:HA	4:D:657:HOH:O	2.17	0.44
1:A:14:PRO:HG3	1:A:21:LEU:HB3	1.99	0.44
1:F:46:ARG:NH1	1:F:48:GLU:OE1	2.51	0.44
1:G:232:PHE:CZ	1:G:234:GLY:HA3	2.51	0.44
1:G:306:ARG:NH1	4:G:692:HOH:O	2.51	0.44
1:G:434:LYS:HD2	4:G:709:HOH:O	2.18	0.44
1:C:122:ARG:NE	1:F:122:ARG:NH2	2.57	0.43
1:E:400:ASP:OD2	1:E:425:ARG:HD2	2.18	0.43
1:B:336:GLU:HG3	1:B:364:GLY:HA2	1.99	0.43
1:D:469:GLU:O	1:D:473:SER:HB2	2.18	0.43
1:E:83:ARG:CD	1:E:86:GLU:OE1	2.66	0.43
1:B:84:LYS:HE2	1:B:84:LYS:HB3	1.73	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:F:465:GLU:HB3	1:F:466:GLY:H	1.58	0.43
1:E:119:MET:CE	1:G:121:ILE:HD11	2.49	0.43
1:F:203:PRO:HA	1:F:204:PRO:HD3	1.80	0.43
1:D:92:THR:HG1	1:D:102:SER:HG	1.59	0.43
2:C:501:NAD:H51A	2:C:501:NAD:H2B	1.56	0.43
1:H:27:ARG:HG3	1:H:41:THR:HG21	1.99	0.43
1:C:31:ARG:HD3	1:C:36:ASP:OD1	2.18	0.43
1:H:13:GLU:O	1:H:43:PRO:HD3	2.19	0.43
1:E:10:VAL:O	1:E:11:ARG:CB	2.66	0.43
1:E:27:ARG:NH1	4:E:769:HOH:O	2.51	0.43
1:D:24:THR:CG2	1:D:26:ASP:O	2.67	0.43
1:C:295:LYS:HE2	1:C:385:GLU:HG3	2.00	0.43
1:D:10:VAL:HG12	1:D:11:ARG:NH2	2.34	0.42
1:A:170:PRO:HB3	1:A:471:MET:HG3	2.00	0.42
1:E:27:ARG:HE	1:E:41:THR:CG2	2.30	0.42
1:D:35:ASN:O	1:D:37:THR:CG2	2.67	0.42
1:F:84:LYS:HE2	1:F:84:LYS:HB3	1.80	0.42
1:G:148:LEU:HD21	1:G:250:ARG:HH22	1.84	0.42
1:H:13:GLU:HG3	1:H:16:ARG:NH1	2.29	0.42
1:D:24:THR:HG22	1:D:26:ASP:O	2.19	0.42
1:A:12:HIS:ND1	1:A:41:THR:HB	2.35	0.42
1:C:122:ARG:NE	1:F:122:ARG:HH22	2.14	0.42
1:C:11:ARG:N	4:C:728:HOH:O	2.52	0.42
2:F:501:NAD:H2B	4:F:800:HOH:O	2.18	0.42
1:H:362:ARG:HG2	1:H:363:SER:N	2.34	0.42
1:G:355:ASP:OD2	1:G:357:LEU:HD21	2.20	0.42
1:C:153:ALA:HB1	1:C:167:LYS:HG2	2.01	0.42
1:F:417:GLY:HA2	1:F:439:ASN:O	2.19	0.42
1:B:121:ILE:HD13	1:D:118:GLN:OE1	2.19	0.42
1:E:108:ARG:HH12	3:E:502:PAE:P	2.43	0.42
1:B:340:ALA:O	1:B:344:GLU:HG3	2.19	0.42
1:F:295:LYS:HE2	1:F:385:GLU:HG3	2.02	0.42
1:F:357:LEU:HD22	4:F:917:HOH:O	2.18	0.42
1:C:123:ASP:OD1	4:C:867:HOH:O	2.21	0.42
1:B:144:MET:HE1	4:H:629:HOH:O	2.18	0.42
1:D:287:SER:HA	1:D:330:LEU:CD1	2.49	0.42
1:H:67:TYR:OH	1:H:71:LYS:HE2	2.19	0.42
1:E:170:PRO:HB3	1:E:471:MET:HG3	2.00	0.42
1:C:260:PRO:HA	1:C:296:ARG:O	2.19	0.42
1:G:84:LYS:HE2	1:G:103:LEU:HD22	2.01	0.42
1:H:376:PRO:HG2	1:H:379:SER:HB3	2.02	0.42
1:E:95:LEU:HD22	1:E:160:PRO:HD3	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:54:PHE:CE1	1:C:179:VAL:HB	2.54	0.41
1:H:122:ARG:HG2	1:H:123:ASP:N	2.35	0.41
1:F:24:THR:HB	1:F:43:PRO:HB3	2.01	0.41
1:B:229:LEU:HD23	1:B:229:LEU:C	2.40	0.41
1:A:118:GLN:HG2	1:H:118:GLN:HG2	2.02	0.41
1:D:246:ALA:CB	1:D:251:GLN:NE2	2.83	0.41
1:E:119:MET:HE2	1:G:121:ILE:HD11	2.02	0.41
1:G:377:HIS:CG	1:G:406:LEU:HD11	2.54	0.41
1:A:13:GLU:O	1:A:43:PRO:HD3	2.19	0.41
1:G:221:MET:HA	1:G:221:MET:CE	2.48	0.41
1:G:260:PRO:HA	1:G:296:ARG:O	2.20	0.41
1:F:232:PHE:CZ	1:F:234:GLY:HA3	2.55	0.41
1:H:128:PHE:HB2	1:H:141:ILE:HB	2.03	0.41
1:E:11:ARG:NH1	4:E:874:HOH:O	2.53	0.41
1:B:83:ARG:HD3	1:B:86:GLU:OE1	2.20	0.41
1:G:70:GLN:CG	1:G:74:LEU:HD22	2.48	0.41
1:B:465:GLU:HB3	1:B:466:GLY:H	1.59	0.41
1:C:27:ARG:HE	1:C:41:THR:HG21	1.85	0.41
1:A:264:LEU:HD12	1:A:420:THR:CB	2.51	0.41
1:A:182:PRO:HD2	1:A:210:VAL:O	2.20	0.41
1:E:118:GLN:HG2	1:G:118:GLN:HG2	2.02	0.41
1:D:310:LEU:O	1:D:314:ARG:HD2	2.21	0.41
1:H:355:ASP:HB2	4:H:808:HOH:O	2.19	0.41
1:D:438:VAL:O	1:H:480:PHE:HA	2.20	0.41
1:D:174:THR:HG22	1:D:176:ASN:OD1	2.19	0.41
1:D:157:PHE:HA	1:D:183:THR:HG21	2.03	0.41
1:H:46:ARG:NH2	4:H:870:HOH:O	2.45	0.41
1:B:67:TYR:CZ	1:H:134:PRO:HG3	2.56	0.41
1:A:83:ARG:CD	1:A:86:GLU:OE1	2.68	0.41
1:H:373:ASP:OD1	1:H:374:ARG:N	2.44	0.41
1:D:125:GLY:HA2	1:D:143:THR:CG2	2.45	0.41
1:A:241:LEU:C	1:A:241:LEU:HD23	2.40	0.41
1:H:157:PHE:C	1:H:157:PHE:CD1	2.94	0.41
1:G:264:LEU:HD12	1:G:420:THR:HB	2.01	0.40
1:F:127:ILE:HD13	1:F:127:ILE:HG21	1.89	0.40
1:B:130:CYS:C	1:B:132:LEU:HD12	2.41	0.40
1:F:256:GLY:HA2	2:F:501:NAD:O2D	2.21	0.40
1:F:234:GLY:O	1:F:255:LEU:HA	2.21	0.40
1:E:161:LEU:HB2	1:E:189:THR:HG21	2.03	0.40
1:B:169:ALA:HB3	1:B:170:PRO:HD3	2.02	0.40
1:C:234:GLY:O	1:C:255:LEU:HA	2.21	0.40
1:B:348:ARG:NH2	1:B:380:ASP:OD2	2.41	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:D:501:NAD:C5N	3:D:502:PAE:O2	2.70	0.40
1:A:169:ALA:HB3	1:A:170:PRO:HD3	2.03	0.40
1:C:186:THR:N	1:C:187:PRO:HD3	2.36	0.40
1:D:223:THR:O	1:D:224:ASN:C	2.58	0.40
1:B:241:LEU:C	1:B:241:LEU:HD23	2.42	0.40
1:C:472:LYS:HE3	4:C:787:HOH:O	2.20	0.40
1:B:319:ARG:HD2	4:B:682:HOH:O	2.21	0.40
1:C:70:GLN:O	1:C:74:LEU:HD22	2.22	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:E:937:HOH:O	4:F:895:HOH:O[2_555]	2.04	0.16
4:C:895:HOH:O	4:E:904:HOH:O[2_545]	2.14	0.06

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	474/488 (97%)	460 (97%)	11 (2%)	3 (1%)	33	20
1	B	472/488 (97%)	454 (96%)	16 (3%)	2 (0%)	43	32
1	C	473/488 (97%)	454 (96%)	17 (4%)	2 (0%)	43	32
1	D	474/488 (97%)	450 (95%)	20 (4%)	4 (1%)	27	14
1	E	474/488 (97%)	451 (95%)	20 (4%)	3 (1%)	33	20
1	F	474/488 (97%)	453 (96%)	20 (4%)	1 (0%)	56	47
1	G	472/488 (97%)	449 (95%)	20 (4%)	3 (1%)	33	20
1	H	474/488 (97%)	448 (94%)	23 (5%)	3 (1%)	33	20
All	All	3787/3904 (97%)	3619 (96%)	147 (4%)	21 (1%)	33	20

All (21) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	136	GLY
1	C	247	HIS
1	D	136	GLY
1	D	215	ALA
1	E	11	ARG
1	E	247	HIS
1	G	215	ALA
1	B	247	HIS
1	A	137	LYS
1	C	392	PRO
1	E	392	PRO
1	H	247	HIS
1	D	216	ASP
1	G	461	ASN
1	A	392	PRO
1	D	392	PRO
1	H	47	ALA
1	H	392	PRO
1	B	392	PRO
1	F	392	PRO
1	G	392	PRO

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	392/401 (98%)	381 (97%)	11 (3%)	56	50
1	B	390/401 (97%)	378 (97%)	12 (3%)	52	45
1	C	391/401 (98%)	382 (98%)	9 (2%)	63	58
1	D	392/401 (98%)	369 (94%)	23 (6%)	28	17
1	E	391/401 (98%)	378 (97%)	13 (3%)	50	42
1	F	392/401 (98%)	380 (97%)	12 (3%)	52	45
1	G	390/401 (97%)	379 (97%)	11 (3%)	56	50
1	H	392/401 (98%)	378 (96%)	14 (4%)	47	39
All	All	3130/3208 (98%)	3025 (97%)	105 (3%)	49	42

All (105) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	ASP
1	A	41	THR
1	A	48	GLU
1	A	74	LEU
1	A	84	LYS
1	A	174	THR
1	A	240	LYS
1	A	255	LEU
1	A	359	HIS
1	A	378	GLN
1	A	386	THR
1	B	23	ASP
1	B	27	ARG
1	B	41	THR
1	B	71	LYS
1	B	74	LEU
1	B	219	MET
1	B	250	ARG
1	B	255	LEU
1	B	337	LYS
1	B	359	HIS
1	B	372	VAL
1	B	406	LEU
1	C	23	ASP
1	C	41	THR
1	C	64	LEU
1	C	74	LEU
1	C	167	LYS
1	C	174	THR
1	C	344	GLU
1	C	359	HIS
1	C	406	LEU
1	D	10	VAL
1	D	11	ARG
1	D	24	THR
1	D	25	ASP
1	D	27	ARG
1	D	37	THR
1	D	39	VAL
1	D	122	ARG
1	D	143	THR
1	D	163	MET

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	174	THR
1	D	191	LEU
1	D	223	THR
1	D	241	LEU
1	D	255	LEU
1	D	284	THR
1	D	313	GLU
1	D	359	HIS
1	D	367	LEU
1	D	386	THR
1	D	406	LEU
1	D	447	ARG
1	D	473	SER
1	E	12	HIS
1	E	23	ASP
1	E	41	THR
1	E	135	HIS
1	E	191	LEU
1	E	250	ARG
1	E	255	LEU
1	E	319	ARG
1	E	336	GLU
1	E	359	HIS
1	E	386	THR
1	E	406	LEU
1	E	473	SER
1	F	20	ARG
1	F	24	THR
1	F	41	THR
1	F	48	GLU
1	F	181	LYS
1	F	219	MET
1	F	223	THR
1	F	316	LYS
1	F	336	GLU
1	F	359	HIS
1	F	406	LEU
1	F	447	ARG
1	G	23	ASP
1	G	24	THR
1	G	74	LEU
1	G	122	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	G	137	LYS
1	G	144	MET
1	G	216	ASP
1	G	241	LEU
1	G	285	LYS
1	G	359	HIS
1	G	406	LEU
1	H	10	VAL
1	H	23	ASP
1	H	41	THR
1	H	52	GLU
1	H	74	LEU
1	H	132	LEU
1	H	163	MET
1	H	216	ASP
1	H	223	THR
1	H	231	THR
1	H	255	LEU
1	H	284	THR
1	H	359	HIS
1	H	406	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	12	HIS
1	D	251	GLN
1	E	176	ASN
1	F	176	ASN
1	F	245	ASN
1	G	176	ASN
1	G	245	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

16 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	NAD	A	501	-	48,48,48	1.20	5 (10%)	73,73,73	2.31	18 (24%)
3	PAE	A	502	-	7,7,7	1.62	2 (28%)	10,10,10	3.34	5 (50%)
2	NAD	B	501	-	48,48,48	1.15	5 (10%)	73,73,73	1.85	12 (16%)
3	PAE	B	502	-	7,7,7	1.73	2 (28%)	10,10,10	2.09	2 (20%)
2	NAD	C	501	-	48,48,48	1.20	4 (8%)	73,73,73	2.38	23 (31%)
3	PAE	C	502	-	7,7,7	1.37	1 (14%)	10,10,10	4.33	3 (30%)
2	NAD	D	501	-	48,48,48	1.36	5 (10%)	73,73,73	2.03	15 (20%)
3	PAE	D	502	-	7,7,7	1.36	1 (14%)	10,10,10	2.04	1 (10%)
2	NAD	E	501	-	48,48,48	1.17	5 (10%)	73,73,73	2.26	21 (28%)
3	PAE	E	502	-	7,7,7	1.17	1 (14%)	10,10,10	2.19	3 (30%)
2	NAD	F	501	-	48,48,48	1.20	3 (6%)	73,73,73	2.10	17 (23%)
3	PAE	F	502	-	7,7,7	1.26	1 (14%)	10,10,10	3.36	4 (40%)
2	NAD	G	501	-	48,48,48	1.10	4 (8%)	73,73,73	2.26	19 (26%)
3	PAE	G	502	-	7,7,7	1.38	1 (14%)	10,10,10	2.78	4 (40%)
2	NAD	H	501	-	48,48,48	1.17	6 (12%)	73,73,73	1.89	11 (15%)
3	PAE	H	502	-	7,7,7	1.62	1 (14%)	10,10,10	3.36	4 (40%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAD	A	501	-	-	0/30/62/62	0/3/5/5
3	PAE	A	502	-	-	0/5/5/5	0/0/0/0
2	NAD	B	501	-	-	0/30/62/62	0/3/5/5
3	PAE	B	502	-	-	0/5/5/5	0/0/0/0
2	NAD	C	501	-	-	0/30/62/62	0/3/5/5
3	PAE	C	502	-	-	0/5/5/5	0/0/0/0
2	NAD	D	501	-	-	0/30/62/62	0/3/5/5
3	PAE	D	502	-	-	0/5/5/5	0/0/0/0
2	NAD	E	501	-	-	0/30/62/62	0/3/5/5
3	PAE	E	502	-	-	0/5/5/5	0/0/0/0
2	NAD	F	501	-	-	0/30/62/62	0/3/5/5
3	PAE	F	502	-	-	0/5/5/5	0/0/0/0
2	NAD	G	501	-	-	0/30/62/62	0/3/5/5
3	PAE	G	502	-	-	0/5/5/5	0/0/0/0
2	NAD	H	501	-	-	0/30/62/62	0/3/5/5
3	PAE	H	502	-	-	0/5/5/5	0/0/0/0

All (47) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	NAD	PN-O2N	3.90	1.57	1.48
2	D	501	NAD	PN-O2N	3.68	1.57	1.48
2	G	501	NAD	C4A-N9A	-3.64	1.32	1.37
2	D	501	NAD	C5A-C4A	3.63	1.48	1.40
2	H	501	NAD	C5A-C4A	3.48	1.48	1.40
2	D	501	NAD	C4A-N9A	-3.33	1.32	1.37
3	H	502	PAE	C1P-C1	-3.31	1.47	1.51
2	F	501	NAD	C4A-N9A	-3.28	1.33	1.37
3	B	502	PAE	C1P-C1	-3.18	1.47	1.51
2	B	501	NAD	C5A-C4A	3.13	1.47	1.40
2	C	501	NAD	O4D-C1D	3.06	1.46	1.41
3	A	502	PAE	C1P-C1	-3.06	1.47	1.51
2	D	501	NAD	O4D-C1D	3.05	1.46	1.41
2	F	501	NAD	C5A-C4A	2.99	1.47	1.40
2	A	501	NAD	C4A-N9A	-2.98	1.33	1.37
2	B	501	NAD	PN-O1N	2.94	1.56	1.48
2	G	501	NAD	O4D-C1D	2.82	1.45	1.41
2	C	501	NAD	PN-O3	2.68	1.65	1.60
3	B	502	PAE	P-O3P	2.67	1.56	1.50
2	G	501	NAD	C5A-C4A	2.64	1.46	1.40
2	E	501	NAD	C4N-C3N	2.61	1.43	1.39
2	E	501	NAD	C5A-C4A	2.60	1.46	1.40
2	G	501	NAD	PN-O1N	2.58	1.55	1.48

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	501	NAD	O5B-C5B	-2.52	1.34	1.44
2	H	501	NAD	PN-O2N	2.52	1.54	1.48
2	B	501	NAD	O4B-C1B	2.52	1.45	1.41
2	F	501	NAD	O4D-C1D	2.45	1.45	1.41
2	C	501	NAD	O5B-C5B	-2.45	1.34	1.44
3	D	502	PAE	O1-C1	-2.44	1.21	1.30
2	D	501	NAD	C4N-C3N	2.43	1.43	1.39
2	B	501	NAD	C4A-N9A	-2.42	1.34	1.37
3	A	502	PAE	O1-C1	-2.42	1.21	1.30
2	H	501	NAD	C4N-C3N	2.39	1.43	1.39
3	F	502	PAE	C1P-C1	-2.34	1.48	1.51
2	E	501	NAD	C4A-N9A	-2.33	1.34	1.37
2	A	501	NAD	C5A-C4A	2.33	1.45	1.40
2	E	501	NAD	PN-O2N	2.28	1.54	1.48
2	C	501	NAD	PN-O1N	2.26	1.54	1.48
2	A	501	NAD	O4D-C1D	2.17	1.44	1.41
3	G	502	PAE	P-O1P	-2.11	1.50	1.54
2	H	501	NAD	PA-O3	2.11	1.63	1.59
2	H	501	NAD	C3N-C7N	2.07	1.54	1.50
3	C	502	PAE	O1-C1	-2.06	1.23	1.30
2	A	501	NAD	C5A-N7A	-2.05	1.32	1.40
2	H	501	NAD	C4A-N9A	-2.04	1.34	1.37
3	E	502	PAE	O1-C1	-2.02	1.23	1.30
2	B	501	NAD	PA-O3	2.01	1.63	1.59

All (162) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	NAD	O4D-C1D-N1N	12.45	120.69	107.95
3	C	502	PAE	P-C1P-C1	-10.95	94.94	113.67
2	G	501	NAD	N3A-C2A-N1A	-9.70	120.60	128.71
3	A	502	PAE	P-C1P-C1	-8.95	98.35	113.67
2	C	501	NAD	O4D-C1D-N1N	8.83	116.99	107.95
3	H	502	PAE	P-C1P-C1	-8.83	98.57	113.67
3	F	502	PAE	P-C1P-C1	-8.79	98.64	113.67
2	H	501	NAD	N3A-C2A-N1A	-8.54	121.57	128.71
2	D	501	NAD	N3A-C2A-N1A	-8.14	121.90	128.71
2	F	501	NAD	N3A-C2A-N1A	-7.95	122.06	128.71
2	G	501	NAD	O4D-C1D-N1N	7.54	115.66	107.95
2	E	501	NAD	N3A-C2A-N1A	-7.51	122.43	128.71
2	C	501	NAD	N3A-C2A-N1A	-7.18	122.71	128.71
3	C	502	PAE	O3P-P-C1P	-7.10	96.02	110.22

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	NAD	N3A-C2A-N1A	-6.89	122.95	128.71
2	E	501	NAD	O4D-C1D-N1N	6.84	114.95	107.95
2	B	501	NAD	N3A-C2A-N1A	-6.81	123.01	128.71
2	F	501	NAD	O4D-C1D-N1N	6.57	114.67	107.95
2	D	501	NAD	O4D-C1D-N1N	6.50	114.60	107.95
3	G	502	PAE	P-C1P-C1	-6.46	102.62	113.67
2	H	501	NAD	O4D-C1D-N1N	6.27	114.36	107.95
2	C	501	NAD	N3A-C4A-N9A	6.05	136.36	125.43
2	C	501	NAD	C5B-C4B-C3B	-5.82	91.91	115.21
2	G	501	NAD	C3N-C7N-N7N	5.70	124.25	117.77
2	A	501	NAD	N3A-C4A-N9A	5.70	135.72	125.43
2	F	501	NAD	C8A-N9A-C4A	5.68	111.23	106.90
3	D	502	PAE	P-C1P-C1	-5.63	104.04	113.67
2	E	501	NAD	C3N-C7N-N7N	-5.39	111.64	117.77
2	H	501	NAD	N3A-C4A-N9A	5.39	135.16	125.43
2	B	501	NAD	N3A-C4A-N9A	5.25	134.91	125.43
2	E	501	NAD	C5B-C4B-C3B	-5.15	94.58	115.21
2	D	501	NAD	N3A-C4A-N9A	5.07	134.59	125.43
2	E	501	NAD	O7N-C7N-C3N	5.04	125.26	119.58
3	B	502	PAE	O3P-P-C1P	-5.00	100.22	110.22
2	D	501	NAD	C3N-C7N-N7N	4.94	123.39	117.77
2	B	501	NAD	O4D-C1D-C2D	-4.73	99.51	106.77
2	E	501	NAD	N3A-C4A-N9A	4.72	133.95	125.43
2	C	501	NAD	C8A-N9A-C4A	4.71	110.49	106.90
2	C	501	NAD	O4B-C1B-N9A	4.68	112.79	108.44
2	F	501	NAD	N3A-C4A-N9A	4.67	133.87	125.43
2	G	501	NAD	C1B-N9A-C4A	-4.56	118.76	126.64
3	E	502	PAE	P-C1P-C1	-4.49	106.00	113.67
2	F	501	NAD	C1B-N9A-C4A	-4.38	119.06	126.64
2	A	501	NAD	O7N-C7N-C3N	4.38	124.52	119.58
2	C	501	NAD	O4B-C4B-C5B	-4.38	93.73	109.36
2	E	501	NAD	O4B-C1B-N9A	4.32	112.46	108.44
2	F	501	NAD	O4B-C1B-N9A	-4.32	104.42	108.44
2	B	501	NAD	C2D-C1D-N1N	-4.22	106.72	113.86
2	G	501	NAD	N3A-C4A-N9A	4.18	132.99	125.43
2	D	501	NAD	C2D-C1D-N1N	-4.15	106.83	113.86
3	G	502	PAE	O2P-P-C1P	-3.93	98.78	106.85
2	E	501	NAD	O4B-C4B-C5B	-3.87	95.55	109.36
2	B	501	NAD	C4A-C5A-N7A	-3.83	106.24	109.52
3	H	502	PAE	O3P-P-C1P	-3.80	102.61	110.22
2	A	501	NAD	C8A-N9A-C4A	3.79	109.79	106.90
2	C	501	NAD	O3-PA-O5B	-3.75	86.63	103.41

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	NAD	O4D-C1D-N1N	3.73	111.76	107.95
2	B	501	NAD	O4B-C1B-N9A	3.70	111.88	108.44
3	F	502	PAE	O3P-P-C1P	-3.60	103.01	110.22
2	G	501	NAD	O7N-C7N-C3N	-3.56	115.57	119.58
3	E	502	PAE	O1P-P-C1P	3.54	114.11	106.85
2	G	501	NAD	O4B-C1B-N9A	3.50	111.70	108.44
2	D	501	NAD	O7N-C7N-C3N	-3.48	115.65	119.58
2	H	501	NAD	O7N-C7N-C3N	3.45	123.46	119.58
2	G	501	NAD	C8A-N9A-C4A	3.35	109.46	106.90
2	B	501	NAD	C5A-C4A-N3A	-3.26	118.61	125.70
2	C	501	NAD	C2D-C1D-N1N	-3.24	108.37	113.86
2	F	501	NAD	O4D-C1D-C2D	-3.24	101.81	106.77
3	E	502	PAE	O3P-P-C1P	-3.19	103.83	110.22
2	C	501	NAD	C5A-C4A-N3A	-3.19	118.76	125.70
2	D	501	NAD	C1B-N9A-C4A	-3.17	121.16	126.64
2	A	501	NAD	C2D-C1D-N1N	-3.15	108.53	113.86
2	D	501	NAD	O4D-C1D-C2D	-3.05	102.10	106.77
2	D	501	NAD	C8A-N9A-C4A	3.00	109.19	106.90
2	H	501	NAD	C5A-C4A-N3A	-2.93	119.32	125.70
2	G	501	NAD	C2A-N3A-C4A	2.91	122.30	114.01
2	A	501	NAD	C4B-O4B-C1B	-2.90	106.60	109.75
2	F	501	NAD	C2D-C1D-N1N	-2.87	109.00	113.86
3	C	502	PAE	O2P-P-O1P	2.86	117.43	108.35
2	E	501	NAD	C4A-C5A-N7A	-2.81	107.11	109.52
2	B	501	NAD	O7N-C7N-C3N	2.81	122.74	119.58
2	A	501	NAD	C5A-C4A-N3A	-2.81	119.59	125.70
2	G	501	NAD	C2D-C1D-N1N	-2.80	109.11	113.86
2	G	501	NAD	C4A-C5A-N7A	-2.77	107.15	109.52
3	F	502	PAE	O2P-P-O1P	2.76	117.11	108.35
3	A	502	PAE	O3P-P-C1P	-2.76	104.69	110.22
2	D	501	NAD	O3-PN-O1N	-2.76	102.23	108.83
2	H	501	NAD	C2A-N3A-C4A	2.75	121.83	114.01
2	E	501	NAD	C2A-N3A-C4A	2.73	121.80	114.01
2	G	501	NAD	C8A-N9A-C1B	2.74	131.77	126.38
2	E	501	NAD	C5A-C4A-N3A	-2.72	119.78	125.70
3	A	502	PAE	O1-C1-C1P	2.70	121.41	113.83
2	B	501	NAD	C2A-N3A-C4A	2.68	121.63	114.01
2	H	501	NAD	O4D-C1D-C2D	-2.66	102.70	106.77
2	F	501	NAD	O3-PN-O1N	-2.63	102.54	108.83
2	H	501	NAD	C8A-N9A-C4A	2.63	108.90	106.90
2	C	501	NAD	O2N-PN-O3	-2.61	101.75	108.79
2	C	501	NAD	O7N-C7N-C3N	2.61	122.51	119.58

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	501	NAD	O4D-C1D-C2D	-2.59	102.80	106.77
3	H	502	PAE	O2-C1-C1P	-2.58	116.33	122.44
2	E	501	NAD	C2D-C1D-N1N	-2.58	109.49	113.86
2	F	501	NAD	C2A-N1A-C6A	2.55	123.37	118.77
3	G	502	PAE	O2-C1-C1P	-2.54	116.42	122.44
2	E	501	NAD	C1B-N9A-C4A	-2.54	122.24	126.64
2	D	501	NAD	O4B-C1B-C2B	-2.54	102.88	106.77
2	D	501	NAD	O2D-C2D-C3D	2.54	120.08	111.83
2	G	501	NAD	O4D-C1D-C2D	-2.50	102.94	106.77
2	D	501	NAD	C5A-C4A-N3A	-2.49	120.28	125.70
2	D	501	NAD	C2A-N3A-C4A	2.45	120.98	114.01
2	H	501	NAD	PN-O5D-C5D	2.44	128.67	120.24
3	H	502	PAE	O2P-P-O1P	2.41	116.00	108.35
2	C	501	NAD	C2A-N3A-C4A	2.40	120.84	114.01
2	F	501	NAD	O7N-C7N-C3N	-2.40	116.88	119.58
2	A	501	NAD	O4B-C1B-C2B	-2.39	103.11	106.77
3	B	502	PAE	P-C1P-C1	-2.38	109.59	113.67
2	E	501	NAD	C2B-C3B-C4B	-2.37	97.94	102.65
2	E	501	NAD	O2A-PA-O5B	2.35	120.37	108.51
2	E	501	NAD	O5B-C5B-C4B	-2.35	100.32	108.94
2	F	501	NAD	O2N-PN-O1N	2.35	125.81	118.72
2	B	501	NAD	O3B-C3B-C2B	-2.33	104.26	111.83
2	C	501	NAD	C1B-N9A-C4A	-2.32	122.63	126.64
2	G	501	NAD	C2A-N1A-C6A	2.31	122.94	118.77
2	A	501	NAD	O4B-C1B-N9A	2.31	110.59	108.44
2	E	501	NAD	C8A-N9A-C4A	2.30	108.66	106.90
2	C	501	NAD	C3B-C2B-C1B	-2.30	97.30	100.91
2	E	501	NAD	O4D-C1D-C2D	-2.29	103.26	106.77
2	E	501	NAD	PN-O5D-C5D	2.29	128.15	120.24
2	F	501	NAD	N6A-C6A-N1A	2.29	123.85	119.36
2	C	501	NAD	O5B-PA-O1A	2.26	118.24	109.37
2	C	501	NAD	O2B-C2B-C3B	2.24	119.13	111.83
2	G	501	NAD	C5A-C4A-N3A	-2.24	120.83	125.70
2	C	501	NAD	N7A-C8A-N9A	-2.23	108.06	114.36
3	F	502	PAE	O2P-P-C1P	-2.23	102.28	106.85
2	C	501	NAD	O2D-C2D-C3D	2.21	119.04	111.83
3	A	502	PAE	O2P-P-C1P	-2.21	102.32	106.85
2	D	501	NAD	C2A-N1A-C6A	2.21	122.75	118.77
2	B	501	NAD	C8A-N9A-C4A	2.20	108.58	106.90
2	A	501	NAD	C2A-N3A-C4A	2.19	120.25	114.01
2	A	501	NAD	O4D-C1D-C2D	-2.18	103.42	106.77
2	F	501	NAD	O3B-C3B-C4B	-2.17	104.70	111.08

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	501	NAD	O2A-PA-O1A	2.16	124.27	112.21
2	G	501	NAD	O4B-C4B-C3B	2.15	109.53	105.17
2	A	501	NAD	N6A-C6A-N1A	2.15	123.58	119.36
2	G	501	NAD	C4B-O4B-C1B	-2.12	107.44	109.75
2	H	501	NAD	C2A-N1A-C6A	2.12	122.60	118.77
2	E	501	NAD	C3D-C2D-C1D	2.10	104.20	100.91
2	G	501	NAD	O2N-PN-O3	-2.09	103.15	108.79
2	A	501	NAD	O2N-PN-O3	2.09	114.41	108.79
2	E	501	NAD	O3-PA-O5B	-2.08	94.11	103.41
2	F	501	NAD	N7A-C8A-N9A	-2.07	108.50	114.36
3	A	502	PAE	O2-C1-C1P	-2.07	117.55	122.44
2	C	501	NAD	O2A-PA-O3	2.06	114.93	105.14
3	G	502	PAE	O1-C1-C1P	2.06	119.63	113.83
2	A	501	NAD	C1B-N9A-C4A	-2.06	123.07	126.64
2	C	501	NAD	C4A-C5A-N7A	-2.06	107.76	109.52
2	H	501	NAD	C4A-C5A-N7A	-2.05	107.76	109.52
2	A	501	NAD	PN-O5D-C5D	2.05	127.34	120.24
2	A	501	NAD	C3N-C7N-N7N	-2.05	115.44	117.77
2	C	501	NAD	N6A-C6A-N1A	2.05	123.39	119.36
2	G	501	NAD	C4D-O4D-C1D	-2.05	107.53	109.75
2	F	501	NAD	C5A-C4A-N9A	-2.04	104.21	107.16
2	A	501	NAD	O2D-C2D-C3D	2.03	118.44	111.83

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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	476/488 (97%)	-0.64	0 100 100	11, 18, 32, 69	0
1	B	474/488 (97%)	-0.54	1 (0%) 93 95	13, 23, 42, 87	0
1	C	475/488 (97%)	-0.37	2 (0%) 90 93	13, 25, 42, 68	0
1	D	476/488 (97%)	-0.48	5 (1%) 77 80	14, 26, 47, 76	0
1	E	476/488 (97%)	-0.52	2 (0%) 90 93	11, 21, 41, 65	0
1	F	476/488 (97%)	-0.39	2 (0%) 90 93	14, 26, 46, 67	0
1	G	474/488 (97%)	-0.42	2 (0%) 90 93	15, 24, 45, 67	0
1	H	476/488 (97%)	-0.33	1 (0%) 93 95	14, 29, 48, 73	0
All	All	3803/3904 (97%)	-0.46	15 (0%) 90 93	11, 24, 43, 87	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	135	HIS	3.5
1	D	135	HIS	3.3
1	E	135	HIS	3.0
1	G	215	ALA	2.9
1	D	215	ALA	2.9
1	H	215	ALA	2.8
1	F	215	ALA	2.6
1	C	135	HIS	2.4
1	G	12	HIS	2.3
1	D	10	VAL	2.3
1	D	25	ASP	2.3
1	F	297	ILE	2.2
1	C	248	TYR	2.2
1	E	134	PRO	2.1
1	D	216	ASP	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	PAE	E	502	8/8	0.11	1.85	31,39,44,44	0
3	PAE	B	502	8/8	0.12	1.62	29,32,38,40	0
3	PAE	D	502	8/8	0.12	1.61	37,41,45,46	0
3	PAE	F	502	8/8	0.11	1.44	39,44,53,55	0
3	PAE	A	502	8/8	0.14	1.17	29,36,42,48	0
3	PAE	H	502	8/8	0.12	0.42	39,49,56,57	0
3	PAE	C	502	8/8	0.13	0.27	35,44,54,56	0
2	NAD	E	501	44/44	0.09	0.24	17,30,40,46	0
2	NAD	F	501	44/44	0.08	-0.47	28,38,48,56	0
2	NAD	D	501	44/44	0.07	-0.62	27,34,43,44	0
2	NAD	H	501	44/44	0.09	-0.63	26,42,54,58	0
2	NAD	C	501	44/44	0.08	-0.69	19,29,37,44	0
2	NAD	G	501	44/44	0.08	-0.78	27,34,41,50	0
2	NAD	B	501	44/44	0.07	-0.81	20,32,36,37	0
3	PAE	G	502	8/8	0.08	-0.86	36,40,43,45	0
2	NAD	A	501	44/44	0.06	-0.92	17,22,31,36	0

6.5 Other polymers ⓘ

There are no such residues in this entry.